



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:28 AM GMT

PDB ID : 3P0A
Title : X-ray structure of pentameric HIV-1 CA
Authors : Pornillos, O.
Deposited on : 2010-09-27
Resolution : 5.95 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

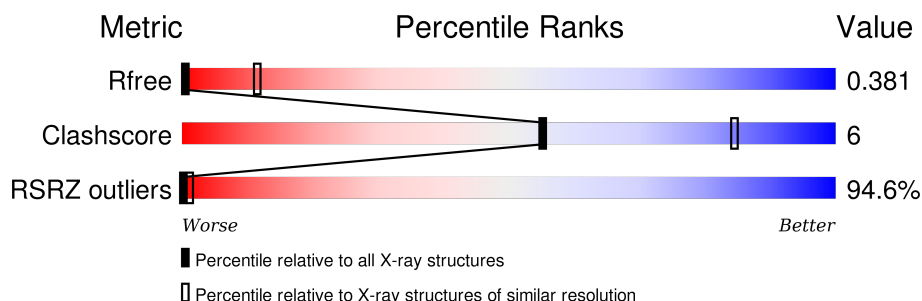
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.95 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	1001 (8.20-3.66)
Clashscore	102246	1049 (8.20-3.70)
RSRZ outliers	91569	1000 (8.20-3.66)

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	231	<div> <div>80%</div> <div> <div></div> <div>84%</div> <div>15%</div> </div> </div>
1	B	231	<div> <div>80%</div> <div> <div></div> <div>85%</div> <div>14%</div> </div> </div>
1	C	231	<div> <div>82%</div> <div> <div></div> <div>84%</div> <div>14%</div> </div> </div>
1	D	231	<div> <div>82%</div> <div> <div></div> <div>85%</div> <div>14%</div> </div> </div>
1	E	231	<div> <div>80%</div> <div> <div></div> <div>84%</div> <div>15%</div> </div> </div>
1	F	231	<div> <div>78%</div> <div> <div></div> <div>84%</div> <div>15%</div> </div> </div>
1	G	231	<div> <div>81%</div> <div> <div></div> <div>84%</div> <div>14%</div> </div> </div>
1	H	231	<div> <div>83%</div> <div> <div></div> <div>85%</div> <div>14%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	I	231	<div>82%</div> <div> <div></div> <div></div> <div></div> </div> <div>84%</div> <div>14%</div>
1	J	231	<div>82%</div> <div> <div></div> <div></div> <div></div> </div> <div>84%</div> <div>15%</div>
1	K	231	<div>81%</div> <div> <div></div> <div></div> <div></div> </div> <div>84%</div> <div>15%</div>
1	L	231	<div>82%</div> <div> <div></div> <div></div> <div></div> </div> <div>84%</div> <div>14%</div>
1	M	231	<div>82%</div> <div> <div></div> <div></div> <div></div> </div> <div>85%</div> <div>14%</div>
1	N	231	<div>82%</div> <div> <div></div> <div></div> <div></div> </div> <div>85%</div> <div>14%</div>
1	O	231	<div>84%</div> <div> <div></div> <div></div> <div></div> </div> <div>84%</div> <div>15%</div>
1	P	231	<div>79%</div> <div> <div></div> <div></div> <div></div> </div> <div>84%</div> <div>15%</div>
1	Q	231	<div>79%</div> <div> <div></div> <div></div> <div></div> </div> <div>85%</div> <div>14%</div>
1	R	231	<div>80%</div> <div> <div></div> <div></div> <div></div> </div> <div>84%</div> <div>14%</div>
1	S	231	<div>81%</div> <div> <div></div> <div></div> <div></div> </div> <div>85%</div> <div>14%</div>
1	T	231	<div>78%</div> <div> <div></div> <div></div> <div></div> </div> <div>84%</div> <div>15%</div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3952 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 HIV-1 CA.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	197	Total C 197 197	0	0	197
1	B	198	Total C 198 198	0	0	198
1	C	198	Total C 198 198	0	0	198
1	D	198	Total C 198 198	0	0	198
1	E	197	Total C 197 197	0	0	197
1	F	197	Total C 197 197	0	0	197
1	G	198	Total C 198 198	0	0	198
1	H	198	Total C 198 198	0	0	198
1	I	198	Total C 198 198	0	0	198
1	J	197	Total C 197 197	0	0	197
1	K	197	Total C 197 197	0	0	197
1	L	198	Total C 198 198	0	0	198
1	M	198	Total C 198 198	0	0	198
1	N	198	Total C 198 198	0	0	198
1	O	197	Total C 197 197	0	0	197
1	P	197	Total C 197 197	0	0	197

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	Q	198	Total C 198 198	0	0	198
1	R	198	Total C 198 198	0	0	198
1	S	198	Total C 198 198	0	0	198
1	T	197	Total C 197 197	0	0	197

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
A	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
A	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
A	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
A	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
B	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
B	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
B	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
B	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
B	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
C	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
C	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
C	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
C	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
C	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
D	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
D	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
D	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
D	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
D	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
E	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
E	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
E	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
E	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
E	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
F	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
F	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
F	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
F	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
F	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
G	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497

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Chain	Residue	Modelled	Actual	Comment	Reference
G	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
G	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
G	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
G	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
H	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
H	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
H	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
H	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
H	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
I	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
I	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
I	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
I	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
I	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
J	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
J	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
J	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
J	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
J	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
K	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
K	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
K	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
K	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
K	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
L	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
L	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
L	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
L	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
L	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
M	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
M	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
M	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
M	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
M	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
N	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
N	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
N	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
N	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
N	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
O	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
O	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
O	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497

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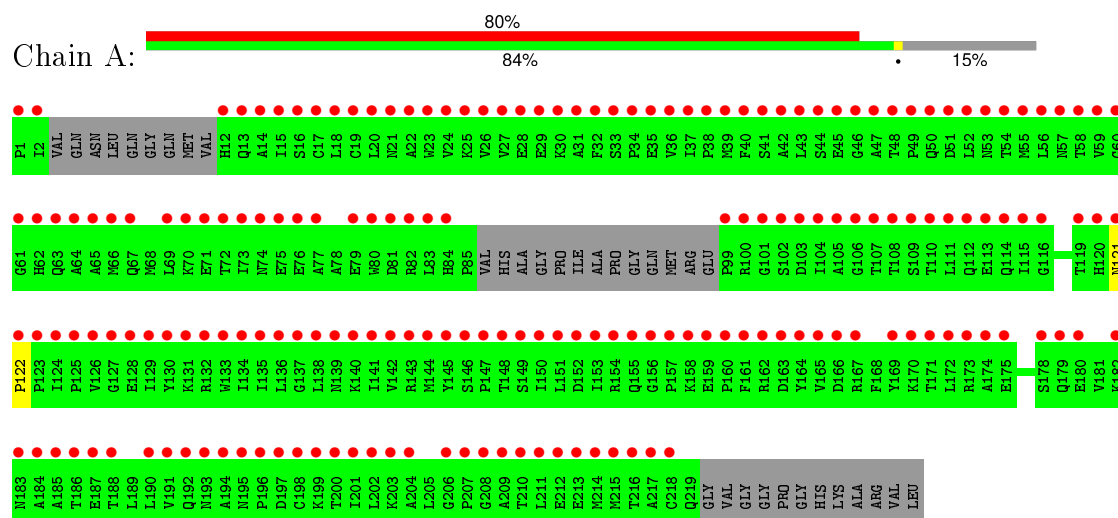
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Chain	Residue	Modelled	Actual	Comment	Reference
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O	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
P	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
P	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
P	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
P	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
P	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
Q	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
Q	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
Q	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
Q	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
Q	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
R	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
R	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
R	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
R	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
R	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
S	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
S	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
S	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
S	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
S	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497
T	17	CYS	PRO	ENGINEERED MUTATION	UNP Q72497
T	18	LEU	ARG	ENGINEERED MUTATION	UNP Q72497
T	19	CYS	THR	ENGINEERED MUTATION	UNP Q72497
T	184	ALA	TRP	ENGINEERED MUTATION	UNP Q72497
T	185	ALA	MET	ENGINEERED MUTATION	UNP Q72497

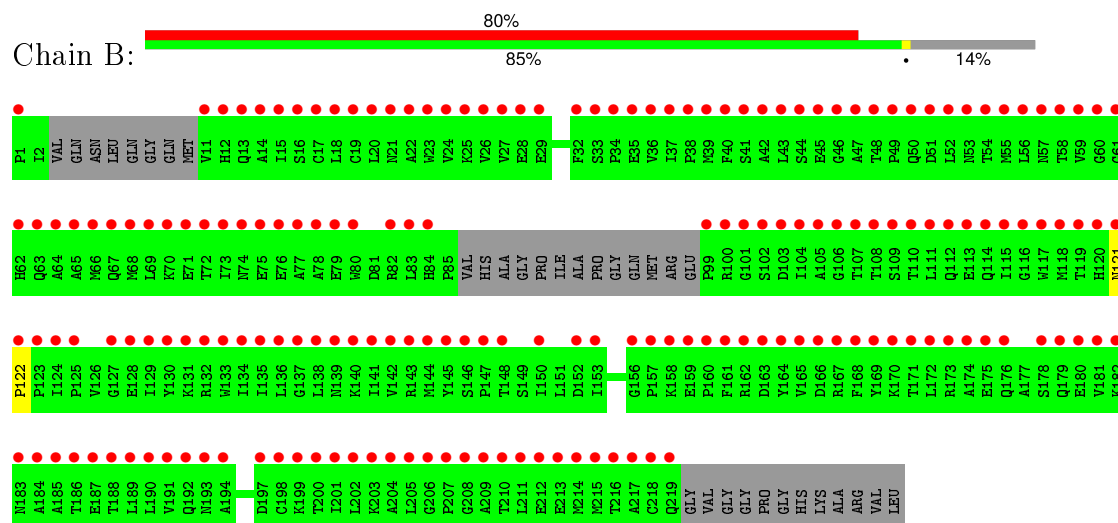
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

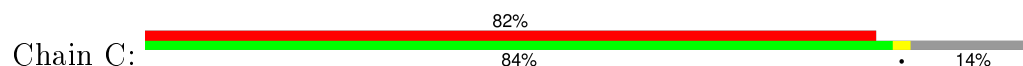
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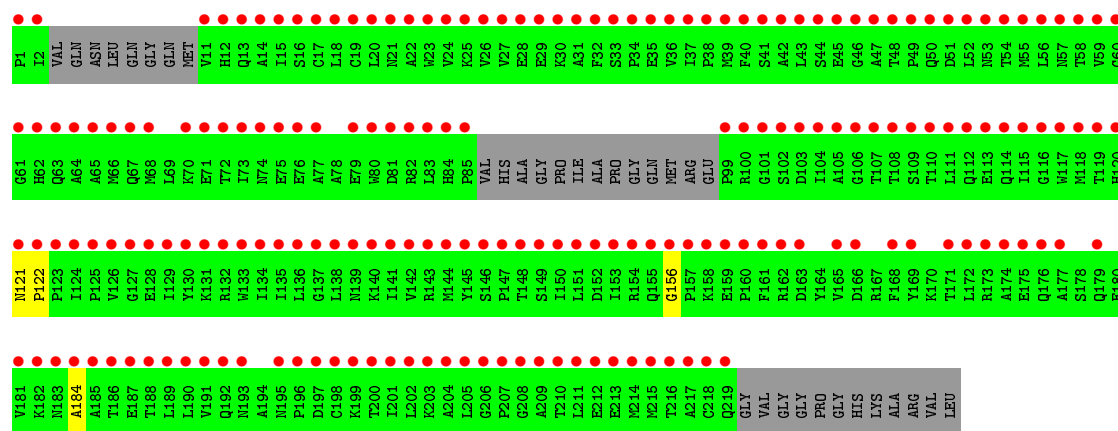


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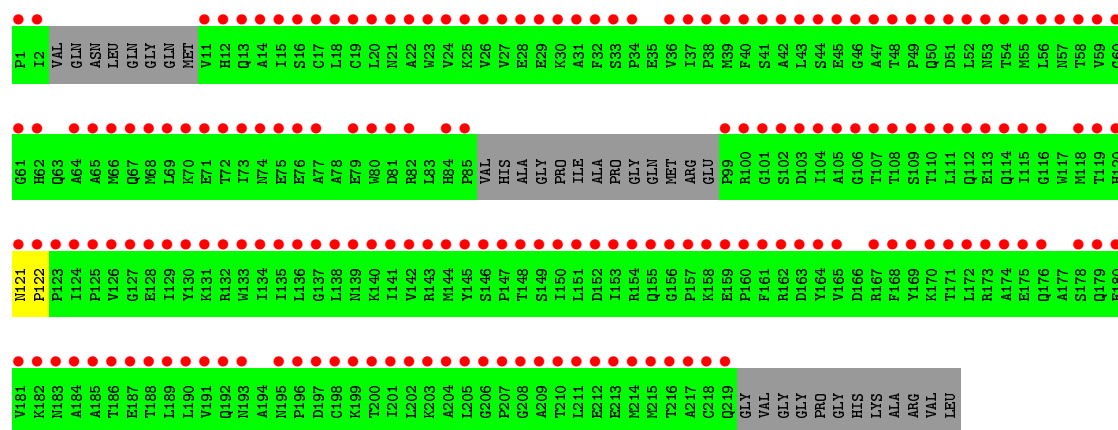
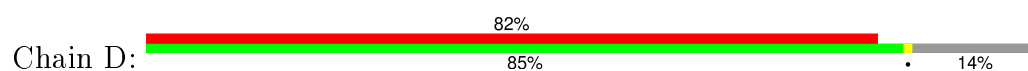


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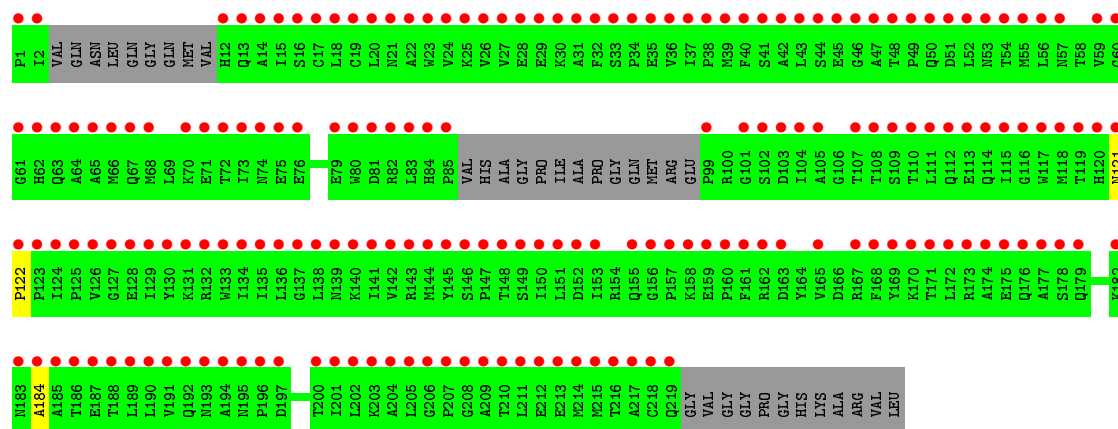
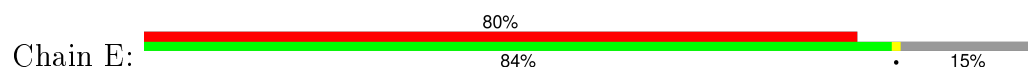




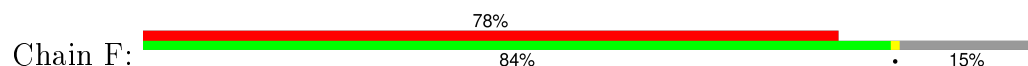
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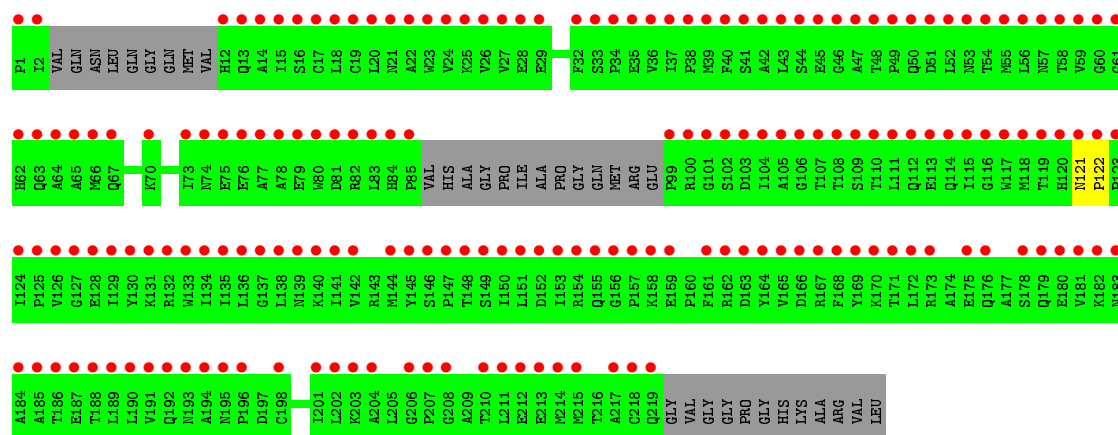


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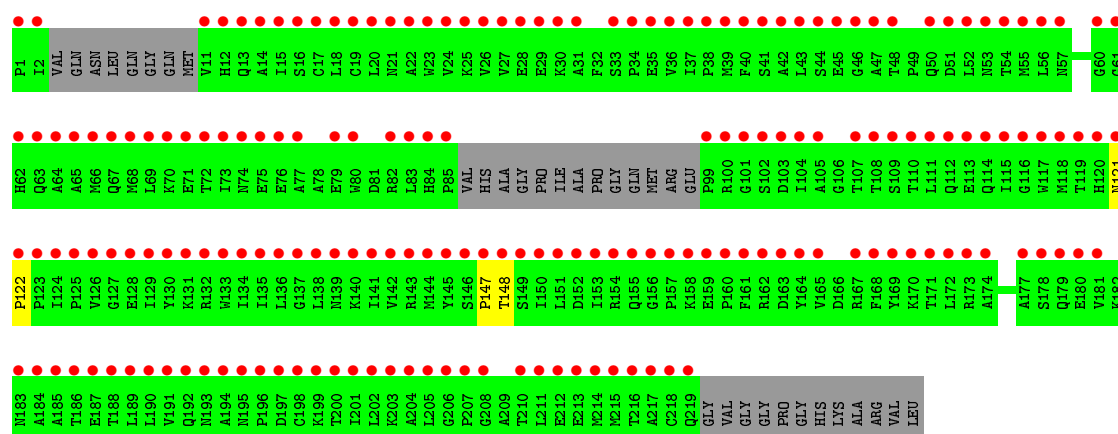
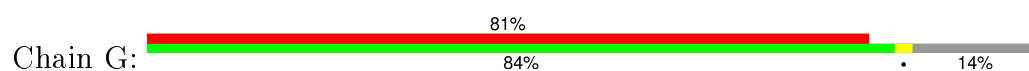


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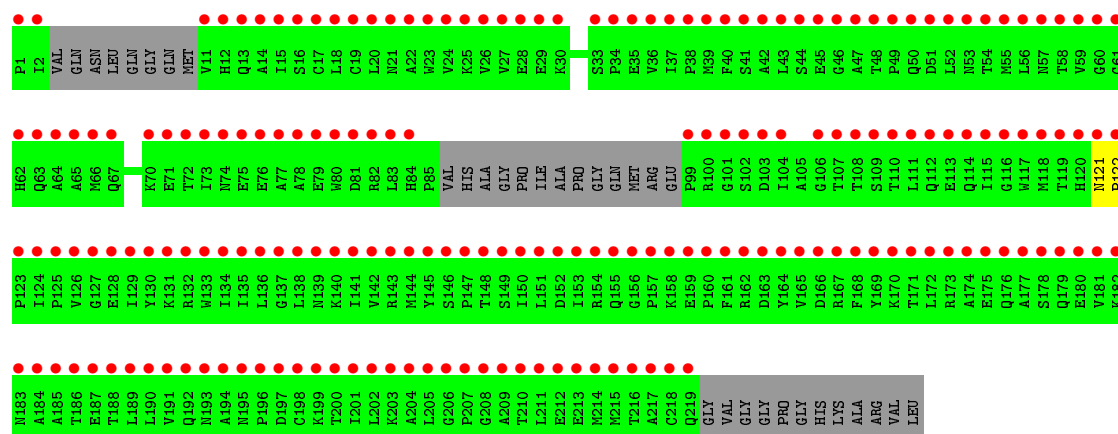
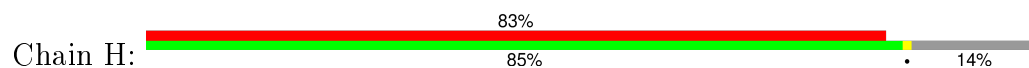




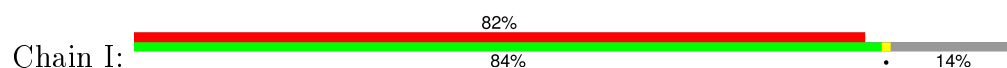
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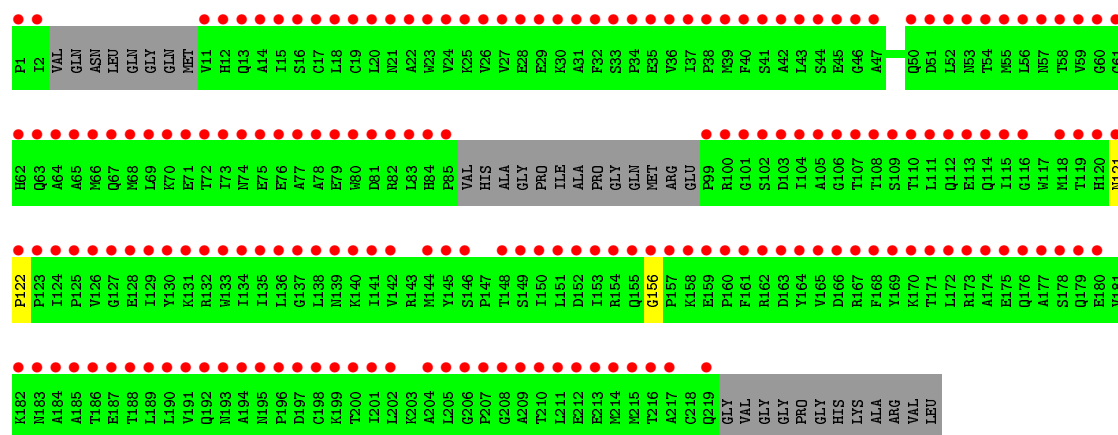


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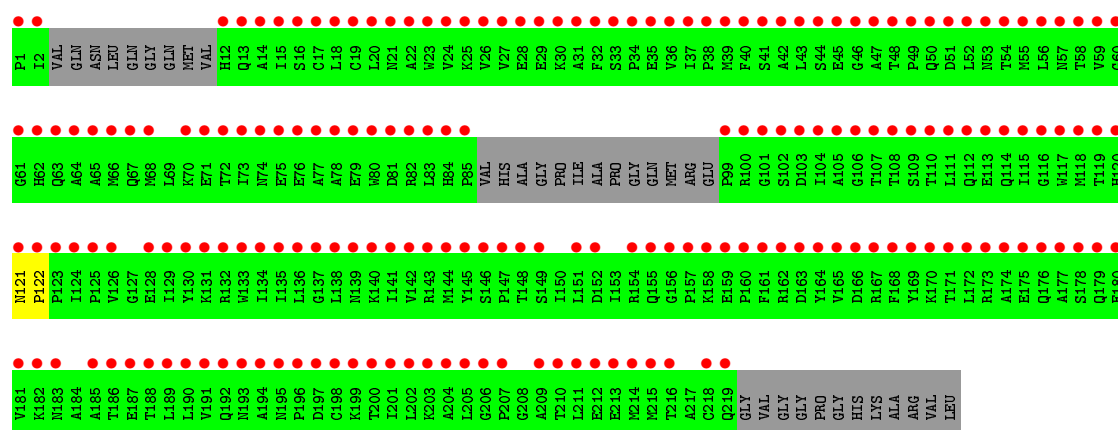
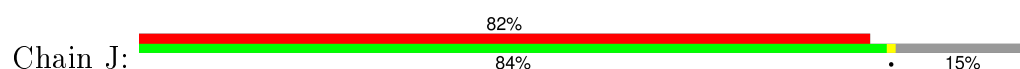


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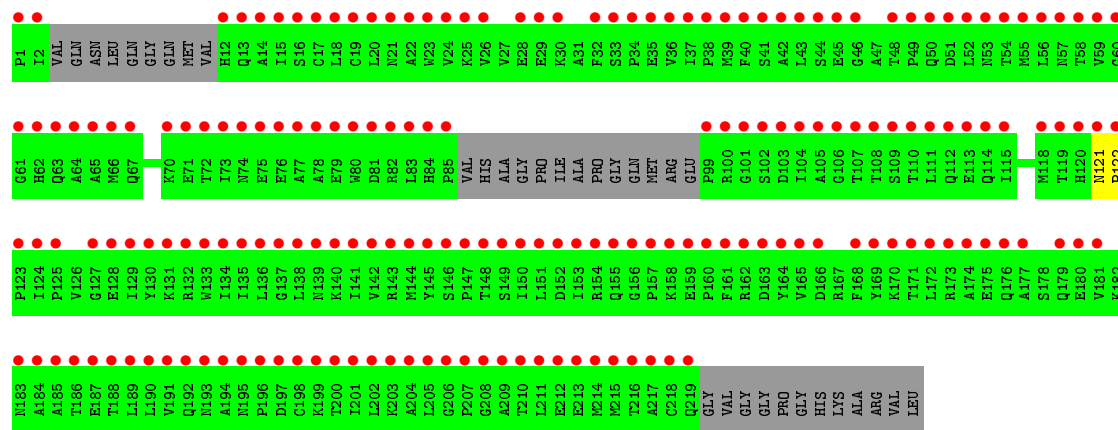
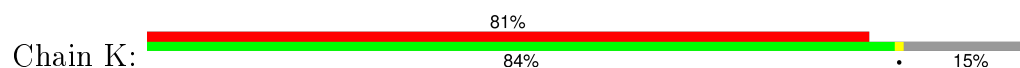




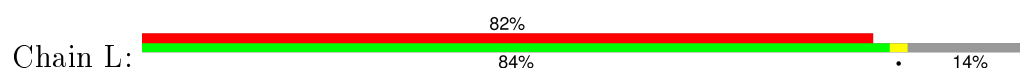
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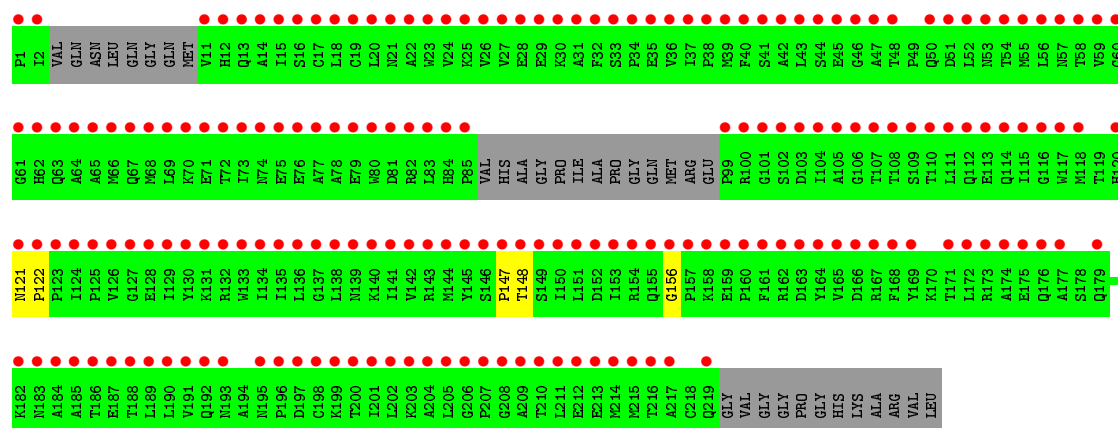


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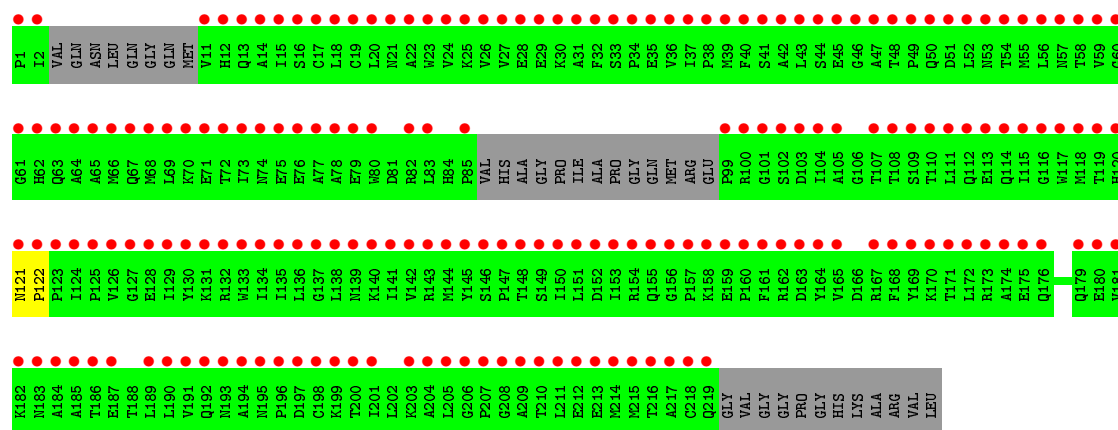
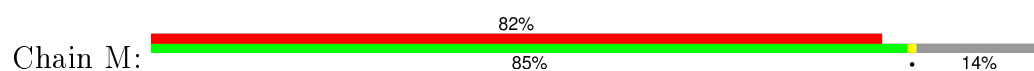


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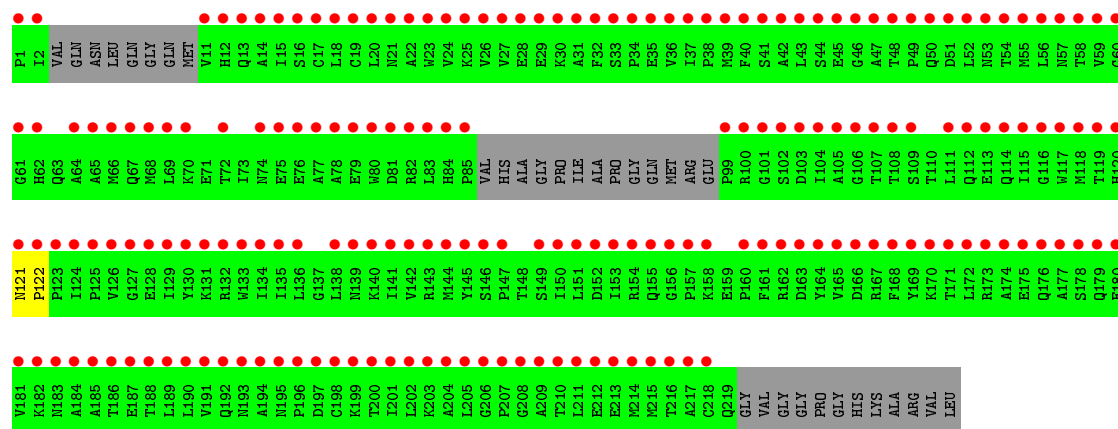
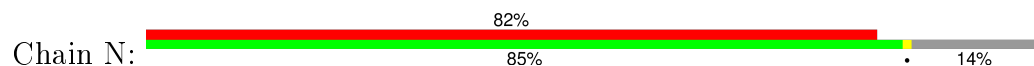




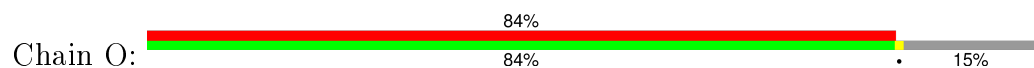
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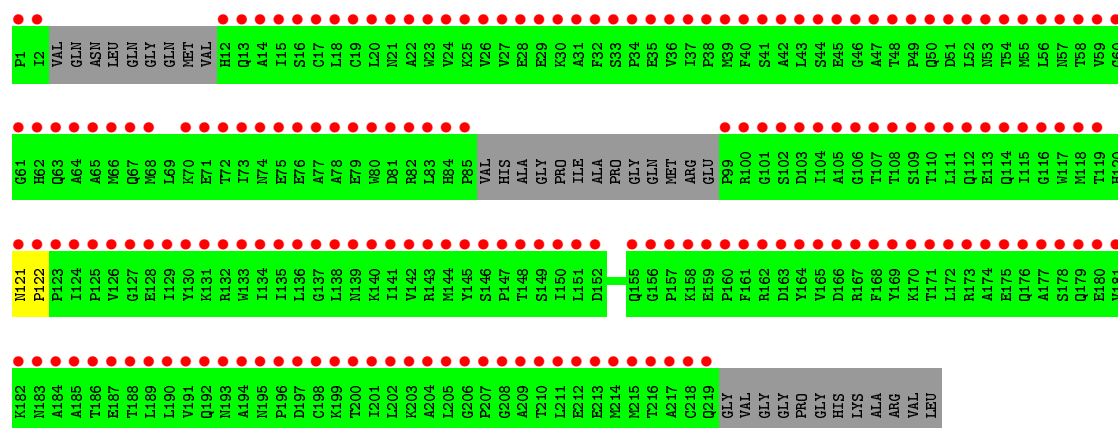


● Molecule 1: HIV-1 CA

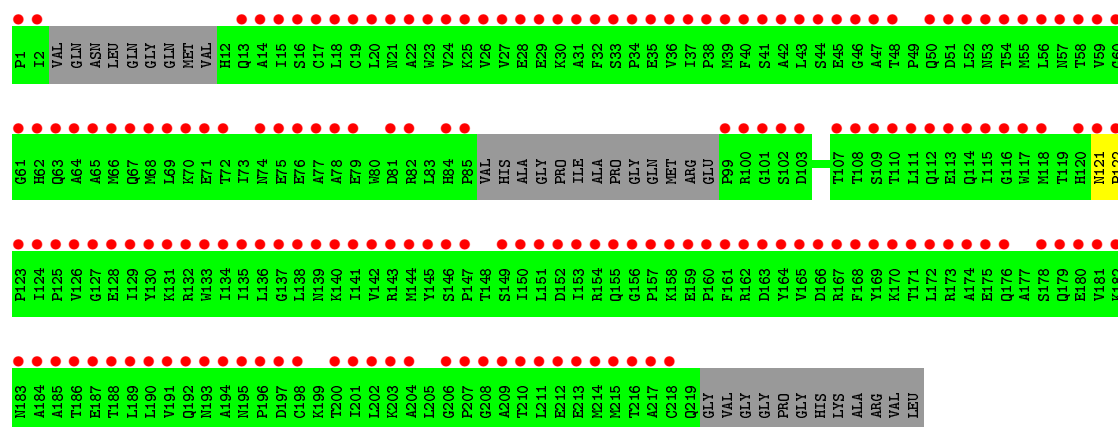
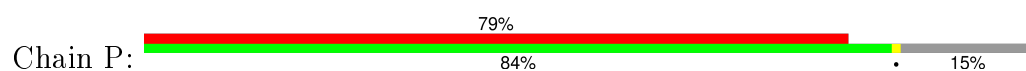


● Molecule 1: HIV-1 CA

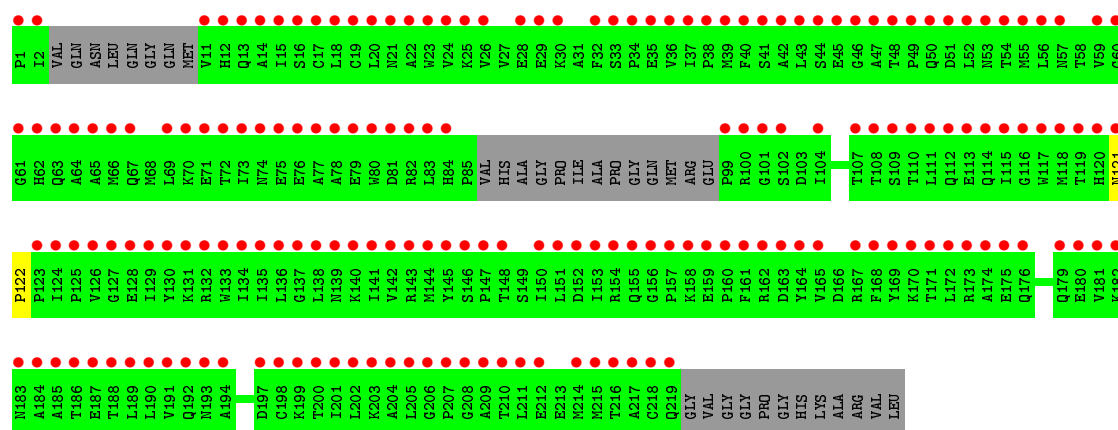
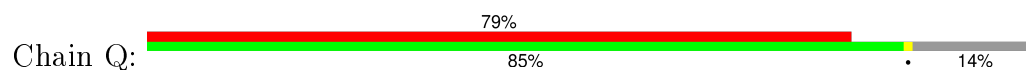




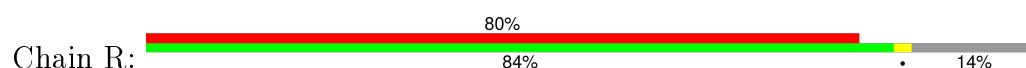
● Molecule 1: HIV-1 CA

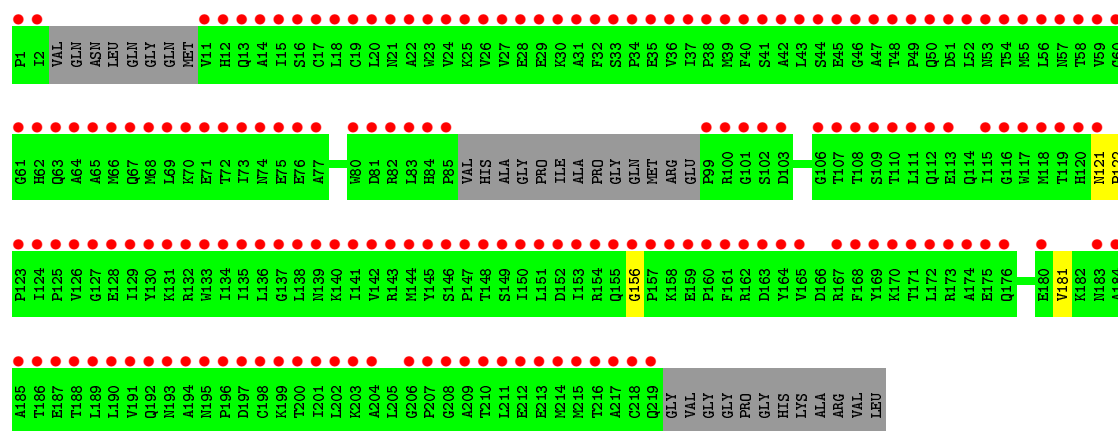


● Molecule 1: HIV-1 CA

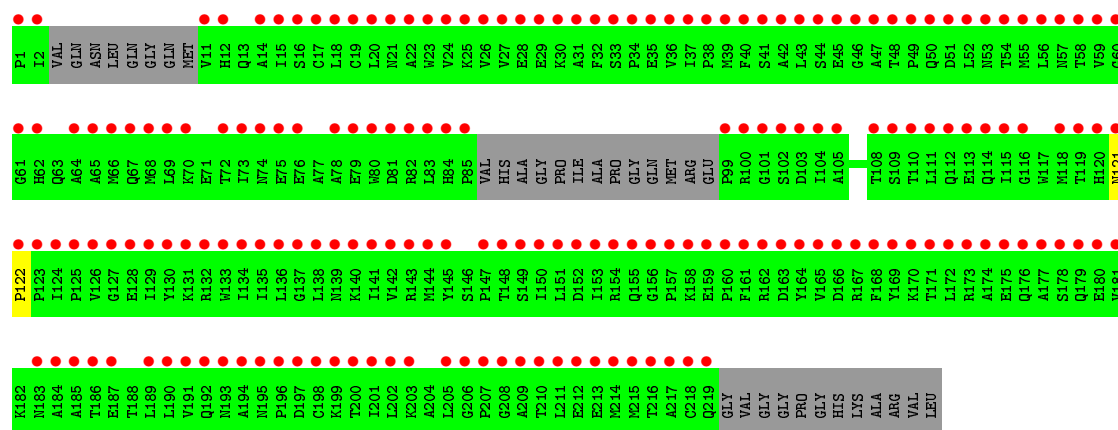
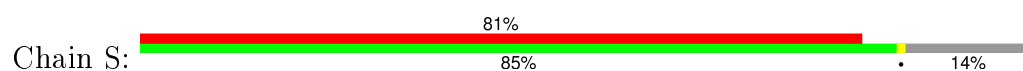


● Molecule 1: HIV-1 CA

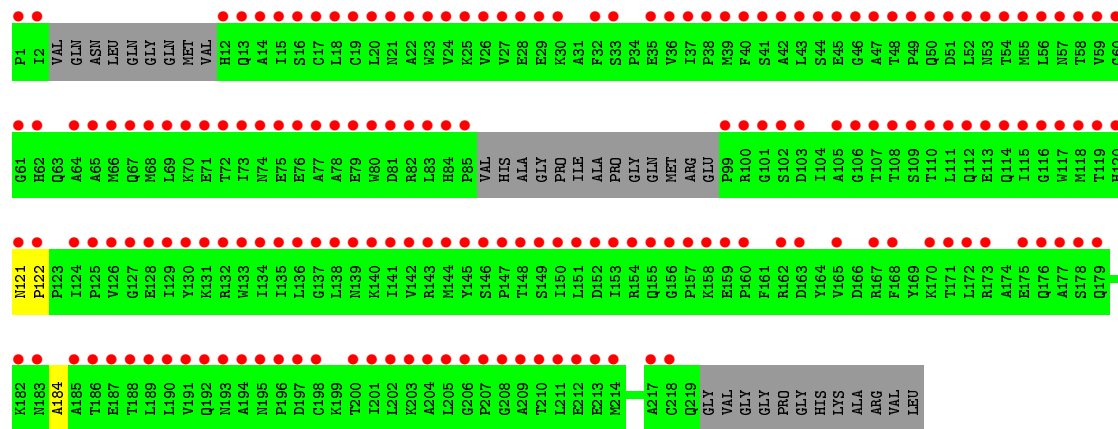
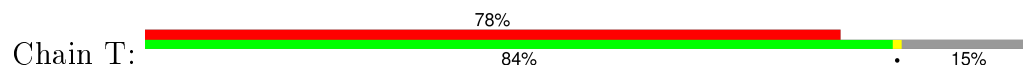




● Molecule 1: HIV-1 CA



● Molecule 1: HIV-1 CA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	86.79 Å 122.13 Å 149.30 Å 74.41° 74.36° 81.48°	Depositor
Resolution (Å)	45.56 – 5.95 49.59 – 5.95	Depositor EDS
% Data completeness (in resolution range)	97.9 (45.56-5.95) 91.1 (49.59-5.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.16 (at 6.15 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, R_{free}	0.297 , 0.316 0.346 , 0.381	Depositor DCC
R_{free} test set	1415 reflections (9.99%)	DCC
Wilson B-factor (Å ²)	287.8	Xtriage
Anisotropy	0.420	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.46 , -10.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 14213 reflections	Xtriage
F_o, F_c correlation	0.79	EDS
Total number of atoms	3952	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.52% 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	197	0	0	1	0
1	B	198	0	0	1	0
1	C	198	0	0	3	0
1	D	198	0	0	1	0
1	E	197	0	0	1	1
1	F	197	0	0	1	0
1	G	198	0	0	2	0
1	H	198	0	0	1	0
1	I	198	0	0	2	0
1	J	197	0	0	1	0
1	K	197	0	0	1	0
1	L	198	0	0	3	0
1	M	198	0	0	1	0
1	N	198	0	0	1	0
1	O	197	0	0	1	0
1	P	197	0	0	1	0
1	Q	198	0	0	1	0
1	R	198	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S	198	0	0	1	0
1	T	197	0	0	1	1
All	All	3952	0	0	25	1

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 6.

All (25) 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)
1:C:156:GLY:CA	1:I:156:GLY:CA	2.58	0.81
1:C:184:ALA:CA	1:R:181:VAL:CA	2.58	0.80
1:G:147:PRO:CA	1:G:148:THR:CA	2.89	0.50
1:L:121:ASN:CA	1:L:122:PRO:CA	2.90	0.50
1:Q:121:ASN:CA	1:Q:122:PRO:CA	2.90	0.49
1:B:121:ASN:CA	1:B:122:PRO:CA	2.90	0.49
1:G:121:ASN:CA	1:G:122:PRO:CA	2.90	0.49
1:E:121:ASN:CA	1:E:122:PRO:CA	2.91	0.48
1:T:121:ASN:CA	1:T:122:PRO:CA	2.91	0.48
1:O:121:ASN:CA	1:O:122:PRO:CA	2.91	0.48
1:J:121:ASN:CA	1:J:122:PRO:CA	2.91	0.48
1:R:121:ASN:CA	1:R:122:PRO:CA	2.92	0.48
1:L:156:GLY:CA	1:R:156:GLY:CA	2.92	0.48
1:C:121:ASN:CA	1:C:122:PRO:CA	2.92	0.48
1:L:147:PRO:CA	1:L:148:THR:CA	2.92	0.47
1:H:121:ASN:CA	1:H:122:PRO:CA	2.92	0.47
1:I:121:ASN:CA	1:I:122:PRO:CA	2.93	0.47
1:P:121:ASN:CA	1:P:122:PRO:CA	2.93	0.47
1:A:121:ASN:CA	1:A:122:PRO:CA	2.93	0.47
1:M:121:ASN:CA	1:M:122:PRO:CA	2.92	0.47
1:D:121:ASN:CA	1:D:122:PRO:CA	2.93	0.47
1:S:121:ASN:CA	1:S:122:PRO:CA	2.93	0.46
1:K:121:ASN:CA	1:K:122:PRO:CA	2.93	0.46
1:F:121:ASN:CA	1:F:122:PRO:CA	2.93	0.46
1:N:121:ASN:CA	1:N:122:PRO:CA	2.93	0.46

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:184:ALA:CA	1:T:184:ALA:CA[1_556]	2.06	0.14

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](#)

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](#)

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	197/231 (85%)	10.59	185 (93%) 0 1	100, 100, 100, 100	0
1	B	198/231 (85%)	9.73	185 (93%) 0 1	100, 100, 100, 100	0
1	C	198/231 (85%)	11.28	190 (95%) 0 1	100, 100, 100, 100	0
1	D	198/231 (85%)	10.99	190 (95%) 0 1	100, 100, 100, 100	0
1	E	197/231 (85%)	10.05	184 (93%) 0 1	100, 100, 100, 100	0
1	F	197/231 (85%)	10.70	181 (91%) 0 1	100, 100, 100, 100	0
1	G	198/231 (85%)	10.20	186 (93%) 0 1	100, 100, 100, 100	0
1	H	198/231 (85%)	11.87	192 (96%) 0 1	100, 100, 100, 100	0
1	I	198/231 (85%)	12.03	190 (95%) 0 1	100, 100, 100, 100	0
1	J	197/231 (85%)	11.04	190 (96%) 0 1	100, 100, 100, 100	0
1	K	197/231 (85%)	10.91	186 (94%) 0 1	100, 100, 100, 100	0
1	L	198/231 (85%)	10.37	190 (95%) 0 1	100, 100, 100, 100	0
1	M	198/231 (85%)	10.80	190 (95%) 0 1	100, 100, 100, 100	0
1	N	198/231 (85%)	10.48	190 (95%) 0 1	100, 100, 100, 100	0
1	O	197/231 (85%)	10.89	193 (97%) 0 1	100, 100, 100, 100	0
1	P	197/231 (85%)	10.64	183 (92%) 0 1	100, 100, 100, 100	0
1	Q	198/231 (85%)	9.58	182 (91%) 0 1	100, 100, 100, 100	0
1	R	198/231 (85%)	10.44	185 (93%) 0 1	100, 100, 100, 100	0
1	S	198/231 (85%)	10.54	187 (94%) 0 1	100, 100, 100, 100	0
1	T	197/231 (85%)	10.11	180 (91%) 0 1	100, 100, 100, 100	0
All	All	3952/4620 (85%)	10.66	3739 (94%) 0 1	100, 100, 100, 100	0

All (3739) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	100	ARG	49.1
1	S	171	THR	46.4
1	I	115	ILE	45.4
1	J	74	ASN	44.7
1	O	125	PRO	44.3
1	D	112	GLN	43.4
1	H	79	GLU	43.1
1	R	100	ARG	42.2
1	H	74	ASN	42.1
1	M	214	MET	42.0
1	H	124	ILE	41.8
1	D	190	LEU	41.5
1	F	52	LEU	39.7
1	I	102	SER	39.6
1	H	107	THR	39.2
1	O	157	PRO	38.9
1	K	201	ILE	38.8
1	K	64	ALA	38.5
1	G	130	TYR	38.5
1	A	210	THR	38.0
1	I	111	LEU	37.8
1	O	74	ASN	37.7
1	A	115	ILE	37.7
1	O	144	MET	37.7
1	S	67	GLN	37.4
1	R	198	CYS	37.4
1	O	156	GLY	37.1
1	Q	192	GLN	36.9
1	C	74	ASN	36.8
1	O	173	ARG	36.8
1	K	219	GLN	36.7
1	P	128	GLU	36.5
1	D	161	PHE	36.4
1	C	200	THR	36.4
1	I	51	ASP	36.4
1	L	157	PRO	36.2
1	S	112	GLN	36.1
1	F	102	SER	35.8
1	N	67	GLN	35.7
1	B	51	ASP	35.7
1	S	193	ASN	35.6
1	K	102	SER	35.5
1	T	210	THR	35.3

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Mol	Chain	Res	Type	RSRZ
1	E	67	GLN	35.2
1	S	190	LEU	34.8
1	M	125	PRO	34.6
1	E	128	GLU	34.5
1	F	139	ASN	34.4
1	I	214	MET	34.2
1	K	192	GLN	34.2
1	M	101	GLY	34.1
1	N	140	LYS	34.1
1	D	211	LEU	34.1
1	J	135	ILE	34.1
1	A	193	ASN	34.0
1	R	118	MET	33.9
1	C	131	LYS	33.5
1	B	158	LYS	33.4
1	Q	115	ILE	33.3
1	A	183	ASN	33.0
1	T	195	ASN	32.5
1	J	113	GLU	32.4
1	J	25	LYS	32.3
1	D	113	GLU	32.0
1	F	51	ASP	32.0
1	I	110	THR	31.9
1	C	108	THR	31.9
1	C	75	GLU	31.8
1	H	83	LEU	31.7
1	R	12	HIS	31.3
1	C	188	THR	31.2
1	I	163	ASP	31.1
1	P	151	LEU	31.0
1	G	124	ILE	31.0
1	E	66	MET	30.9
1	H	139	ASN	30.9
1	D	51	ASP	30.9
1	F	53	ASN	30.8
1	T	206	GLY	30.8
1	I	152	ASP	30.7
1	E	160	PRO	30.6
1	I	153	ILE	30.4
1	A	152	ASP	30.3
1	Q	169	TYR	30.3
1	F	130	TYR	30.2

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Mol	Chain	Res	Type	RSRZ
1	I	137	GLY	30.1
1	O	71	GLU	30.1
1	R	51	ASP	30.1
1	J	119	THR	30.1
1	F	186	THR	29.9
1	C	130	TYR	29.9
1	M	112	GLN	29.7
1	D	173	ARG	29.7
1	I	40	PHE	29.7
1	G	218	CYS	29.5
1	P	157	PRO	29.5
1	H	112	GLN	29.4
1	M	215	MET	29.4
1	F	115	ILE	29.3
1	R	11	VAL	29.3
1	M	128	GLU	29.2
1	S	119	THR	29.2
1	D	144	MET	29.2
1	F	112	GLN	29.1
1	E	81	ASP	29.1
1	B	165	VAL	29.1
1	M	141	ILE	29.0
1	T	211	LEU	28.9
1	F	191	VAL	28.7
1	Q	129	ILE	28.7
1	L	115	ILE	28.6
1	K	193	ASN	28.6
1	R	127	GLY	28.5
1	F	2	ILE	28.5
1	T	135	ILE	28.4
1	R	108	THR	28.3
1	G	186	THR	28.2
1	M	129	ILE	28.1
1	G	107	THR	28.0
1	F	125	PRO	28.0
1	E	102	SER	27.9
1	O	162	ARG	27.9
1	N	58	THR	27.9
1	T	65	ALA	27.9
1	R	195	ASN	27.9
1	D	170	LYS	27.8
1	J	144	MET	27.7

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Mol	Chain	Res	Type	RSRZ
1	T	67	GLN	27.7
1	P	152	ASP	27.7
1	K	66	MET	27.5
1	C	76	GLU	27.4
1	O	129	ILE	27.3
1	N	115	ILE	27.3
1	K	202	LEU	27.3
1	T	53	ASN	27.2
1	K	145	TYR	27.2
1	B	164	TYR	27.1
1	D	129	ILE	27.1
1	L	156	GLY	27.1
1	C	157	PRO	27.1
1	R	197	ASP	27.1
1	N	213	GLU	27.0
1	L	201	ILE	27.0
1	K	80	TRP	26.9
1	H	108	THR	26.9
1	K	200	THR	26.9
1	M	16	SER	26.9
1	R	162	ARG	26.8
1	A	157	PRO	26.7
1	F	153	ILE	26.7
1	G	13	GLN	26.7
1	S	162	ARG	26.6
1	S	186	THR	26.6
1	R	128	GLU	26.6
1	H	80	TRP	26.4
1	H	128	GLU	26.3
1	S	84	HIS	26.3
1	I	173	ARG	26.3
1	Q	160	PRO	26.2
1	A	114	GLN	26.2
1	Q	193	ASN	26.2
1	R	109	SER	26.2
1	J	173	ARG	26.1
1	B	156	GLY	26.1
1	G	108	THR	26.1
1	L	202	LEU	26.0
1	A	161	PHE	26.0
1	D	145	TYR	25.9
1	M	115	ILE	25.9

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Mol	Chain	Res	Type	RSRZ
1	S	111	LEU	25.9
1	S	102	SER	25.8
1	H	51	ASP	25.8
1	A	182	LYS	25.8
1	O	46	GLY	25.8
1	C	208	GLY	25.7
1	Q	190	LEU	25.6
1	D	41	SER	25.6
1	J	66	MET	25.5
1	I	150	ILE	25.4
1	S	214	MET	25.4
1	M	162	ARG	25.4
1	Q	207	PRO	25.4
1	T	112	GLN	25.4
1	N	29	GLU	25.4
1	D	186	THR	25.3
1	O	113	GLU	25.3
1	O	141	ILE	25.3
1	T	207	PRO	25.2
1	N	152	ASP	25.2
1	P	28	GLU	25.2
1	R	199	LYS	25.2
1	T	172	LEU	25.2
1	S	36	VAL	25.1
1	E	151	LEU	25.0
1	M	28	GLU	24.9
1	D	76	GLU	24.9
1	T	134	ILE	24.9
1	D	210	THR	24.9
1	Q	171	THR	24.9
1	I	112	GLN	24.8
1	M	66	MET	24.8
1	N	80	TRP	24.8
1	L	50	GLN	24.7
1	D	183	ASN	24.7
1	F	152	ASP	24.7
1	L	192	GLN	24.7
1	D	212	GLU	24.6
1	T	144	MET	24.6
1	J	36	VAL	24.6
1	C	198	CYS	24.6
1	A	144	MET	24.6

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Mol	Chain	Res	Type	RSRZ
1	T	139	ASN	24.5
1	L	116	GLY	24.5
1	M	212	GLU	24.4
1	K	35	GLU	24.4
1	D	37	ILE	24.4
1	J	163	ASP	24.3
1	P	67	GLN	24.3
1	T	212	GLU	24.3
1	D	171	THR	24.3
1	N	108	THR	24.3
1	D	132	ARG	24.3
1	J	162	ARG	24.3
1	F	167	ARG	24.2
1	E	203	LYS	24.2
1	J	67	GLN	24.1
1	J	133	TRP	24.1
1	I	157	PRO	24.1
1	G	155	GLN	24.1
1	L	67	GLN	24.0
1	G	132	ARG	24.0
1	C	214	MET	24.0
1	N	38	PRO	24.0
1	P	125	PRO	23.9
1	K	2	ILE	23.9
1	C	158	LYS	23.8
1	F	185	ALA	23.7
1	T	145	TYR	23.6
1	L	162	ARG	23.6
1	B	200	THR	23.5
1	B	186	THR	23.5
1	G	168	PHE	23.4
1	S	212	GLU	23.4
1	O	114	GLN	23.4
1	A	51	ASP	23.3
1	R	107	THR	23.3
1	J	149	SER	23.3
1	B	173	ARG	23.2
1	I	36	VAL	23.2
1	M	51	ASP	23.1
1	J	219	GLN	23.1
1	O	128	GLU	23.1
1	B	135	ILE	23.1

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Mol	Chain	Res	Type	RSRZ
1	K	51	ASP	23.1
1	E	118	MET	23.1
1	I	130	TYR	23.1
1	H	50	GLN	23.0
1	B	193	ASN	23.0
1	C	197	ASP	23.0
1	S	139	ASN	22.9
1	N	151	LEU	22.9
1	S	83	LEU	22.9
1	R	134	ILE	22.9
1	B	163	ASP	22.9
1	S	143	ARG	22.9
1	C	124	ILE	22.9
1	B	171	THR	22.9
1	F	67	GLN	22.8
1	Q	200	THR	22.8
1	P	145	TYR	22.8
1	J	170	LYS	22.8
1	L	75	GLU	22.8
1	J	38	PRO	22.7
1	K	76	GLU	22.7
1	B	76	GLU	22.7
1	P	26	VAL	22.7
1	E	186	THR	22.6
1	I	56	LEU	22.6
1	B	159	GLU	22.6
1	J	26	VAL	22.5
1	C	107	THR	22.5
1	O	172	LEU	22.5
1	E	51	ASP	22.4
1	G	203	LYS	22.4
1	G	173	ARG	22.4
1	D	162	ARG	22.4
1	R	119	THR	22.4
1	R	208	GLY	22.3
1	H	132	ARG	22.3
1	I	129	ILE	22.3
1	H	142	VAL	22.2
1	P	186	THR	22.2
1	N	121	ASN	22.2
1	D	180	GLU	22.2
1	F	35	GLU	22.2

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Mol	Chain	Res	Type	RSRZ
1	J	65	ALA	22.2
1	H	171	THR	22.2
1	C	64	ALA	22.1
1	D	67	GLN	22.1
1	P	56	LEU	22.1
1	M	76	GLU	22.1
1	C	139	ASN	22.1
1	N	65	ALA	22.1
1	J	139	ASN	22.0
1	R	132	ARG	22.0
1	G	217	ALA	22.0
1	H	125	PRO	22.0
1	G	169	TYR	21.9
1	T	42	ALA	21.9
1	A	165	VAL	21.9
1	L	40	PHE	21.9
1	A	172	LEU	21.9
1	C	201	ILE	21.8
1	J	136	LEU	21.8
1	P	130	TYR	21.8
1	C	199	LYS	21.7
1	K	101	GLY	21.7
1	C	122	PRO	21.6
1	Q	133	TRP	21.6
1	C	163	ASP	21.6
1	M	130	TYR	21.5
1	S	128	GLU	21.5
1	L	53	ASN	21.5
1	F	128	GLU	21.5
1	A	17	CYS	21.5
1	J	77	ALA	21.5
1	E	103	ASP	21.4
1	O	139	ASN	21.4
1	S	129	ILE	21.4
1	I	165	VAL	21.3
1	S	35	GLU	21.3
1	A	102	SER	21.3
1	S	170	LYS	21.3
1	G	210	THR	21.3
1	P	214	MET	21.3
1	P	50	GLN	21.3
1	H	200	THR	21.2

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Mol	Chain	Res	Type	RSRZ
1	J	210	THR	21.2
1	Q	159	GLU	21.2
1	F	206	GLY	21.2
1	J	49	PRO	21.2
1	J	41	SER	21.2
1	Q	25	LYS	21.1
1	M	74	ASN	21.1
1	T	100	ARG	21.1
1	J	16	SER	21.0
1	R	196	PRO	21.0
1	N	35	GLU	21.0
1	O	101	GLY	21.0
1	F	17	CYS	21.0
1	I	158	LYS	21.0
1	B	50	GLN	21.0
1	P	39	MET	21.0
1	A	66	MET	21.0
1	P	115	ILE	20.9
1	Q	100	ARG	20.9
1	C	99	PRO	20.9
1	H	12	HIS	20.9
1	N	76	GLU	20.9
1	E	150	ILE	20.9
1	F	140	LYS	20.9
1	F	126	VAL	20.9
1	G	140	LYS	20.9
1	C	187	GLU	20.9
1	J	13	GLN	20.9
1	A	195	ASN	20.8
1	N	50	GLN	20.8
1	J	120	HIS	20.7
1	H	156	GLY	20.7
1	K	216	THR	20.7
1	N	195	ASN	20.7
1	I	54	THR	20.7
1	Q	139	ASN	20.7
1	K	152	ASP	20.7
1	A	67	GLN	20.6
1	F	16	SER	20.6
1	I	50	GLN	20.6
1	A	112	GLN	20.6
1	L	132	ARG	20.6

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Mol	Chain	Res	Type	RSRZ
1	M	131	LYS	20.6
1	H	129	ILE	20.6
1	P	191	VAL	20.6
1	P	203	LYS	20.6
1	M	65	ALA	20.6
1	A	153	ILE	20.6
1	G	172	LEU	20.6
1	T	186	THR	20.5
1	E	112	GLN	20.5
1	T	143	ARG	20.5
1	H	113	GLU	20.5
1	G	113	GLU	20.5
1	A	111	LEU	20.5
1	C	2	ILE	20.5
1	E	24	VAL	20.5
1	C	66	MET	20.5
1	K	50	GLN	20.5
1	P	20	LEU	20.4
1	N	109	SER	20.4
1	O	48	THR	20.4
1	R	76	GLU	20.4
1	L	66	MET	20.4
1	T	68	MET	20.4
1	C	112	GLN	20.3
1	H	109	SER	20.3
1	G	129	ILE	20.3
1	A	166	ASP	20.2
1	Q	53	ASN	20.2
1	F	50	GLN	20.2
1	R	171	THR	20.2
1	S	42	ALA	20.2
1	H	192	GLN	20.2
1	R	61	GLY	20.2
1	C	129	ILE	20.2
1	M	26	VAL	20.1
1	C	193	ASN	20.1
1	H	81	ASP	20.0
1	S	174	ALA	20.0
1	G	38	PRO	20.0
1	P	179	GLN	20.0
1	S	173	ARG	20.0
1	E	134	ILE	19.9

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Mol	Chain	Res	Type	RSRZ
1	G	157	PRO	19.9
1	S	31	ALA	19.9
1	P	185	ALA	19.9
1	L	51	ASP	19.9
1	E	25	LYS	19.9
1	J	209	ALA	19.9
1	R	36	VAL	19.8
1	F	109	SER	19.8
1	P	57	ASN	19.8
1	G	41	SER	19.8
1	R	158	LYS	19.8
1	A	141	ILE	19.8
1	Q	212	GLU	19.8
1	Q	83	LEU	19.7
1	M	190	LEU	19.7
1	K	103	ASP	19.7
1	P	190	LEU	19.7
1	J	29	GLU	19.7
1	O	75	GLU	19.7
1	G	213	GLU	19.7
1	F	124	ILE	19.6
1	S	169	TYR	19.6
1	P	133	TRP	19.6
1	J	110	THR	19.6
1	T	208	GLY	19.6
1	Q	211	LEU	19.6
1	M	211	LEU	19.6
1	C	206	GLY	19.5
1	N	56	LEU	19.5
1	D	125	PRO	19.5
1	K	214	MET	19.5
1	T	51	ASP	19.5
1	O	115	ILE	19.5
1	K	212	GLU	19.5
1	B	175	GLU	19.4
1	R	210	THR	19.4
1	P	42	ALA	19.4
1	E	193	ASN	19.4
1	H	152	ASP	19.3
1	F	131	LYS	19.3
1	A	160	PRO	19.3
1	J	131	LYS	19.3

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Mol	Chain	Res	Type	RSRZ
1	S	2	ILE	19.3
1	Q	131	LYS	19.3
1	K	141	ILE	19.3
1	H	172	LEU	19.3
1	O	51	ASP	19.3
1	E	84	HIS	19.3
1	T	50	GLN	19.3
1	O	203	LYS	19.2
1	T	39	MET	19.2
1	A	113	GLU	19.2
1	B	162	ARG	19.2
1	K	75	GLU	19.2
1	I	191	VAL	19.2
1	A	130	TYR	19.2
1	G	46	GLY	19.2
1	O	118	MET	19.2
1	N	75	GLU	19.2
1	Q	130	TYR	19.2
1	K	37	ILE	19.2
1	N	100	ARG	19.1
1	M	67	GLN	19.1
1	K	159	GLU	19.1
1	S	200	THR	19.1
1	C	196	PRO	19.0
1	C	189	LEU	18.9
1	P	126	VAL	18.9
1	O	108	THR	18.9
1	R	200	THR	18.9
1	E	135	ILE	18.9
1	I	45	GLU	18.9
1	B	210	THR	18.8
1	G	167	ARG	18.8
1	F	42	ALA	18.8
1	J	75	GLU	18.8
1	I	172	LEU	18.8
1	H	157	PRO	18.7
1	I	74	ASN	18.7
1	F	40	PHE	18.7
1	S	202	LEU	18.7
1	A	21	ASN	18.7
1	G	145	TYR	18.7
1	B	101	GLY	18.7

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Mol	Chain	Res	Type	RSRZ
1	N	206	GLY	18.6
1	H	76	GLU	18.6
1	P	131	LYS	18.6
1	A	122	PRO	18.6
1	I	160	PRO	18.6
1	H	193	ASN	18.5
1	O	213	GLU	18.5
1	D	130	TYR	18.5
1	L	191	VAL	18.5
1	G	139	ASN	18.4
1	G	131	LYS	18.4
1	D	184	ALA	18.4
1	M	35	GLU	18.4
1	P	102	SER	18.4
1	K	85	PRO	18.3
1	N	134	ILE	18.3
1	K	77	ALA	18.3
1	K	142	VAL	18.3
1	O	53	ASN	18.3
1	S	125	PRO	18.3
1	T	2	ILE	18.3
1	I	192	GLN	18.3
1	C	1	PRO	18.3
1	N	133	TRP	18.2
1	Q	202	LEU	18.2
1	N	39	MET	18.2
1	N	165	VAL	18.2
1	L	153	ILE	18.2
1	I	154	ARG	18.2
1	R	135	ILE	18.1
1	Q	102	SER	18.1
1	M	80	TRP	18.1
1	D	66	MET	18.1
1	F	99	PRO	18.1
1	F	192	GLN	18.1
1	T	20	LEU	18.0
1	P	17	CYS	18.0
1	Q	172	LEU	18.0
1	G	76	GLU	18.0
1	I	125	PRO	18.0
1	C	121	ASN	18.0
1	O	158	LYS	18.0

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Mol	Chain	Res	Type	RSRZ
1	O	38	PRO	17.9
1	K	125	PRO	17.9
1	S	144	MET	17.9
1	P	212	GLU	17.9
1	A	164	TYR	17.9
1	H	1	PRO	17.9
1	O	1	PRO	17.9
1	J	23	TRP	17.8
1	H	145	TYR	17.8
1	B	53	ASN	17.8
1	G	112	GLN	17.8
1	I	164	TYR	17.8
1	E	206	GLY	17.8
1	P	59	VAL	17.8
1	P	111	LEU	17.8
1	J	215	MET	17.8
1	A	192	GLN	17.8
1	E	172	LEU	17.7
1	L	42	ALA	17.7
1	P	192	GLN	17.7
1	C	210	THR	17.7
1	M	218	CYS	17.7
1	A	59	VAL	17.7
1	G	187	GLU	17.7
1	M	17	CYS	17.7
1	K	121	ASN	17.7
1	R	125	PRO	17.7
1	J	111	LEU	17.7
1	H	41	SER	17.7
1	T	151	LEU	17.7
1	B	17	CYS	17.6
1	C	141	ILE	17.6
1	J	193	ASN	17.6
1	G	171	THR	17.6
1	L	133	TRP	17.6
1	J	51	ASP	17.5
1	M	11	VAL	17.5
1	G	74	ASN	17.5
1	I	198	CYS	17.5
1	T	103	ASP	17.5
1	C	140	LYS	17.5
1	G	170	LYS	17.5

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Mol	Chain	Res	Type	RSRZ
1	L	39	MET	17.5
1	H	84	HIS	17.5
1	P	187	GLU	17.5
1	B	112	GLN	17.5
1	L	1	PRO	17.5
1	L	158	LYS	17.5
1	P	134	ILE	17.5
1	H	210	THR	17.5
1	N	24	VAL	17.4
1	D	150	ILE	17.4
1	I	41	SER	17.4
1	C	31	ALA	17.4
1	L	111	LEU	17.4
1	I	132	ARG	17.4
1	G	102	SER	17.4
1	O	152	ASP	17.4
1	L	35	GLU	17.4
1	R	53	ASN	17.4
1	I	184	ALA	17.4
1	D	115	ILE	17.3
1	A	121	ASN	17.3
1	J	12	HIS	17.3
1	N	139	ASN	17.3
1	I	53	ASN	17.3
1	B	21	ASN	17.3
1	A	158	LYS	17.3
1	H	163	ASP	17.3
1	A	203	LYS	17.3
1	N	103	ASP	17.3
1	O	130	TYR	17.2
1	P	101	GLY	17.2
1	Q	134	ILE	17.2
1	C	50	GLN	17.2
1	C	65	ALA	17.2
1	N	25	LYS	17.2
1	K	48	THR	17.2
1	T	194	ALA	17.2
1	C	216	THR	17.1
1	F	133	TRP	17.1
1	M	197	ASP	17.1
1	M	20	LEU	17.1
1	R	139	ASN	17.1

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Mol	Chain	Res	Type	RSRZ
1	M	132	ARG	17.1
1	G	39	MET	17.1
1	L	113	GLU	17.1
1	A	26	VAL	17.0
1	M	103	ASP	17.0
1	H	133	TRP	17.0
1	Q	51	ASP	17.0
1	P	141	ILE	17.0
1	C	128	GLU	17.0
1	B	191	VAL	17.0
1	O	2	ILE	17.0
1	S	65	ALA	17.0
1	P	149	SER	17.0
1	L	41	SER	17.0
1	E	136	LEU	16.9
1	N	201	ILE	16.9
1	H	16	SER	16.9
1	C	203	LYS	16.9
1	M	102	SER	16.9
1	M	38	PRO	16.9
1	F	135	ILE	16.9
1	A	65	ALA	16.9
1	D	47	ALA	16.8
1	P	40	PHE	16.8
1	H	147	PRO	16.8
1	N	162	ARG	16.8
1	C	159	GLU	16.8
1	L	135	ILE	16.8
1	T	159	GLU	16.8
1	I	12	HIS	16.8
1	O	99	PRO	16.8
1	D	187	GLU	16.7
1	G	156	GLY	16.7
1	I	183	ASN	16.7
1	C	134	ILE	16.7
1	P	129	ILE	16.7
1	N	77	ALA	16.7
1	B	141	ILE	16.7
1	D	141	ILE	16.7
1	R	65	ALA	16.7
1	Q	216	THR	16.6
1	H	138	LEU	16.6

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Mol	Chain	Res	Type	RSRZ
1	R	190	LEU	16.6
1	Q	208	GLY	16.6
1	P	139	ASN	16.6
1	R	165	VAL	16.6
1	N	198	CYS	16.6
1	C	63	GLN	16.6
1	J	158	LYS	16.6
1	R	163	ASP	16.6
1	N	36	VAL	16.5
1	C	191	VAL	16.5
1	J	151	LEU	16.5
1	H	199	LYS	16.5
1	D	200	THR	16.5
1	O	180	GLU	16.5
1	P	44	SER	16.5
1	A	134	ILE	16.5
1	N	173	ARG	16.5
1	L	183	ASN	16.5
1	H	72	THR	16.4
1	A	126	VAL	16.4
1	M	77	ALA	16.4
1	L	173	ARG	16.4
1	I	212	GLU	16.4
1	N	59	VAL	16.4
1	T	192	GLN	16.4
1	D	36	VAL	16.4
1	A	53	ASN	16.4
1	I	135	ILE	16.4
1	E	108	THR	16.4
1	M	176	GLN	16.4
1	A	140	LYS	16.4
1	O	103	ASP	16.4
1	R	112	GLN	16.4
1	K	53	ASN	16.4
1	H	11	VAL	16.4
1	C	156	GLY	16.4
1	L	165	VAL	16.4
1	E	129	ILE	16.3
1	M	27	VAL	16.3
1	H	53	ASN	16.3
1	G	196	PRO	16.3
1	R	172	LEU	16.3

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Mol	Chain	Res	Type	RSRZ
1	P	138	LEU	16.3
1	O	140	LYS	16.3
1	D	169	TYR	16.3
1	M	217	ALA	16.3
1	A	162	ARG	16.3
1	T	130	TYR	16.3
1	H	202	LEU	16.3
1	J	100	ARG	16.3
1	Q	163	ASP	16.2
1	D	40	PHE	16.2
1	J	129	ILE	16.2
1	T	52	LEU	16.2
1	R	17	CYS	16.2
1	G	52	LEU	16.2
1	P	110	THR	16.2
1	F	121	ASN	16.2
1	A	60	GLY	16.2
1	N	149	SER	16.2
1	D	102	SER	16.2
1	I	13	GLN	16.2
1	J	152	ASP	16.2
1	E	21	ASN	16.1
1	A	52	LEU	16.1
1	Q	210	THR	16.1
1	B	113	GLU	16.1
1	L	130	TYR	16.1
1	M	99	PRO	16.1
1	P	18	LEU	16.1
1	E	187	GLU	16.0
1	C	144	MET	16.0
1	Q	128	GLU	16.0
1	L	219	GLN	16.0
1	B	65	ALA	16.0
1	L	125	PRO	16.0
1	J	101	GLY	16.0
1	T	152	ASP	16.0
1	E	173	ARG	16.0
1	I	171	THR	16.0
1	D	164	TYR	16.0
1	H	18	LEU	16.0
1	J	115	ILE	16.0
1	H	67	GLN	15.9

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Mol	Chain	Res	Type	RSRZ
1	P	55	MET	15.9
1	H	165	VAL	15.9
1	P	135	ILE	15.9
1	H	183	ASN	15.9
1	B	183	ASN	15.9
1	G	197	ASP	15.9
1	D	158	LYS	15.9
1	O	138	LEU	15.9
1	Q	183	ASN	15.9
1	A	58	THR	15.8
1	K	21	ASN	15.8
1	K	180	GLU	15.8
1	G	14	ALA	15.8
1	H	39	MET	15.8
1	B	130	TYR	15.8
1	L	147	PRO	15.8
1	M	40	PHE	15.8
1	A	36	VAL	15.8
1	J	145	TYR	15.8
1	I	133	TRP	15.8
1	Q	76	GLU	15.8
1	R	130	TYR	15.8
1	B	57	ASN	15.7
1	O	39	MET	15.7
1	P	121	ASN	15.7
1	K	39	MET	15.7
1	A	50	GLN	15.7
1	K	33	SER	15.7
1	I	131	LYS	15.7
1	O	192	GLN	15.7
1	G	207	PRO	15.7
1	C	53	ASN	15.7
1	N	135	ILE	15.7
1	J	132	ARG	15.6
1	P	58	THR	15.6
1	B	157	PRO	15.6
1	N	28	GLU	15.6
1	G	61	GLY	15.6
1	N	156	GLY	15.6
1	C	24	VAL	15.6
1	Q	197	ASP	15.6
1	I	182	LYS	15.6

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Mol	Chain	Res	Type	RSRZ
1	E	61	GLY	15.6
1	Q	50	GLN	15.6
1	D	168	PHE	15.6
1	J	125	PRO	15.6
1	T	23	TRP	15.6
1	Q	20	LEU	15.6
1	E	125	PRO	15.6
1	G	99	PRO	15.6
1	M	29	GLU	15.6
1	D	52	LEU	15.6
1	P	211	LEU	15.5
1	A	129	ILE	15.5
1	S	110	THR	15.5
1	H	37	ILE	15.5
1	K	138	LEU	15.5
1	E	216	THR	15.5
1	Q	127	GLY	15.5
1	S	1	PRO	15.5
1	L	152	ASP	15.5
1	N	197	ASP	15.5
1	S	11	VAL	15.5
1	R	214	MET	15.5
1	A	28	GLU	15.5
1	E	130	TYR	15.5
1	H	102	SER	15.4
1	S	30	LYS	15.4
1	K	205	LEU	15.4
1	F	113	GLU	15.4
1	K	183	ASN	15.4
1	K	203	LYS	15.4
1	B	56	LEU	15.4
1	D	151	LEU	15.4
1	Q	114	GLN	15.4
1	N	112	GLN	15.3
1	F	80	TRP	15.3
1	M	53	ASN	15.3
1	N	79	GLU	15.3
1	B	99	PRO	15.3
1	J	138	LEU	15.3
1	B	212	GLU	15.3
1	Q	101	GLY	15.3
1	N	51	ASP	15.3

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Mol	Chain	Res	Type	RSRZ
1	K	204	ALA	15.3
1	C	126	VAL	15.2
1	F	107	THR	15.2
1	G	161	PHE	15.2
1	H	179	GLN	15.2
1	P	166	ASP	15.2
1	R	124	ILE	15.2
1	I	55	MET	15.2
1	O	214	MET	15.2
1	H	180	GLU	15.2
1	C	211	LEU	15.2
1	Q	24	VAL	15.2
1	M	216	THR	15.2
1	M	180	GLU	15.2
1	F	24	VAL	15.2
1	B	42	ALA	15.2
1	D	157	PRO	15.2
1	T	120	HIS	15.2
1	G	79	GLU	15.1
1	H	206	GLY	15.1
1	P	132	ARG	15.1
1	D	197	ASP	15.1
1	J	76	GLU	15.1
1	L	137	GLY	15.1
1	F	172	LEU	15.1
1	E	183	ASN	15.1
1	T	56	LEU	15.1
1	T	160	PRO	15.1
1	I	67	GLN	15.1
1	N	60	GLY	15.1
1	R	21	ASN	15.1
1	O	211	LEU	15.0
1	J	186	THR	15.0
1	P	173	ARG	15.0
1	S	216	THR	15.0
1	E	217	ALA	15.0
1	B	84	HIS	15.0
1	E	75	GLU	15.0
1	H	130	TYR	15.0
1	F	21	ASN	15.0
1	N	157	PRO	15.0
1	R	29	GLU	15.0

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Mol	Chain	Res	Type	RSRZ
1	K	79	GLU	14.9
1	G	45	GLU	14.9
1	H	126	VAL	14.9
1	B	45	GLU	14.9
1	A	44	SER	14.9
1	M	55	MET	14.9
1	H	218	CYS	14.9
1	F	179	GLN	14.9
1	J	64	ALA	14.9
1	L	159	GLU	14.9
1	G	47	ALA	14.9
1	R	156	GLY	14.9
1	G	134	ILE	14.9
1	Q	77	ALA	14.9
1	M	163	ASP	14.8
1	O	186	THR	14.8
1	S	185	ALA	14.8
1	R	38	PRO	14.8
1	F	132	ARG	14.8
1	G	44	SER	14.8
1	N	37	ILE	14.8
1	Q	152	ASP	14.8
1	K	107	THR	14.8
1	E	56	LEU	14.8
1	P	66	MET	14.8
1	K	208	GLY	14.8
1	R	211	LEU	14.8
1	S	175	GLU	14.8
1	N	41	SER	14.8
1	L	172	LEU	14.8
1	C	151	LEU	14.8
1	H	215	MET	14.8
1	N	210	THR	14.8
1	T	190	LEU	14.7
1	E	169	TYR	14.7
1	K	139	ASN	14.7
1	T	40	PHE	14.7
1	H	36	VAL	14.7
1	I	156	GLY	14.7
1	J	20	LEU	14.7
1	R	133	TRP	14.7
1	T	49	PRO	14.7

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Mol	Chain	Res	Type	RSRZ
1	K	206	GLY	14.7
1	K	172	LEU	14.7
1	R	40	PHE	14.7
1	F	129	ILE	14.6
1	Q	38	PRO	14.6
1	C	207	PRO	14.6
1	M	12	HIS	14.6
1	F	147	PRO	14.6
1	J	30	LYS	14.6
1	N	32	PHE	14.6
1	J	40	PHE	14.6
1	J	72	THR	14.6
1	L	128	GLU	14.6
1	Q	186	THR	14.6
1	C	132	ARG	14.6
1	E	48	THR	14.6
1	F	146	SER	14.6
1	B	20	LEU	14.6
1	G	42	ALA	14.5
1	E	41	SER	14.5
1	O	217	ALA	14.5
1	A	147	PRO	14.5
1	B	217	ALA	14.5
1	P	24	VAL	14.5
1	K	215	MET	14.5
1	E	65	ALA	14.5
1	T	197	ASP	14.5
1	N	214	MET	14.5
1	M	186	THR	14.5
1	E	55	MET	14.5
1	F	171	THR	14.5
1	H	173	ARG	14.5
1	L	129	ILE	14.4
1	M	161	PHE	14.4
1	O	200	THR	14.4
1	O	212	GLU	14.4
1	N	132	ARG	14.4
1	I	169	TYR	14.4
1	K	136	LEU	14.4
1	F	203	LYS	14.4
1	H	186	THR	14.4
1	L	69	LEU	14.4

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Mol	Chain	Res	Type	RSRZ
1	J	126	VAL	14.4
1	S	213	GLU	14.4
1	A	108	THR	14.4
1	C	192	GLN	14.4
1	I	44	SER	14.3
1	E	209	ALA	14.3
1	I	35	GLU	14.3
1	M	213	GLU	14.3
1	K	1	PRO	14.3
1	P	169	TYR	14.3
1	N	172	LEU	14.3
1	S	138	LEU	14.3
1	C	21	ASN	14.3
1	S	25	LYS	14.3
1	H	115	ILE	14.3
1	E	12	HIS	14.3
1	S	145	TYR	14.2
1	D	134	ILE	14.2
1	L	20	LEU	14.2
1	C	72	THR	14.2
1	S	52	LEU	14.2
1	L	76	GLU	14.2
1	O	199	LYS	14.2
1	S	131	LYS	14.2
1	E	119	THR	14.2
1	J	165	VAL	14.2
1	N	131	LYS	14.2
1	A	170	LYS	14.2
1	K	173	ARG	14.2
1	D	135	ILE	14.2
1	H	24	VAL	14.2
1	N	125	PRO	14.2
1	K	165	VAL	14.2
1	P	25	LYS	14.1
1	A	41	SER	14.1
1	S	29	GLU	14.1
1	K	146	SER	14.1
1	C	117	TRP	14.1
1	A	125	PRO	14.1
1	N	119	THR	14.1
1	J	28	GLU	14.1
1	S	50	GLN	14.1

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Mol	Chain	Res	Type	RSRZ
1	F	165	VAL	14.1
1	I	81	ASP	14.1
1	O	131	LYS	14.1
1	O	132	ARG	14.1
1	Q	17	CYS	14.1
1	H	205	LEU	14.1
1	H	159	GLU	14.1
1	S	180	GLU	14.0
1	T	66	MET	14.0
1	R	141	ILE	14.0
1	D	192	GLN	14.0
1	B	203	LYS	14.0
1	R	26	VAL	14.0
1	N	160	PRO	14.0
1	R	207	PRO	14.0
1	C	51	ASP	14.0
1	I	103	ASP	14.0
1	T	213	GLU	13.9
1	R	111	LEU	13.9
1	S	43	LEU	13.9
1	O	35	GLU	13.9
1	C	123	PRO	13.9
1	T	83	LEU	13.9
1	F	64	ALA	13.9
1	I	23	TRP	13.9
1	N	124	ILE	13.9
1	R	30	LYS	13.9
1	P	183	ASN	13.9
1	R	131	LYS	13.9
1	D	13	GLN	13.9
1	H	146	SER	13.9
1	R	1	PRO	13.9
1	O	111	LEU	13.9
1	J	35	GLU	13.9
1	A	211	LEU	13.9
1	O	34	PRO	13.9
1	Q	140	LYS	13.9
1	S	82	ARG	13.9
1	J	62	HIS	13.8
1	P	172	LEU	13.8
1	H	103	ASP	13.8
1	L	37	ILE	13.8

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Mol	Chain	Res	Type	RSRZ
1	E	204	ALA	13.8
1	T	162	ARG	13.8
1	N	190	LEU	13.8
1	O	47	ALA	13.8
1	E	159	GLU	13.8
1	L	112	GLN	13.8
1	F	164	TYR	13.8
1	D	202	LEU	13.8
1	S	126	VAL	13.8
1	I	141	ILE	13.8
1	D	53	ASN	13.7
1	P	52	LEU	13.7
1	F	211	LEU	13.7
1	H	15	ILE	13.7
1	F	103	ASP	13.7
1	D	42	ALA	13.7
1	T	173	ARG	13.7
1	F	214	MET	13.7
1	S	123	PRO	13.7
1	B	192	GLN	13.7
1	C	109	SER	13.7
1	I	170	LYS	13.7
1	L	57	ASN	13.7
1	L	196	PRO	13.7
1	E	50	GLN	13.6
1	S	85	PRO	13.6
1	E	120	HIS	13.6
1	J	50	GLN	13.6
1	E	39	MET	13.6
1	I	28	GLU	13.6
1	M	173	ARG	13.6
1	K	84	HIS	13.6
1	I	57	ASN	13.5
1	P	41	SER	13.5
1	T	156	GLY	13.5
1	P	51	ASP	13.5
1	N	61	GLY	13.5
1	O	67	GLN	13.5
1	A	190	LEU	13.5
1	O	177	ALA	13.5
1	C	30	LYS	13.4
1	R	110	THR	13.4

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Mol	Chain	Res	Type	RSRZ
1	C	12	HIS	13.4
1	G	43	LEU	13.4
1	A	109	SER	13.4
1	L	52	LEU	13.4
1	N	66	MET	13.4
1	J	169	TYR	13.4
1	T	107	THR	13.4
1	B	55	MET	13.4
1	F	1	PRO	13.4
1	E	147	PRO	13.4
1	E	33	SER	13.4
1	L	19	CYS	13.4
1	K	143	ARG	13.4
1	T	129	ILE	13.4
1	D	111	LEU	13.3
1	I	66	MET	13.3
1	H	219	GLN	13.3
1	K	207	PRO	13.3
1	M	113	GLU	13.3
1	P	109	SER	13.3
1	D	25	LYS	13.3
1	R	187	GLU	13.3
1	I	38	PRO	13.3
1	I	64	ALA	13.3
1	B	47	ALA	13.3
1	E	162	ARG	13.3
1	C	26	VAL	13.3
1	Q	151	LEU	13.3
1	N	17	CYS	13.3
1	S	99	PRO	13.3
1	T	102	SER	13.3
1	I	176	GLN	13.3
1	O	44	SER	13.2
1	T	138	LEU	13.2
1	E	53	ASN	13.2
1	I	211	LEU	13.2
1	F	41	SER	13.2
1	D	46	GLY	13.2
1	L	43	LEU	13.2
1	S	51	ASP	13.2
1	K	135	ILE	13.2
1	F	193	ASN	13.2

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Mol	Chain	Res	Type	RSRZ
1	L	103	ASP	13.2
1	H	149	SER	13.2
1	I	210	THR	13.2
1	T	146	SER	13.2
1	M	14	ALA	13.2
1	B	131	LYS	13.1
1	E	72	THR	13.1
1	P	158	LYS	13.1
1	L	189	LEU	13.1
1	Q	13	GLN	13.1
1	F	74	ASN	13.1
1	B	211	LEU	13.1
1	L	107	THR	13.1
1	T	48	THR	13.1
1	A	37	ILE	13.1
1	G	215	MET	13.1
1	A	217	ALA	13.1
1	L	55	MET	13.1
1	M	160	PRO	13.0
1	F	134	ILE	13.0
1	L	139	ASN	13.0
1	I	75	GLU	13.0
1	Q	141	ILE	13.0
1	M	23	TRP	13.0
1	G	75	GLU	13.0
1	P	19	CYS	13.0
1	A	34	PRO	13.0
1	M	170	LYS	13.0
1	D	165	VAL	13.0
1	O	215	MET	13.0
1	O	40	PHE	13.0
1	I	179	GLN	13.0
1	P	182	LYS	13.0
1	B	41	SER	13.0
1	H	197	ASP	13.0
1	L	168	PHE	13.0
1	B	215	MET	13.0
1	M	138	LEU	13.0
1	A	150	ILE	13.0
1	L	34	PRO	13.0
1	O	147	PRO	13.0
1	R	151	LEU	12.9

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Mol	Chain	Res	Type	RSRZ
1	J	190	LEU	12.9
1	I	149	SER	12.9
1	R	75	GLU	12.9
1	K	190	LEU	12.9
1	O	151	LEU	12.9
1	P	206	GLY	12.9
1	A	55	MET	12.9
1	D	75	GLU	12.9
1	K	131	LYS	12.9
1	P	35	GLU	12.9
1	T	41	SER	12.9
1	G	56	LEU	12.9
1	I	128	GLU	12.9
1	P	29	GLU	12.9
1	F	66	MET	12.9
1	P	195	ASN	12.9
1	Q	132	ARG	12.9
1	J	128	GLU	12.9
1	S	62	HIS	12.9
1	C	190	LEU	12.9
1	B	124	ILE	12.8
1	G	188	THR	12.8
1	M	140	LYS	12.8
1	S	184	ALA	12.8
1	M	149	SER	12.8
1	G	71	GLU	12.8
1	S	215	MET	12.8
1	K	144	MET	12.8
1	K	162	ARG	12.8
1	Q	46	GLY	12.8
1	Q	55	MET	12.7
1	E	59	VAL	12.7
1	G	143	ARG	12.7
1	P	170	LYS	12.7
1	P	100	ARG	12.7
1	G	128	GLU	12.7
1	S	41	SER	12.7
1	M	158	LYS	12.7
1	E	214	MET	12.7
1	J	60	GLY	12.7
1	G	192	GLN	12.7
1	P	178	SER	12.7

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Mol	Chain	Res	Type	RSRZ
1	K	186	THR	12.7
1	Q	201	ILE	12.7
1	F	190	LEU	12.7
1	Q	73	ILE	12.6
1	F	60	GLY	12.6
1	N	107	THR	12.6
1	Q	184	ALA	12.6
1	H	176	GLN	12.6
1	T	45	GLU	12.6
1	O	170	LYS	12.6
1	T	21	ASN	12.6
1	F	162	ARG	12.6
1	T	44	SER	12.6
1	E	40	PHE	12.6
1	I	189	LEU	12.6
1	B	75	GLU	12.6
1	C	138	LEU	12.6
1	I	113	GLU	12.6
1	A	2	ILE	12.6
1	S	135	ILE	12.6
1	I	195	ASN	12.5
1	P	30	LYS	12.5
1	M	118	MET	12.5
1	I	62	HIS	12.5
1	D	213	GLU	12.5
1	H	21	ASN	12.5
1	O	50	GLN	12.5
1	I	16	SER	12.5
1	D	101	GLY	12.5
1	O	207	PRO	12.5
1	G	162	ARG	12.5
1	G	178	SER	12.5
1	Q	135	ILE	12.5
1	O	70	LYS	12.5
1	F	213	GLU	12.5
1	L	163	ASP	12.5
1	L	33	SER	12.5
1	P	154	ARG	12.5
1	L	216	THR	12.5
1	D	203	LYS	12.5
1	I	80	TRP	12.5
1	S	130	TYR	12.5

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Mol	Chain	Res	Type	RSRZ
1	H	75	GLU	12.4
1	O	145	TYR	12.4
1	O	77	ALA	12.4
1	B	25	LYS	12.4
1	L	26	VAL	12.4
1	J	141	ILE	12.4
1	N	44	SER	12.4
1	B	13	GLN	12.4
1	L	140	LYS	12.4
1	N	30	LYS	12.4
1	I	26	VAL	12.4
1	R	41	SER	12.4
1	R	99	PRO	12.4
1	B	37	ILE	12.4
1	G	138	LEU	12.4
1	M	175	GLU	12.4
1	P	113	GLU	12.4
1	S	183	ASN	12.4
1	J	53	ASN	12.4
1	L	45	GLU	12.4
1	T	153	ILE	12.4
1	M	54	THR	12.4
1	H	26	VAL	12.4
1	F	37	ILE	12.4
1	B	185	ALA	12.4
1	J	80	TRP	12.3
1	O	176	GLN	12.3
1	T	29	GLU	12.3
1	I	25	LYS	12.3
1	Q	99	PRO	12.3
1	C	127	GLY	12.3
1	T	150	ILE	12.3
1	D	14	ALA	12.3
1	F	65	ALA	12.3
1	A	213	GLU	12.3
1	I	168	PHE	12.3
1	D	189	LEU	12.3
1	N	170	LYS	12.3
1	P	116	GLY	12.3
1	T	25	LYS	12.3
1	D	2	ILE	12.3
1	M	172	LEU	12.3

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Mol	Chain	Res	Type	RSRZ
1	Q	203	LYS	12.3
1	C	160	PRO	12.3
1	B	102	SER	12.3
1	C	120	HIS	12.3
1	R	164	TYR	12.3
1	S	114	GLN	12.3
1	C	162	ARG	12.2
1	G	51	ASP	12.2
1	B	39	MET	12.2
1	F	127	GLY	12.2
1	D	23	TRP	12.2
1	M	13	GLN	12.2
1	E	123	PRO	12.2
1	S	157	PRO	12.2
1	B	140	LYS	12.2
1	L	123	PRO	12.2
1	J	216	THR	12.2
1	T	132	ARG	12.2
1	S	207	PRO	12.2
1	L	100	ARG	12.2
1	I	20	LEU	12.2
1	A	173	ARG	12.2
1	C	172	LEU	12.2
1	N	12	HIS	12.2
1	I	21	ASN	12.2
1	F	75	GLU	12.2
1	B	214	MET	12.2
1	L	2	ILE	12.2
1	Q	215	MET	12.2
1	N	179	GLN	12.1
1	L	154	ARG	12.1
1	D	120	HIS	12.1
1	H	65	ALA	12.1
1	H	144	MET	12.1
1	H	143	ARG	12.1
1	M	134	ILE	12.1
1	O	161	PHE	12.1
1	H	191	VAL	12.1
1	E	60	GLY	12.1
1	Q	41	SER	12.1
1	B	134	ILE	12.1
1	N	150	ILE	12.1

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Mol	Chain	Res	Type	RSRZ
1	F	184	ALA	12.1
1	F	100	ARG	12.1
1	P	193	ASN	12.1
1	K	210	THR	12.1
1	I	99	PRO	12.1
1	J	214	MET	12.1
1	J	107	THR	12.0
1	O	84	HIS	12.0
1	O	60	GLY	12.0
1	M	121	ASN	12.0
1	B	125	PRO	12.0
1	N	186	THR	12.0
1	N	55	MET	12.0
1	P	122	PRO	12.0
1	P	14	ALA	12.0
1	I	217	ALA	12.0
1	H	162	ARG	12.0
1	K	115	ILE	12.0
1	A	15	ILE	12.0
1	I	52	LEU	12.0
1	M	15	ILE	12.0
1	D	100	ARG	12.0
1	C	125	PRO	11.9
1	I	201	ILE	11.9
1	K	188	THR	11.9
1	I	196	PRO	11.9
1	I	24	VAL	11.9
1	I	84	HIS	11.9
1	H	123	PRO	11.9
1	K	20	LEU	11.9
1	A	145	TYR	11.9
1	F	108	THR	11.9
1	P	160	PRO	11.9
1	I	213	GLU	11.9
1	H	136	LEU	11.9
1	K	130	TYR	11.9
1	A	46	GLY	11.9
1	G	216	THR	11.9
1	B	205	LEU	11.9
1	P	140	LYS	11.9
1	G	219	GLN	11.8
1	S	113	GLU	11.8

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Mol	Chain	Res	Type	RSRZ
1	H	170	LYS	11.8
1	N	200	THR	11.8
1	E	42	ALA	11.8
1	L	74	ASN	11.8
1	D	32	PHE	11.8
1	D	216	THR	11.8
1	F	14	ALA	11.8
1	C	150	ILE	11.8
1	L	124	ILE	11.8
1	C	46	GLY	11.8
1	O	216	THR	11.8
1	N	171	THR	11.8
1	D	72	THR	11.8
1	I	215	MET	11.8
1	H	28	GLU	11.8
1	Q	45	GLU	11.8
1	K	134	ILE	11.8
1	A	132	ARG	11.7
1	D	139	ASN	11.7
1	I	15	ILE	11.7
1	R	85	PRO	11.7
1	G	135	ILE	11.7
1	R	144	MET	11.7
1	B	161	PHE	11.7
1	E	213	GLU	11.7
1	A	20	LEU	11.7
1	F	156	GLY	11.7
1	F	207	PRO	11.7
1	N	53	ASN	11.7
1	M	50	GLN	11.7
1	M	56	LEU	11.7
1	D	43	LEU	11.7
1	D	207	PRO	11.7
1	G	70	LYS	11.7
1	M	18	LEU	11.7
1	N	57	ASN	11.7
1	E	143	ARG	11.7
1	B	103	ASP	11.7
1	F	25	LYS	11.7
1	I	126	VAL	11.7
1	J	171	THR	11.7
1	O	126	VAL	11.7

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Mol	Chain	Res	Type	RSRZ
1	B	67	GLN	11.6
1	G	55	MET	11.6
1	I	65	ALA	11.6
1	K	82	ARG	11.6
1	M	145	TYR	11.6
1	B	43	LEU	11.6
1	J	56	LEU	11.6
1	S	81	ASP	11.6
1	A	185	ALA	11.6
1	D	39	MET	11.6
1	A	133	TRP	11.6
1	L	187	GLU	11.6
1	L	184	ALA	11.6
1	E	28	GLU	11.6
1	I	159	GLU	11.6
1	R	213	GLU	11.6
1	H	111	LEU	11.6
1	R	186	THR	11.6
1	L	38	PRO	11.6
1	E	197	ASP	11.6
1	S	105	ALA	11.6
1	L	171	THR	11.6
1	S	17	CYS	11.6
1	J	164	TYR	11.5
1	J	181	VAL	11.5
1	S	189	LEU	11.5
1	L	155	GLN	11.5
1	L	197	ASP	11.5
1	R	67	GLN	11.5
1	R	106	GLY	11.5
1	E	29	GLU	11.5
1	R	173	ARG	11.5
1	A	43	LEU	11.5
1	B	169	TYR	11.5
1	K	74	ASN	11.5
1	H	77	ALA	11.5
1	M	110	THR	11.5
1	E	141	ILE	11.4
1	J	212	GLU	11.4
1	E	124	ILE	11.4
1	O	56	LEU	11.4
1	N	11	VAL	11.4

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Mol	Chain	Res	Type	RSRZ
1	K	129	ILE	11.4
1	Q	173	ARG	11.4
1	S	40	PHE	11.4
1	M	206	GLY	11.4
1	D	12	HIS	11.4
1	G	144	MET	11.4
1	L	211	LEU	11.4
1	F	114	GLN	11.4
1	I	161	PHE	11.4
1	B	61	GLY	11.4
1	F	36	VAL	11.4
1	Q	126	VAL	11.4
1	G	183	ASN	11.4
1	G	117	TRP	11.4
1	H	140	LYS	11.4
1	I	42	ALA	11.4
1	Q	75	GLU	11.4
1	A	206	GLY	11.3
1	B	176	GLN	11.3
1	L	12	HIS	11.3
1	T	176	GLN	11.3
1	B	133	TRP	11.3
1	C	176	GLN	11.3
1	E	104	ILE	11.3
1	K	36	VAL	11.3
1	J	108	THR	11.3
1	R	20	LEU	11.3
1	D	121	ASN	11.3
1	P	112	GLN	11.3
1	H	161	PHE	11.3
1	R	2	ILE	11.3
1	A	151	LEU	11.3
1	S	26	VAL	11.3
1	H	207	PRO	11.3
1	Q	32	PHE	11.3
1	R	62	HIS	11.3
1	S	199	LYS	11.3
1	S	132	ARG	11.3
1	D	119	THR	11.3
1	A	40	PHE	11.2
1	K	133	TRP	11.2
1	M	114	GLN	11.2

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Mol	Chain	Res	Type	RSRZ
1	M	41	SER	11.2
1	C	32	PHE	11.2
1	I	61	GLY	11.2
1	I	106	GLY	11.2
1	L	99	PRO	11.2
1	P	144	MET	11.2
1	E	210	THR	11.2
1	K	72	THR	11.2
1	O	100	ARG	11.2
1	G	57	ASN	11.2
1	T	108	THR	11.2
1	A	64	ALA	11.2
1	B	46	GLY	11.2
1	F	212	GLU	11.2
1	H	43	LEU	11.2
1	K	128	GLU	11.2
1	N	203	LYS	11.2
1	C	44	SER	11.2
1	G	80	TRP	11.2
1	M	44	SER	11.2
1	A	120	HIS	11.2
1	H	45	GLU	11.2
1	I	1	PRO	11.2
1	J	172	LEU	11.2
1	R	48	THR	11.1
1	M	30	LYS	11.1
1	A	202	LEU	11.1
1	D	45	GLU	11.1
1	I	216	THR	11.1
1	N	64	ALA	11.1
1	N	184	ALA	11.1
1	E	20	LEU	11.1
1	C	36	VAL	11.1
1	K	67	GLN	11.1
1	I	202	LEU	11.1
1	I	58	THR	11.1
1	P	53	ASN	11.1
1	K	189	LEU	11.1
1	L	144	MET	11.1
1	A	16	SER	11.1
1	O	42	ALA	11.1
1	Q	67	GLN	11.1

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Mol	Chain	Res	Type	RSRZ
1	K	211	LEU	11.0
1	T	115	ILE	11.0
1	Q	37	ILE	11.0
1	D	123	PRO	11.0
1	F	79	GLU	11.0
1	E	71	GLU	11.0
1	R	55	MET	11.0
1	T	214	MET	11.0
1	H	187	GLU	11.0
1	L	18	LEU	11.0
1	A	127	GLY	11.0
1	H	211	LEU	11.0
1	N	128	GLU	11.0
1	I	17	CYS	11.0
1	L	44	SER	11.0
1	J	109	SER	11.0
1	G	36	VAL	11.0
1	B	152	ASP	11.0
1	L	61	GLY	11.0
1	G	53	ASN	10.9
1	H	73	ILE	10.9
1	B	83	LEU	10.9
1	K	112	GLN	10.9
1	A	13	GLN	10.9
1	G	212	GLU	10.9
1	M	43	LEU	10.9
1	O	208	GLY	10.9
1	Q	162	ARG	10.9
1	G	50	GLN	10.9
1	J	46	GLY	10.9
1	A	80	TRP	10.9
1	Q	44	SER	10.9
1	D	79	GLU	10.9
1	M	150	ILE	10.9
1	F	77	ALA	10.9
1	R	50	GLN	10.9
1	C	42	ALA	10.9
1	G	211	LEU	10.9
1	J	44	SER	10.9
1	J	114	GLN	10.9
1	G	133	TRP	10.8
1	D	114	GLN	10.8

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Mol	Chain	Res	Type	RSRZ
1	C	152	ASP	10.8
1	L	214	MET	10.8
1	B	128	GLU	10.8
1	I	46	GLY	10.8
1	N	130	TYR	10.8
1	P	216	THR	10.8
1	H	190	LEU	10.8
1	C	169	TYR	10.8
1	D	128	GLU	10.8
1	H	169	TYR	10.8
1	L	28	GLU	10.8
1	E	163	ASP	10.8
1	N	16	SER	10.8
1	C	49	PRO	10.8
1	Q	138	LEU	10.8
1	A	184	ALA	10.8
1	I	138	LEU	10.8
1	K	110	THR	10.8
1	O	45	GLU	10.8
1	F	43	LEU	10.8
1	S	24	VAL	10.8
1	B	70	LYS	10.7
1	G	110	THR	10.7
1	O	135	ILE	10.7
1	F	76	GLU	10.7
1	B	11	VAL	10.7
1	T	187	GLU	10.7
1	H	35	GLU	10.7
1	C	113	GLU	10.7
1	A	107	THR	10.7
1	E	175	GLU	10.7
1	P	43	LEU	10.7
1	T	22	ALA	10.7
1	T	55	MET	10.7
1	G	15	ILE	10.7
1	K	120	HIS	10.7
1	M	171	THR	10.7
1	E	70	LYS	10.7
1	Q	21	ASN	10.7
1	I	145	TYR	10.6
1	N	183	ASN	10.6
1	I	197	ASP	10.6

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Mol	Chain	Res	Type	RSRZ
1	P	15	ILE	10.6
1	M	31	ALA	10.6
1	E	140	LYS	10.6
1	T	61	GLY	10.6
1	K	24	VAL	10.6
1	R	147	PRO	10.6
1	T	16	SER	10.6
1	N	34	PRO	10.6
1	O	178	SER	10.6
1	A	139	ASN	10.6
1	F	55	MET	10.6
1	L	80	TRP	10.6
1	P	21	ASN	10.6
1	K	177	ALA	10.6
1	Q	112	GLN	10.6
1	I	11	VAL	10.6
1	E	208	GLY	10.6
1	R	201	ILE	10.6
1	O	102	SER	10.6
1	J	55	MET	10.5
1	K	40	PHE	10.5
1	P	204	ALA	10.5
1	C	41	SER	10.5
1	E	145	TYR	10.5
1	O	33	SER	10.5
1	E	47	ALA	10.5
1	J	48	THR	10.5
1	M	70	LYS	10.5
1	B	16	SER	10.5
1	D	11	VAL	10.5
1	O	43	LEU	10.5
1	R	64	ALA	10.5
1	E	131	LYS	10.5
1	M	154	ARG	10.5
1	T	24	VAL	10.5
1	A	128	GLU	10.5
1	L	188	THR	10.5
1	N	161	PHE	10.5
1	H	134	ILE	10.5
1	C	33	SER	10.4
1	S	206	GLY	10.4
1	K	111	LEU	10.4

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Mol	Chain	Res	Type	RSRZ
1	D	204	ALA	10.4
1	M	144	MET	10.4
1	B	28	GLU	10.4
1	A	54	THR	10.4
1	H	155	GLN	10.4
1	E	133	TRP	10.4
1	H	212	GLU	10.4
1	R	129	ILE	10.4
1	M	39	MET	10.4
1	P	99	PRO	10.4
1	J	24	VAL	10.4
1	A	31	ALA	10.4
1	E	32	PHE	10.4
1	D	179	GLN	10.4
1	J	42	ALA	10.4
1	A	179	GLN	10.4
1	C	45	GLU	10.3
1	R	140	LYS	10.3
1	A	212	GLU	10.3
1	A	207	PRO	10.3
1	N	1	PRO	10.3
1	K	55	MET	10.3
1	K	132	ARG	10.3
1	K	45	GLU	10.3
1	L	72	THR	10.3
1	A	56	LEU	10.3
1	H	135	ILE	10.3
1	O	116	GLY	10.3
1	H	99	PRO	10.3
1	R	101	GLY	10.3
1	C	119	THR	10.3
1	C	83	LEU	10.3
1	J	37	ILE	10.3
1	L	134	ILE	10.3
1	O	148	THR	10.3
1	C	40	PHE	10.3
1	T	85	PRO	10.3
1	H	25	LYS	10.3
1	L	11	VAL	10.3
1	J	99	PRO	10.3
1	S	161	PHE	10.3
1	H	131	LYS	10.3

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Mol	Chain	Res	Type	RSRZ
1	D	57	ASN	10.3
1	B	153	ILE	10.2
1	I	162	ARG	10.2
1	F	180	GLU	10.2
1	T	121	ASN	10.2
1	B	138	LEU	10.2
1	J	73	ILE	10.2
1	L	190	LEU	10.2
1	G	208	GLY	10.2
1	M	183	ASN	10.2
1	T	70	LYS	10.2
1	F	218	CYS	10.2
1	C	143	ARG	10.2
1	D	127	GLY	10.2
1	H	203	LYS	10.2
1	M	75	GLU	10.2
1	N	106	GLY	10.2
1	D	44	SER	10.2
1	M	142	VAL	10.2
1	B	213	GLU	10.2
1	P	45	GLU	10.2
1	M	52	LEU	10.2
1	K	49	PRO	10.2
1	M	42	ALA	10.2
1	R	56	LEU	10.2
1	O	65	ALA	10.2
1	P	63	GLN	10.2
1	L	138	LEU	10.2
1	Q	145	TYR	10.2
1	I	185	ALA	10.2
1	M	105	ALA	10.2
1	F	155	GLN	10.2
1	P	33	SER	10.1
1	K	105	ALA	10.1
1	R	70	LYS	10.1
1	T	37	ILE	10.1
1	G	141	ILE	10.1
1	A	169	TYR	10.1
1	G	18	LEU	10.1
1	N	142	VAL	10.1
1	E	171	THR	10.1
1	M	49	PRO	10.1

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Mol	Chain	Res	Type	RSRZ
1	O	17	CYS	10.1
1	Q	147	PRO	10.1
1	G	109	SER	10.1
1	M	136	LEU	10.1
1	E	146	SER	10.1
1	E	13	GLN	10.1
1	L	15	ILE	10.1
1	S	172	LEU	10.1
1	O	26	VAL	10.1
1	O	61	GLY	10.1
1	B	147	PRO	10.1
1	E	212	GLU	10.0
1	P	150	ILE	10.0
1	H	40	PHE	10.0
1	D	21	ASN	10.0
1	A	186	THR	10.0
1	K	56	LEU	10.0
1	D	140	LYS	10.0
1	A	75	GLU	10.0
1	G	17	CYS	10.0
1	N	129	ILE	10.0
1	T	119	THR	10.0
1	D	17	CYS	10.0
1	B	129	ILE	10.0
1	I	193	ASN	10.0
1	A	84	HIS	10.0
1	C	11	VAL	10.0
1	N	118	MET	10.0
1	H	42	ALA	10.0
1	L	136	LEU	10.0
1	O	52	LEU	10.0
1	B	216	THR	10.0
1	T	170	LYS	10.0
1	T	204	ALA	10.0
1	T	60	GLY	10.0
1	C	135	ILE	10.0
1	M	79	GLU	10.0
1	N	101	GLY	9.9
1	Q	54	THR	9.9
1	I	72	THR	9.9
1	B	111	LEU	9.9
1	Q	16	SER	9.9

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Mol	Chain	Res	Type	RSRZ
1	R	206	GLY	9.9
1	A	99	PRO	9.9
1	J	27	VAL	9.9
1	A	214	MET	9.9
1	S	208	GLY	9.9
1	D	136	LEU	9.9
1	O	106	GLY	9.9
1	C	147	PRO	9.9
1	M	123	PRO	9.9
1	T	125	PRO	9.9
1	P	118	MET	9.9
1	K	213	GLU	9.8
1	A	14	ALA	9.8
1	J	175	GLU	9.8
1	B	36	VAL	9.8
1	T	217	ALA	9.8
1	T	203	LYS	9.8
1	O	193	ASN	9.8
1	F	45	GLU	9.8
1	R	188	THR	9.8
1	E	74	ASN	9.8
1	M	61	GLY	9.8
1	G	103	ASP	9.8
1	F	46	GLY	9.8
1	K	18	LEU	9.8
1	K	171	THR	9.8
1	E	152	ASP	9.8
1	F	145	TYR	9.7
1	C	25	LYS	9.7
1	B	219	GLN	9.7
1	N	188	THR	9.7
1	S	57	ASN	9.7
1	P	210	THR	9.7
1	P	146	SER	9.7
1	L	16	SER	9.7
1	M	45	GLU	9.7
1	A	25	LYS	9.7
1	Q	110	THR	9.7
1	K	209	ALA	9.7
1	P	207	PRO	9.7
1	I	27	VAL	9.7
1	F	33	SER	9.7

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Mol	Chain	Res	Type	RSRZ
1	K	52	LEU	9.7
1	A	30	LYS	9.7
1	B	54	THR	9.7
1	L	198	CYS	9.6
1	Q	176	GLN	9.6
1	D	65	ALA	9.6
1	S	141	ILE	9.6
1	N	82	ARG	9.6
1	L	169	TYR	9.6
1	T	177	ALA	9.6
1	B	35	GLU	9.6
1	O	210	THR	9.6
1	C	148	THR	9.6
1	T	12	HIS	9.6
1	B	148	THR	9.6
1	Q	107	THR	9.6
1	K	42	ALA	9.6
1	D	61	GLY	9.6
1	J	118	MET	9.6
1	L	62	HIS	9.6
1	Q	74	ASN	9.6
1	A	57	ASN	9.6
1	K	114	GLN	9.6
1	E	200	THR	9.6
1	D	28	GLU	9.6
1	D	99	PRO	9.6
1	A	48	THR	9.6
1	E	190	LEU	9.6
1	S	66	MET	9.6
1	D	70	LYS	9.5
1	T	191	VAL	9.5
1	J	194	ALA	9.5
1	N	207	PRO	9.5
1	F	44	SER	9.5
1	S	39	MET	9.5
1	F	18	LEU	9.5
1	F	56	LEU	9.5
1	I	180	GLU	9.5
1	O	190	LEU	9.5
1	O	218	CYS	9.5
1	D	56	LEU	9.5
1	Q	49	PRO	9.5

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Mol	Chain	Res	Type	RSRZ
1	S	140	LYS	9.5
1	I	188	THR	9.5
1	J	71	GLU	9.5
1	M	108	THR	9.5
1	E	45	GLU	9.5
1	G	35	GLU	9.5
1	Q	39	MET	9.5
1	M	151	LEU	9.5
1	D	49	PRO	9.5
1	T	111	LEU	9.5
1	P	27	VAL	9.5
1	O	189	LEU	9.4
1	H	188	THR	9.4
1	P	71	GLU	9.4
1	N	42	ALA	9.4
1	N	136	LEU	9.4
1	F	39	MET	9.4
1	A	137	GLY	9.4
1	O	28	GLU	9.4
1	N	27	VAL	9.4
1	A	178	SER	9.4
1	T	147	PRO	9.4
1	H	30	LYS	9.4
1	H	2	ILE	9.4
1	I	207	PRO	9.4
1	J	176	GLN	9.4
1	C	23	TRP	9.4
1	K	151	LEU	9.4
1	C	115	ILE	9.4
1	O	105	ALA	9.4
1	E	218	CYS	9.4
1	L	14	ALA	9.4
1	E	68	MET	9.4
1	J	140	LYS	9.4
1	L	131	LYS	9.4
1	Q	154	ARG	9.4
1	Q	170	LYS	9.4
1	F	202	LEU	9.4
1	N	13	GLN	9.4
1	P	163	ASP	9.4
1	C	55	MET	9.4
1	E	14	ALA	9.3

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Mol	Chain	Res	Type	RSRZ
1	O	134	ILE	9.3
1	B	197	ASP	9.3
1	I	190	LEU	9.3
1	J	180	GLU	9.3
1	Q	70	LYS	9.3
1	M	100	ARG	9.3
1	C	184	ALA	9.3
1	P	217	ALA	9.3
1	Q	109	SER	9.3
1	T	47	ALA	9.3
1	D	58	THR	9.3
1	K	122	PRO	9.3
1	M	72	THR	9.3
1	M	122	PRO	9.3
1	M	73	ILE	9.3
1	S	44	SER	9.3
1	F	20	LEU	9.3
1	T	82	ARG	9.3
1	E	211	LEU	9.3
1	B	33	SER	9.3
1	K	160	PRO	9.3
1	B	201	ILE	9.3
1	H	209	ALA	9.3
1	K	41	SER	9.3
1	H	141	ILE	9.3
1	H	137	GLY	9.3
1	N	52	LEU	9.3
1	E	76	GLU	9.2
1	H	167	ARG	9.2
1	J	17	CYS	9.2
1	Q	14	ALA	9.2
1	R	42	ALA	9.2
1	S	48	THR	9.2
1	R	18	LEU	9.2
1	D	85	PRO	9.2
1	B	139	ASN	9.2
1	C	13	GLN	9.2
1	C	20	LEU	9.2
1	I	206	GLY	9.2
1	K	17	CYS	9.2
1	L	47	ALA	9.2
1	H	213	GLU	9.2

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Mol	Chain	Res	Type	RSRZ
1	O	181	VAL	9.2
1	Q	119	THR	9.2
1	S	69	LEU	9.2
1	A	24	VAL	9.2
1	K	108	THR	9.2
1	L	146	SER	9.2
1	G	34	PRO	9.2
1	S	38	PRO	9.2
1	Q	40	PHE	9.2
1	P	13	GLN	9.1
1	G	16	SER	9.1
1	S	12	HIS	9.1
1	L	106	GLY	9.1
1	N	194	ALA	9.1
1	G	158	LYS	9.1
1	C	80	TRP	9.1
1	I	187	GLU	9.1
1	J	191	VAL	9.1
1	L	213	GLU	9.1
1	A	45	GLU	9.1
1	E	52	LEU	9.1
1	O	18	LEU	9.1
1	I	208	GLY	9.1
1	K	78	ALA	9.1
1	O	155	GLN	9.1
1	S	61	GLY	9.1
1	J	18	LEU	9.1
1	H	150	ILE	9.1
1	D	62	HIS	9.1
1	M	120	HIS	9.1
1	Q	43	LEU	9.1
1	P	175	GLU	9.1
1	G	177	ALA	9.1
1	H	82	ARG	9.0
1	L	36	VAL	9.0
1	M	189	LEU	9.0
1	A	131	LYS	9.0
1	I	134	ILE	9.0
1	E	115	ILE	9.0
1	H	52	LEU	9.0
1	E	192	GLN	9.0
1	J	134	ILE	9.0

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Mol	Chain	Res	Type	RSRZ
1	J	43	LEU	9.0
1	R	103	ASP	9.0
1	F	173	ARG	9.0
1	K	124	ILE	9.0
1	C	77	ALA	9.0
1	Q	198	CYS	9.0
1	J	160	PRO	9.0
1	O	20	LEU	9.0
1	B	107	THR	9.0
1	T	183	ASN	9.0
1	N	40	PHE	9.0
1	E	22	ALA	9.0
1	Q	113	GLU	9.0
1	I	219	GLN	9.0
1	P	64	ALA	9.0
1	P	74	ASN	8.9
1	C	56	LEU	8.9
1	P	127	GLY	8.9
1	S	160	PRO	8.9
1	S	20	LEU	8.9
1	E	195	ASN	8.9
1	O	183	ASN	8.9
1	E	17	CYS	8.9
1	I	39	MET	8.9
1	D	172	LEU	8.9
1	I	121	ASN	8.9
1	Q	136	LEU	8.9
1	K	154	ARG	8.9
1	N	74	ASN	8.9
1	J	45	GLU	8.9
1	D	160	PRO	8.9
1	E	62	HIS	8.9
1	E	207	PRO	8.9
1	F	111	LEU	8.9
1	I	63	GLN	8.9
1	F	183	ASN	8.8
1	D	181	VAL	8.8
1	S	151	LEU	8.8
1	P	36	VAL	8.8
1	A	100	ARG	8.8
1	D	71	GLU	8.8
1	M	62	HIS	8.8

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Mol	Chain	Res	Type	RSRZ
1	O	29	GLU	8.8
1	Q	23	TRP	8.8
1	S	137	GLY	8.8
1	M	119	THR	8.8
1	Q	185	ALA	8.8
1	R	33	SER	8.8
1	F	85	PRO	8.8
1	S	152	ASP	8.8
1	O	23	TRP	8.8
1	M	1	PRO	8.8
1	T	196	PRO	8.8
1	H	110	THR	8.8
1	T	142	VAL	8.8
1	M	2	ILE	8.8
1	M	60	GLY	8.7
1	O	21	ASN	8.7
1	B	40	PHE	8.7
1	N	99	PRO	8.7
1	I	2	ILE	8.7
1	P	70	LYS	8.7
1	T	198	CYS	8.7
1	G	64	ALA	8.7
1	N	211	LEU	8.7
1	R	84	HIS	8.7
1	C	16	SER	8.7
1	R	126	VAL	8.7
1	E	113	GLU	8.7
1	B	52	LEU	8.7
1	M	135	ILE	8.7
1	R	145	TYR	8.7
1	B	19	CYS	8.7
1	D	131	LYS	8.7
1	N	208	GLY	8.7
1	O	136	LEU	8.7
1	R	24	VAL	8.7
1	C	84	HIS	8.7
1	Q	125	PRO	8.7
1	E	182	LYS	8.7
1	G	67	GLN	8.7
1	K	191	VAL	8.7
1	P	184	ALA	8.7
1	M	168	PHE	8.7

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Mol	Chain	Res	Type	RSRZ
1	K	57	ASN	8.7
1	N	126	VAL	8.7
1	M	152	ASP	8.6
1	H	158	LYS	8.6
1	B	60	GLY	8.6
1	H	119	THR	8.6
1	M	191	VAL	8.6
1	R	22	ALA	8.6
1	H	127	GLY	8.6
1	S	118	MET	8.6
1	D	176	GLN	8.6
1	M	32	PHE	8.6
1	I	144	MET	8.6
1	B	38	PRO	8.6
1	F	157	PRO	8.6
1	T	79	GLU	8.6
1	I	140	LYS	8.6
1	L	21	ASN	8.6
1	A	101	GLY	8.6
1	T	131	LYS	8.6
1	A	138	LEU	8.6
1	G	136	LEU	8.6
1	E	176	GLN	8.6
1	L	29	GLU	8.6
1	D	156	GLY	8.6
1	R	192	GLN	8.6
1	H	34	PRO	8.6
1	K	140	LYS	8.6
1	H	48	THR	8.6
1	R	175	GLU	8.6
1	O	83	LEU	8.6
1	S	60	GLY	8.5
1	C	52	LEU	8.5
1	O	174	ALA	8.5
1	T	36	VAL	8.5
1	K	169	TYR	8.5
1	T	99	PRO	8.5
1	D	29	GLU	8.5
1	B	77	ALA	8.5
1	R	193	ASN	8.5
1	D	73	ILE	8.5
1	Q	65	ALA	8.5

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Mol	Chain	Res	Type	RSRZ
1	Q	167	ARG	8.5
1	T	46	GLY	8.5
1	G	40	PHE	8.5
1	E	23	TRP	8.5
1	K	218	CYS	8.5
1	F	210	THR	8.5
1	H	122	PRO	8.5
1	J	31	ALA	8.5
1	N	45	GLU	8.5
1	C	186	THR	8.5
1	G	69	LEU	8.5
1	O	127	GLY	8.5
1	C	57	ASN	8.5
1	T	57	ASN	8.5
1	D	26	VAL	8.5
1	D	50	GLN	8.5
1	S	68	MET	8.5
1	O	80	TRP	8.5
1	L	25	LYS	8.5
1	B	184	ALA	8.5
1	L	65	ALA	8.5
1	S	75	GLU	8.5
1	F	175	GLU	8.5
1	B	174	ALA	8.5
1	E	37	ILE	8.5
1	O	66	MET	8.4
1	L	121	ASN	8.4
1	K	81	ASP	8.4
1	N	120	HIS	8.4
1	B	121	ASN	8.4
1	D	149	SER	8.4
1	L	210	THR	8.4
1	O	14	ALA	8.4
1	Q	56	LEU	8.4
1	S	19	CYS	8.4
1	R	189	LEU	8.4
1	S	156	GLY	8.4
1	T	109	SER	8.4
1	K	196	PRO	8.4
1	H	66	MET	8.4
1	A	42	ALA	8.4
1	G	190	LEU	8.4

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Mol	Chain	Res	Type	RSRZ
1	D	20	LEU	8.4
1	I	175	GLU	8.4
1	K	43	LEU	8.4
1	H	208	GLY	8.4
1	B	166	ASP	8.4
1	Q	64	ALA	8.3
1	N	193	ASN	8.3
1	A	198	CYS	8.3
1	J	213	GLU	8.3
1	I	29	GLU	8.3
1	C	153	ILE	8.3
1	B	32	PHE	8.3
1	R	184	ALA	8.3
1	L	161	PHE	8.3
1	N	43	LEU	8.3
1	C	137	GLY	8.3
1	K	123	PRO	8.3
1	N	192	GLN	8.3
1	C	133	TRP	8.3
1	K	197	ASP	8.3
1	L	77	ALA	8.3
1	S	32	PHE	8.3
1	D	126	VAL	8.3
1	S	127	GLY	8.3
1	C	183	ASN	8.3
1	C	18	LEU	8.3
1	C	215	MET	8.3
1	S	168	PHE	8.3
1	N	104	ILE	8.3
1	P	62	HIS	8.3
1	D	146	SER	8.2
1	O	163	ASP	8.2
1	I	32	PHE	8.2
1	E	179	GLN	8.2
1	D	205	LEU	8.2
1	P	156	GLY	8.2
1	S	176	GLN	8.2
1	J	14	ALA	8.2
1	Q	155	GLN	8.2
1	C	17	CYS	8.2
1	R	16	SER	8.2
1	H	61	GLY	8.2

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Mol	Chain	Res	Type	RSRZ
1	E	44	SER	8.2
1	O	175	GLU	8.2
1	T	15	ILE	8.2
1	J	202	LEU	8.2
1	D	77	ALA	8.2
1	L	175	GLU	8.2
1	H	151	LEU	8.2
1	R	72	THR	8.2
1	F	201	ILE	8.1
1	R	152	ASP	8.1
1	J	102	SER	8.1
1	M	210	THR	8.1
1	H	14	ALA	8.1
1	I	60	GLY	8.1
1	J	103	ASP	8.1
1	N	217	ALA	8.1
1	D	15	ILE	8.1
1	F	12	HIS	8.1
1	T	201	ILE	8.1
1	F	154	ARG	8.1
1	J	52	LEU	8.1
1	N	212	GLU	8.1
1	D	208	GLY	8.1
1	F	149	SER	8.1
1	K	65	ALA	8.1
1	J	218	CYS	8.1
1	O	112	GLN	8.1
1	S	33	SER	8.1
1	H	104	ILE	8.1
1	B	170	LYS	8.1
1	C	14	ALA	8.1
1	A	33	SER	8.1
1	J	197	ASP	8.1
1	G	111	LEU	8.1
1	D	84	HIS	8.1
1	Q	158	LYS	8.1
1	F	166	ASP	8.0
1	O	150	ILE	8.0
1	S	124	ILE	8.0
1	G	2	ILE	8.0
1	H	33	SER	8.0
1	O	167	ARG	8.0

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Mol	Chain	Res	Type	RSRZ
1	Q	33	SER	8.0
1	D	104	ILE	8.0
1	E	121	ASN	8.0
1	T	13	GLN	8.0
1	K	22	ALA	8.0
1	C	43	LEU	8.0
1	T	163	ASP	8.0
1	F	138	LEU	8.0
1	S	122	PRO	8.0
1	S	74	ASN	8.0
1	K	147	PRO	8.0
1	S	100	ARG	8.0
1	C	161	PHE	8.0
1	P	54	THR	7.9
1	G	82	ARG	7.9
1	N	123	PRO	7.9
1	F	150	ILE	7.9
1	S	154	ARG	7.9
1	T	158	LYS	7.9
1	H	214	MET	7.9
1	L	32	PHE	7.9
1	N	147	PRO	7.9
1	R	54	THR	7.9
1	P	165	VAL	7.9
1	E	54	THR	7.9
1	R	137	GLY	7.9
1	M	57	ASN	7.9
1	A	191	VAL	7.9
1	G	165	VAL	7.9
1	O	179	GLN	7.9
1	A	124	ILE	7.9
1	N	189	LEU	7.9
1	S	27	VAL	7.9
1	S	23	TRP	7.9
1	B	208	GLY	7.9
1	E	144	MET	7.9
1	Q	111	LEU	7.9
1	L	176	GLN	7.8
1	Q	18	LEU	7.8
1	F	169	TYR	7.8
1	K	54	THR	7.8
1	L	24	VAL	7.8

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Mol	Chain	Res	Type	RSRZ
1	P	85	PRO	7.8
1	P	162	ARG	7.8
1	I	107	THR	7.8
1	R	212	GLU	7.8
1	L	17	CYS	7.8
1	S	76	GLU	7.8
1	L	64	ALA	7.8
1	C	111	LEU	7.8
1	H	216	THR	7.8
1	M	193	ASN	7.8
1	L	206	GLY	7.8
1	Q	191	VAL	7.8
1	G	48	THR	7.8
1	O	121	ASN	7.8
1	S	149	SER	7.8
1	B	115	ILE	7.8
1	G	160	PRO	7.8
1	J	22	ALA	7.8
1	O	197	ASP	7.8
1	R	32	PHE	7.8
1	Q	66	MET	7.8
1	D	33	SER	7.8
1	R	138	LEU	7.8
1	S	164	TYR	7.8
1	S	45	GLU	7.8
1	H	71	GLU	7.8
1	R	14	ALA	7.8
1	N	158	LYS	7.8
1	F	15	ILE	7.8
1	B	82	ARG	7.7
1	T	78	ALA	7.7
1	R	43	LEU	7.7
1	G	21	ASN	7.7
1	G	191	VAL	7.7
1	S	209	ALA	7.7
1	P	77	ALA	7.7
1	I	18	LEU	7.7
1	S	198	CYS	7.7
1	E	16	SER	7.7
1	F	123	PRO	7.7
1	H	189	LEU	7.7
1	P	114	GLN	7.7

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Mol	Chain	Res	Type	RSRZ
1	S	21	ASN	7.7
1	R	31	ALA	7.7
1	R	217	ALA	7.7
1	T	155	GLN	7.7
1	Q	36	VAL	7.7
1	A	29	GLU	7.7
1	S	120	HIS	7.7
1	L	164	TYR	7.7
1	A	110	THR	7.7
1	H	17	CYS	7.7
1	M	124	ILE	7.6
1	O	12	HIS	7.7
1	T	171	THR	7.7
1	L	102	SER	7.6
1	L	145	TYR	7.6
1	J	63	GLN	7.6
1	N	178	SER	7.6
1	H	168	PHE	7.6
1	I	33	SER	7.6
1	H	46	GLY	7.6
1	N	169	TYR	7.6
1	E	201	ILE	7.6
1	K	176	GLN	7.6
1	P	108	THR	7.6
1	N	202	LEU	7.6
1	O	169	TYR	7.6
1	R	35	GLU	7.6
1	A	76	GLU	7.6
1	M	126	VAL	7.6
1	F	32	PHE	7.6
1	K	29	GLU	7.6
1	P	76	GLU	7.6
1	T	205	LEU	7.6
1	R	81	ASP	7.6
1	R	146	SER	7.6
1	E	46	GLY	7.6
1	J	32	PHE	7.6
1	R	44	SER	7.6
1	B	71	GLU	7.6
1	T	133	TRP	7.6
1	B	66	MET	7.6
1	N	21	ASN	7.6

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Mol	Chain	Res	Type	RSRZ
1	G	63	GLN	7.5
1	A	143	ARG	7.5
1	F	204	ALA	7.5
1	S	181	VAL	7.5
1	E	107	THR	7.5
1	S	203	LYS	7.5
1	K	187	GLU	7.5
1	S	53	ASN	7.5
1	A	156	GLY	7.5
1	I	22	ALA	7.5
1	J	21	ASN	7.5
1	R	39	MET	7.5
1	B	136	LEU	7.5
1	P	136	LEU	7.5
1	T	59	VAL	7.5
1	O	15	ILE	7.5
1	J	167	ARG	7.5
1	I	118	MET	7.5
1	B	59	VAL	7.5
1	B	198	CYS	7.5
1	G	146	SER	7.5
1	S	109	SER	7.5
1	K	150	ILE	7.5
1	M	164	TYR	7.5
1	N	182	LYS	7.5
1	R	37	ILE	7.5
1	P	16	SER	7.5
1	J	116	GLY	7.4
1	N	145	TYR	7.4
1	T	141	ILE	7.4
1	T	81	ASP	7.4
1	I	116	GLY	7.4
1	P	82	ARG	7.4
1	Q	82	ARG	7.4
1	D	1	PRO	7.4
1	F	187	GLU	7.4
1	M	83	LEU	7.4
1	D	82	ARG	7.4
1	K	161	PHE	7.4
1	G	28	GLU	7.4
1	I	127	GLY	7.4
1	D	68	MET	7.4

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Mol	Chain	Res	Type	RSRZ
1	D	74	ASN	7.4
1	I	82	ARG	7.4
1	D	38	PRO	7.4
1	S	115	ILE	7.4
1	C	136	LEU	7.4
1	D	122	PRO	7.4
1	H	13	GLN	7.4
1	E	158	LYS	7.4
1	F	195	ASN	7.4
1	T	149	SER	7.4
1	A	136	LEU	7.4
1	H	70	LYS	7.4
1	F	208	GLY	7.4
1	Q	42	ALA	7.4
1	S	159	GLU	7.4
1	M	59	VAL	7.4
1	S	79	GLU	7.4
1	R	23	TRP	7.4
1	B	119	THR	7.4
1	H	62	HIS	7.3
1	N	185	ALA	7.4
1	S	16	SER	7.3
1	O	107	THR	7.3
1	D	30	LYS	7.3
1	J	33	SER	7.3
1	G	29	GLU	7.3
1	B	108	THR	7.3
1	G	202	LEU	7.3
1	L	151	LEU	7.3
1	I	101	GLY	7.3
1	Q	15	ILE	7.3
1	T	64	ALA	7.3
1	B	24	VAL	7.3
1	J	196	PRO	7.3
1	K	127	GLY	7.3
1	I	14	ALA	7.3
1	L	204	ALA	7.3
1	D	148	THR	7.2
1	Q	19	CYS	7.2
1	D	214	MET	7.2
1	M	25	LYS	7.2
1	J	205	LEU	7.2

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Mol	Chain	Res	Type	RSRZ
1	H	194	ALA	7.2
1	D	138	LEU	7.2
1	B	190	LEU	7.2
1	F	116	GLY	7.2
1	Q	144	MET	7.2
1	B	62	HIS	7.2
1	T	80	TRP	7.2
1	D	24	VAL	7.2
1	D	147	PRO	7.2
1	F	120	HIS	7.2
1	K	100	ARG	7.2
1	R	143	ARG	7.2
1	S	192	GLN	7.2
1	B	74	ASN	7.2
1	E	15	ILE	7.2
1	B	168	PHE	7.2
1	C	62	HIS	7.2
1	S	165	VAL	7.2
1	L	199	LYS	7.2
1	C	54	THR	7.1
1	H	60	GLY	7.1
1	S	56	LEU	7.1
1	M	207	PRO	7.1
1	D	54	THR	7.1
1	E	83	LEU	7.1
1	H	44	SER	7.1
1	F	38	PRO	7.1
1	T	136	LEU	7.1
1	A	1	PRO	7.1
1	Q	180	GLU	7.1
1	T	185	ALA	7.1
1	F	110	THR	7.1
1	N	33	SER	7.1
1	D	159	GLU	7.1
1	H	78	ALA	7.1
1	C	102	SER	7.1
1	C	73	ILE	7.1
1	F	188	THR	7.1
1	H	49	PRO	7.1
1	A	23	TRP	7.1
1	B	172	LEU	7.1
1	I	85	PRO	7.1

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Mol	Chain	Res	Type	RSRZ
1	O	36	VAL	7.1
1	F	29	GLU	7.1
1	L	48	THR	7.1
1	O	13	GLN	7.1
1	H	204	ALA	7.1
1	O	109	SER	7.1
1	H	166	ASP	7.1
1	F	54	THR	7.1
1	C	171	THR	7.1
1	R	209	ALA	7.1
1	L	73	ILE	7.0
1	L	150	ILE	7.0
1	K	15	ILE	7.0
1	Q	108	THR	7.0
1	B	49	PRO	7.0
1	L	207	PRO	7.0
1	T	179	GLN	7.0
1	J	124	ILE	7.0
1	P	137	GLY	7.0
1	Q	157	PRO	7.0
1	C	61	GLY	7.0
1	G	1	PRO	7.0
1	C	209	ALA	7.0
1	O	160	PRO	7.0
1	P	38	PRO	7.0
1	E	82	ARG	7.0
1	C	165	VAL	7.0
1	I	76	GLU	7.0
1	D	209	ALA	7.0
1	P	161	PHE	7.0
1	E	126	VAL	7.0
1	G	125	PRO	7.0
1	J	159	GLU	7.0
1	M	153	ILE	7.0
1	F	189	LEU	6.9
1	B	14	ALA	6.9
1	K	157	PRO	6.9
1	F	178	SER	6.9
1	S	147	PRO	6.9
1	B	144	MET	6.9
1	P	107	THR	6.9
1	D	133	TRP	6.9

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Mol	Chain	Res	Type	RSRZ
1	D	116	GLY	6.9
1	F	105	ALA	6.9
1	H	29	GLU	6.9
1	H	101	GLY	6.9
1	C	145	TYR	6.9
1	P	23	TRP	6.9
1	Q	209	ALA	6.9
1	R	60	GLY	6.9
1	S	15	ILE	6.9
1	B	79	GLU	6.9
1	B	202	LEU	6.8
1	M	139	ASN	6.8
1	E	148	THR	6.8
1	R	73	ILE	6.8
1	N	2	ILE	6.8
1	C	37	ILE	6.8
1	C	149	SER	6.8
1	B	114	GLN	6.8
1	G	77	ALA	6.8
1	G	214	MET	6.8
1	E	170	LYS	6.8
1	R	68	MET	6.8
1	K	71	GLU	6.8
1	B	15	ILE	6.8
1	G	189	LEU	6.8
1	K	119	THR	6.8
1	B	69	LEU	6.8
1	E	194	ALA	6.8
1	O	137	GLY	6.8
1	M	22	ALA	6.8
1	C	39	MET	6.8
1	C	71	GLU	6.8
1	E	2	ILE	6.8
1	I	194	ALA	6.8
1	N	20	LEU	6.8
1	R	150	ILE	6.8
1	H	196	PRO	6.8
1	N	153	ILE	6.8
1	N	155	GLN	6.7
1	T	54	THR	6.7
1	O	76	GLU	6.7
1	N	114	GLN	6.7

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Mol	Chain	Res	Type	RSRZ
1	N	146	SER	6.7
1	I	19	CYS	6.7
1	M	111	LEU	6.7
1	O	49	PRO	6.7
1	G	54	THR	6.7
1	C	82	ARG	6.7
1	G	85	PRO	6.7
1	J	112	GLN	6.7
1	L	120	HIS	6.7
1	F	104	ILE	6.7
1	N	143	ARG	6.7
1	H	56	LEU	6.7
1	O	25	LYS	6.7
1	S	205	LEU	6.7
1	B	218	CYS	6.7
1	G	72	THR	6.7
1	L	23	TRP	6.7
1	O	55	MET	6.7
1	C	204	ALA	6.7
1	G	152	ASP	6.7
1	K	106	GLY	6.7
1	T	77	ALA	6.7
1	P	31	ALA	6.6
1	O	59	VAL	6.6
1	D	64	ALA	6.6
1	H	20	LEU	6.6
1	R	102	SER	6.6
1	T	71	GLU	6.6
1	F	148	THR	6.6
1	G	119	THR	6.6
1	B	160	PRO	6.6
1	E	196	PRO	6.6
1	P	124	ILE	6.6
1	D	118	MET	6.6
1	Q	35	GLU	6.6
1	R	113	GLU	6.6
1	C	142	VAL	6.6
1	M	198	CYS	6.6
1	E	122	PRO	6.6
1	L	68	MET	6.6
1	F	57	ASN	6.6
1	P	202	LEU	6.6

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Mol	Chain	Res	Type	RSRZ
1	R	47	ALA	6.6
1	N	122	PRO	6.6
1	F	28	GLU	6.6
1	I	136	LEU	6.6
1	Q	168	PHE	6.6
1	A	123	PRO	6.6
1	I	139	ASN	6.6
1	O	122	PRO	6.6
1	P	215	MET	6.6
1	G	20	LEU	6.6
1	J	168	PHE	6.6
1	Q	79	GLU	6.6
1	L	46	GLY	6.6
1	L	108	THR	6.6
1	N	116	GLY	6.6
1	P	208	GLY	6.6
1	N	113	GLU	6.6
1	Q	219	GLN	6.6
1	L	118	MET	6.6
1	M	37	ILE	6.6
1	M	201	ILE	6.6
1	P	218	CYS	6.6
1	A	135	ILE	6.5
1	N	144	MET	6.5
1	K	63	GLN	6.5
1	O	68	MET	6.5
1	N	196	PRO	6.5
1	D	16	SER	6.5
1	F	59	VAL	6.5
1	J	137	GLY	6.5
1	K	62	HIS	6.5
1	I	200	THR	6.5
1	J	177	ALA	6.5
1	S	211	LEU	6.5
1	I	77	ALA	6.5
1	O	72	THR	6.5
1	E	155	GLN	6.5
1	C	213	GLU	6.5
1	L	81	ASP	6.5
1	S	18	LEU	6.5
1	L	56	LEU	6.5
1	O	202	LEU	6.5

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Mol	Chain	Res	Type	RSRZ
1	B	58	THR	6.5
1	K	163	ASP	6.5
1	B	44	SER	6.5
1	E	30	LYS	6.5
1	M	36	VAL	6.5
1	C	15	ILE	6.5
1	D	199	LYS	6.5
1	O	188	THR	6.5
1	R	25	LYS	6.5
1	B	143	ARG	6.5
1	H	182	LYS	6.5
1	G	181	VAL	6.5
1	E	138	LEU	6.5
1	H	23	TRP	6.5
1	A	38	PRO	6.4
1	A	216	THR	6.4
1	R	28	GLU	6.4
1	A	63	GLN	6.4
1	G	12	HIS	6.4
1	T	72	THR	6.4
1	B	12	HIS	6.4
1	E	85	PRO	6.4
1	O	204	ALA	6.4
1	L	126	VAL	6.4
1	G	24	VAL	6.4
1	L	160	PRO	6.4
1	B	73	ILE	6.4
1	Q	52	LEU	6.4
1	O	219	GLN	6.4
1	A	61	GLY	6.4
1	H	64	ALA	6.4
1	A	83	LEU	6.4
1	A	154	ARG	6.4
1	M	199	LYS	6.4
1	T	32	PHE	6.4
1	K	149	SER	6.4
1	G	33	SER	6.3
1	C	217	ALA	6.3
1	O	196	PRO	6.3
1	E	142	VAL	6.3
1	J	15	ILE	6.3
1	E	111	LEU	6.3

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Mol	Chain	Res	Type	RSRZ
1	R	115	ILE	6.3
1	B	80	TRP	6.3
1	S	37	ILE	6.3
1	J	211	LEU	6.3
1	K	34	PRO	6.3
1	J	104	ILE	6.3
1	O	185	ALA	6.3
1	L	22	ALA	6.3
1	I	70	LYS	6.3
1	T	113	GLU	6.3
1	P	34	PRO	6.3
1	G	121	ASN	6.3
1	L	58	THR	6.3
1	Q	116	GLY	6.3
1	T	74	ASN	6.3
1	R	45	GLU	6.3
1	B	26	VAL	6.3
1	L	200	THR	6.3
1	F	26	VAL	6.2
1	L	212	GLU	6.2
1	O	41	SER	6.2
1	G	150	ILE	6.2
1	E	149	SER	6.2
1	E	191	VAL	6.2
1	M	117	TRP	6.2
1	J	121	ASN	6.2
1	K	73	ILE	6.2
1	Q	72	THR	6.2
1	M	104	ILE	6.2
1	L	179	GLN	6.2
1	R	123	PRO	6.2
1	K	12	HIS	6.2
1	K	217	ALA	6.2
1	G	19	CYS	6.2
1	I	151	LEU	6.2
1	C	60	GLY	6.2
1	T	69	LEU	6.2
1	N	216	THR	6.2
1	F	62	HIS	6.2
1	B	18	LEU	6.1
1	G	23	TRP	6.2
1	K	118	MET	6.1

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Mol	Chain	Res	Type	RSRZ
1	R	136	LEU	6.1
1	Q	153	ILE	6.1
1	E	34	PRO	6.1
1	A	163	ASP	6.1
1	K	156	GLY	6.1
1	L	70	LYS	6.1
1	P	196	PRO	6.1
1	G	11	VAL	6.1
1	J	148	THR	6.1
1	T	128	GLU	6.1
1	H	154	ARG	6.1
1	T	167	ARG	6.1
1	G	127	GLY	6.1
1	M	68	MET	6.1
1	E	99	PRO	6.1
1	I	43	LEU	6.1
1	K	23	TRP	6.1
1	L	148	THR	6.1
1	J	143	ARG	6.1
1	G	123	PRO	6.1
1	O	206	GLY	6.1
1	B	123	PRO	6.1
1	M	34	PRO	6.1
1	R	157	PRO	6.1
1	K	199	LYS	6.1
1	I	37	ILE	6.1
1	E	79	GLU	6.1
1	G	66	MET	6.1
1	H	55	MET	6.1
1	P	213	GLU	6.1
1	Q	71	GLU	6.1
1	P	201	ILE	6.1
1	K	113	GLU	6.1
1	S	64	ALA	6.1
1	M	182	LYS	6.1
1	K	198	CYS	6.1
1	H	47	ALA	6.1
1	P	143	ARG	6.0
1	F	151	LEU	6.0
1	H	201	ILE	6.0
1	A	201	ILE	6.0
1	C	118	MET	6.0

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Mol	Chain	Res	Type	RSRZ
1	T	114	GLN	6.0
1	G	159	GLU	6.0
1	S	55	MET	6.0
1	T	178	SER	6.0
1	G	201	ILE	6.0
1	L	195	ASN	6.0
1	L	114	GLN	6.0
1	I	59	VAL	6.0
1	B	29	GLU	6.0
1	R	49	PRO	6.0
1	E	132	ARG	6.0
1	R	77	ALA	6.0
1	H	116	GLY	6.0
1	B	120	HIS	6.0
1	O	58	THR	6.0
1	G	118	MET	6.0
1	E	19	CYS	6.0
1	C	114	GLN	6.0
1	H	63	GLN	6.0
1	D	18	LEU	6.0
1	M	133	TRP	5.9
1	M	24	VAL	5.9
1	R	27	VAL	5.9
1	Q	204	ALA	5.9
1	D	174	ALA	5.9
1	D	191	VAL	5.9
1	T	154	ARG	5.9
1	L	54	THR	5.9
1	C	173	ARG	5.9
1	E	156	GLY	5.9
1	T	117	TRP	5.9
1	N	84	HIS	5.9
1	R	52	LEU	5.9
1	K	158	LYS	5.9
1	L	30	LYS	5.9
1	P	171	THR	5.9
1	D	196	PRO	5.9
1	O	16	SER	5.9
1	A	180	GLU	5.9
1	C	28	GLU	5.9
1	K	44	SER	5.9
1	N	181	VAL	5.9

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Mol	Chain	Res	Type	RSRZ
1	T	193	ASN	5.9
1	O	119	THR	5.9
1	E	36	VAL	5.9
1	G	100	ARG	5.9
1	N	14	ALA	5.9
1	N	62	HIS	5.9
1	L	13	GLN	5.8
1	Q	63	GLN	5.8
1	B	206	GLY	5.8
1	N	18	LEU	5.8
1	F	122	PRO	5.8
1	F	137	GLY	5.8
1	T	30	LYS	5.8
1	S	59	VAL	5.8
1	E	177	ALA	5.8
1	C	59	VAL	5.8
1	M	174	ALA	5.8
1	Q	194	ALA	5.8
1	I	68	MET	5.8
1	D	60	GLY	5.8
1	G	151	LEU	5.8
1	H	118	MET	5.8
1	T	75	GLU	5.8
1	C	34	PRO	5.8
1	K	99	PRO	5.8
1	J	187	GLU	5.8
1	O	19	CYS	5.7
1	P	75	GLU	5.7
1	Q	26	VAL	5.7
1	F	23	TRP	5.7
1	J	70	LYS	5.7
1	J	178	SER	5.7
1	M	19	CYS	5.7
1	S	148	THR	5.7
1	B	34	PRO	5.7
1	N	70	LYS	5.7
1	E	27	VAL	5.7
1	E	189	LEU	5.7
1	G	148	THR	5.7
1	M	137	GLY	5.7
1	N	187	GLU	5.7
1	O	117	TRP	5.7

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Mol	Chain	Res	Type	RSRZ
1	M	71	GLU	5.7
1	G	122	PRO	5.7
1	E	188	THR	5.7
1	C	19	CYS	5.7
1	Q	123	PRO	5.7
1	M	156	GLY	5.6
1	H	120	HIS	5.6
1	H	185	ALA	5.6
1	J	106	GLY	5.6
1	D	59	VAL	5.6
1	T	118	MET	5.6
1	K	104	ILE	5.6
1	H	19	CYS	5.6
1	L	60	GLY	5.6
1	Q	189	LEU	5.6
1	L	101	GLY	5.6
1	K	181	VAL	5.6
1	Q	205	LEU	5.6
1	D	108	THR	5.6
1	T	58	THR	5.6
1	E	117	TRP	5.6
1	F	13	GLN	5.6
1	L	63	GLN	5.6
1	L	79	GLU	5.6
1	M	21	ASN	5.6
1	G	154	ARG	5.6
1	S	218	CYS	5.5
1	K	16	SER	5.5
1	R	15	ILE	5.5
1	I	199	LYS	5.5
1	B	109	SER	5.5
1	S	104	ILE	5.5
1	K	59	VAL	5.5
1	T	14	ALA	5.5
1	R	149	SER	5.5
1	J	207	PRO	5.5
1	E	109	SER	5.5
1	E	153	ILE	5.5
1	F	27	VAL	5.5
1	F	47	ALA	5.5
1	G	114	GLN	5.5
1	P	153	ILE	5.5

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Mol	Chain	Res	Type	RSRZ
1	G	163	ASP	5.5
1	E	80	TRP	5.5
1	G	164	TYR	5.5
1	J	78	ALA	5.5
1	K	19	CYS	5.5
1	K	32	PHE	5.5
1	E	185	ALA	5.5
1	T	28	GLU	5.5
1	L	84	HIS	5.5
1	O	143	ARG	5.5
1	T	17	CYS	5.5
1	K	60	GLY	5.5
1	N	163	ASP	5.5
1	C	67	GLN	5.5
1	E	26	VAL	5.5
1	S	187	GLU	5.5
1	G	206	GLY	5.4
1	Q	206	GLY	5.4
1	O	133	TRP	5.4
1	O	146	SER	5.4
1	T	43	LEU	5.4
1	M	64	ALA	5.4
1	R	66	MET	5.4
1	S	150	ILE	5.4
1	B	23	TRP	5.4
1	Q	117	TRP	5.4
1	F	101	GLY	5.4
1	F	182	LYS	5.4
1	Q	57	ASN	5.4
1	S	28	GLU	5.4
1	E	139	ASN	5.4
1	S	47	ALA	5.4
1	L	83	LEU	5.4
1	D	155	GLN	5.4
1	R	13	GLN	5.4
1	J	200	THR	5.4
1	N	141	ILE	5.4
1	T	84	HIS	5.4
1	A	171	THR	5.4
1	H	175	GLU	5.4
1	M	185	ALA	5.4
1	Q	59	VAL	5.3

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Mol	Chain	Res	Type	RSRZ
1	L	217	ALA	5.3
1	H	198	CYS	5.3
1	R	183	ASN	5.3
1	D	48	THR	5.3
1	C	116	GLY	5.3
1	J	61	GLY	5.3
1	O	184	ALA	5.3
1	G	126	VAL	5.3
1	G	153	ILE	5.3
1	L	208	GLY	5.3
1	K	170	LYS	5.3
1	R	69	LEU	5.3
1	A	199	LYS	5.3
1	H	100	ARG	5.3
1	J	105	ALA	5.3
1	E	127	GLY	5.3
1	R	216	THR	5.3
1	B	132	ARG	5.3
1	O	22	ALA	5.3
1	C	100	ARG	5.3
1	S	167	ARG	5.3
1	L	27	VAL	5.3
1	A	194	ALA	5.3
1	B	116	GLY	5.2
1	M	181	VAL	5.2
1	N	15	ILE	5.2
1	M	33	SER	5.2
1	T	148	THR	5.2
1	G	204	ALA	5.2
1	O	198	CYS	5.2
1	I	186	THR	5.2
1	A	116	GLY	5.2
1	E	43	LEU	5.2
1	K	61	GLY	5.2
1	I	34	PRO	5.2
1	G	200	THR	5.2
1	M	165	VAL	5.2
1	F	170	LYS	5.2
1	J	54	THR	5.2
1	K	194	ALA	5.2
1	C	38	PRO	5.2
1	I	79	GLU	5.2

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Mol	Chain	Res	Type	RSRZ
1	N	46	GLY	5.2
1	C	48	THR	5.2
1	G	25	LYS	5.2
1	C	22	ALA	5.2
1	J	166	ASP	5.2
1	P	123	PRO	5.2
1	E	215	MET	5.2
1	L	110	THR	5.2
1	C	168	PHE	5.2
1	E	73	ILE	5.2
1	K	168	PHE	5.2
1	O	187	GLU	5.2
1	T	209	ALA	5.1
1	C	27	VAL	5.1
1	R	161	PHE	5.1
1	E	205	LEU	5.1
1	F	61	GLY	5.1
1	T	140	LYS	5.1
1	F	70	LYS	5.1
1	F	136	LEU	5.1
1	Q	188	THR	5.1
1	H	148	THR	5.1
1	K	137	GLY	5.1
1	M	63	GLN	5.1
1	C	146	SER	5.1
1	P	180	GLU	5.1
1	T	175	GLU	5.1
1	B	127	GLY	5.1
1	Q	80	TRP	5.0
1	F	83	LEU	5.0
1	B	100	ARG	5.0
1	R	176	GLN	5.0
1	J	123	PRO	5.0
1	A	159	GLU	5.0
1	P	194	ALA	5.0
1	E	110	THR	5.0
1	R	155	GLN	5.0
1	P	159	GLU	5.0
1	E	18	LEU	5.0
1	I	109	SER	5.0
1	J	189	LEU	5.0
1	Q	104	ILE	5.0

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Mol	Chain	Res	Type	RSRZ
1	S	134	ILE	5.0
1	Q	146	SER	5.0
1	S	73	ILE	5.0
1	L	127	GLY	5.0
1	E	57	ASN	5.0
1	F	181	VAL	5.0
1	F	219	GLN	5.0
1	C	177	ALA	5.0
1	N	117	TRP	5.0
1	B	122	PRO	5.0
1	D	217	ALA	5.0
1	N	168	PHE	5.0
1	K	70	LYS	4.9
1	K	109	SER	4.9
1	G	180	GLU	4.9
1	P	46	GLY	4.9
1	D	185	ALA	4.9
1	D	188	THR	4.9
1	M	127	GLY	4.9
1	Q	11	VAL	4.9
1	R	71	GLU	4.9
1	B	199	LYS	4.9
1	P	1	PRO	4.9
1	R	160	PRO	4.9
1	H	54	THR	4.9
1	J	34	PRO	4.9
1	F	194	ALA	4.9
1	J	192	GLN	4.9
1	A	142	VAL	4.9
1	C	154	ARG	4.9
1	A	104	ILE	4.9
1	S	34	PRO	4.9
1	J	206	GLY	4.9
1	A	196	PRO	4.9
1	B	179	GLN	4.9
1	C	185	ALA	4.9
1	G	147	PRO	4.9
1	D	103	ASP	4.8
1	N	177	ALA	4.8
1	O	124	ILE	4.8
1	O	78	ALA	4.8
1	G	104	ILE	4.8

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Mol	Chain	Res	Type	RSRZ
1	L	142	VAL	4.8
1	J	122	PRO	4.8
1	R	59	VAL	4.8
1	A	27	VAL	4.8
1	C	81	ASP	4.8
1	D	55	MET	4.8
1	D	80	TRP	4.8
1	L	186	THR	4.8
1	C	101	GLY	4.8
1	T	73	ILE	4.8
1	D	153	ILE	4.8
1	R	219	GLN	4.8
1	R	19	CYS	4.8
1	C	70	LYS	4.8
1	E	38	PRO	4.8
1	I	123	PRO	4.8
1	O	149	SER	4.7
1	A	200	THR	4.7
1	A	204	ALA	4.7
1	F	48	THR	4.7
1	N	81	ASP	4.7
1	A	39	MET	4.7
1	B	207	PRO	4.7
1	P	142	VAL	4.7
1	S	201	ILE	4.7
1	A	22	ALA	4.7
1	D	107	THR	4.7
1	C	58	THR	4.7
1	F	196	PRO	4.7
1	R	57	ASN	4.7
1	M	208	GLY	4.7
1	H	27	VAL	4.7
1	I	83	LEU	4.7
1	B	180	GLU	4.7
1	D	19	CYS	4.7
1	F	217	ALA	4.7
1	P	65	ALA	4.7
1	S	101	GLY	4.7
1	D	198	CYS	4.7
1	O	54	THR	4.7
1	A	187	GLU	4.6
1	H	181	VAL	4.6

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Mol	Chain	Res	Type	RSRZ
1	J	130	TYR	4.6
1	R	142	VAL	4.6
1	I	122	PRO	4.6
1	J	146	SER	4.6
1	Q	143	ARG	4.6
1	G	31	ALA	4.6
1	L	185	ALA	4.6
1	B	27	VAL	4.6
1	O	82	ARG	4.6
1	O	57	ASN	4.6
1	S	177	ALA	4.6
1	F	198	CYS	4.6
1	E	157	PRO	4.6
1	N	85	PRO	4.6
1	N	164	TYR	4.6
1	H	57	ASN	4.6
1	L	104	ILE	4.6
1	Q	22	ALA	4.6
1	L	182	LYS	4.6
1	L	71	GLU	4.6
1	G	30	LYS	4.6
1	B	64	ALA	4.6
1	K	153	ILE	4.6
1	B	187	GLU	4.6
1	C	79	GLU	4.6
1	P	176	GLN	4.6
1	Q	120	HIS	4.6
1	D	34	PRO	4.5
1	D	152	ASP	4.5
1	N	26	VAL	4.5
1	P	188	THR	4.5
1	M	58	THR	4.5
1	P	81	ASP	4.5
1	T	110	THR	4.5
1	F	141	ILE	4.5
1	I	120	HIS	4.5
1	M	200	THR	4.5
1	S	210	THR	4.5
1	F	142	VAL	4.5
1	H	160	PRO	4.5
1	N	48	THR	4.5
1	S	54	THR	4.5

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Mol	Chain	Res	Type	RSRZ
1	I	71	GLU	4.5
1	T	18	LEU	4.5
1	M	82	ARG	4.5
1	A	148	THR	4.5
1	K	38	PRO	4.5
1	N	105	ALA	4.5
1	A	146	SER	4.5
1	B	104	ILE	4.5
1	S	49	PRO	4.5
1	M	78	ALA	4.5
1	P	68	MET	4.5
1	N	191	VAL	4.4
1	J	204	ALA	4.4
1	I	146	SER	4.4
1	L	82	ARG	4.4
1	R	83	LEU	4.4
1	K	46	GLY	4.4
1	L	59	VAL	4.4
1	Q	62	HIS	4.4
1	B	146	SER	4.4
1	L	177	ALA	4.4
1	J	201	ILE	4.4
1	P	167	ARG	4.4
1	T	188	THR	4.4
1	E	31	ALA	4.4
1	T	26	VAL	4.4
1	S	58	THR	4.4
1	R	159	GLU	4.4
1	S	197	ASP	4.4
1	M	157	PRO	4.3
1	Q	181	VAL	4.3
1	Q	217	ALA	4.3
1	Q	156	GLY	4.3
1	O	64	ALA	4.3
1	K	148	THR	4.3
1	N	23	TRP	4.3
1	C	175	GLU	4.3
1	Q	1	PRO	4.3
1	B	63	GLN	4.3
1	C	219	GLN	4.3
1	T	19	CYS	4.3
1	A	81	ASP	4.3

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Mol	Chain	Res	Type	RSRZ
1	D	69	LEU	4.3
1	E	174	ALA	4.3
1	I	73	ILE	4.3
1	J	155	GLN	4.3
1	H	184	ALA	4.3
1	R	74	ASN	4.3
1	A	197	ASP	4.3
1	P	48	THR	4.2
1	G	185	ALA	4.2
1	L	209	ALA	4.2
1	S	70	LYS	4.2
1	O	79	GLU	4.2
1	C	105	ALA	4.2
1	L	117	TRP	4.2
1	C	35	GLU	4.2
1	C	106	GLY	4.2
1	G	184	ALA	4.2
1	I	204	ALA	4.2
1	D	218	CYS	4.2
1	Q	61	GLY	4.2
1	S	163	ASP	4.2
1	Q	29	GLU	4.2
1	O	37	ILE	4.2
1	J	185	ALA	4.2
1	O	24	VAL	4.1
1	B	1	PRO	4.1
1	T	168	PHE	4.1
1	P	117	TRP	4.1
1	J	68	MET	4.1
1	T	62	HIS	4.1
1	B	189	LEU	4.1
1	M	192	GLN	4.1
1	C	29	GLU	4.1
1	J	199	LYS	4.1
1	Q	179	GLN	4.1
1	D	175	GLU	4.1
1	J	81	ASP	4.1
1	E	168	PHE	4.1
1	P	147	PRO	4.1
1	F	19	CYS	4.1
1	P	47	ALA	4.1
1	K	30	LYS	4.1

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Mol	Chain	Res	Type	RSRZ
1	L	167	ARG	4.1
1	P	120	HIS	4.1
1	B	204	ALA	4.1
1	M	116	GLY	4.1
1	J	39	MET	4.1
1	E	64	ALA	4.1
1	M	195	ASN	4.0
1	L	143	ARG	4.0
1	R	148	THR	4.0
1	F	78	ALA	4.0
1	R	34	PRO	4.0
1	B	118	MET	4.0
1	I	178	SER	4.0
1	T	122	PRO	4.0
1	T	137	GLY	4.0
1	B	181	VAL	4.0
1	D	154	ARG	4.0
1	F	168	PHE	4.0
1	F	159	GLU	4.0
1	T	189	LEU	4.0
1	G	137	GLY	4.0
1	N	204	ALA	4.0
1	J	82	ARG	4.0
1	L	193	ASN	4.0
1	F	215	MET	4.0
1	L	141	ILE	4.0
1	F	84	HIS	4.0
1	G	142	VAL	4.0
1	A	79	GLU	4.0
1	J	161	PHE	4.0
1	A	105	ALA	4.0
1	L	166	ASP	4.0
1	D	31	ALA	3.9
1	T	33	SER	3.9
1	S	178	SER	3.9
1	M	209	ALA	3.9
1	G	193	ASN	3.9
1	L	215	MET	3.9
1	C	205	LEU	3.9
1	R	185	ALA	3.9
1	L	174	ALA	3.9
1	T	76	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	R	191	VAL	3.9
1	I	105	ALA	3.9
1	B	167	ARG	3.9
1	H	38	PRO	3.9
1	H	59	VAL	3.9
1	A	71	GLU	3.9
1	P	84	HIS	3.9
1	F	163	ASP	3.9
1	T	101	GLY	3.9
1	B	106	GLY	3.8
1	I	124	ILE	3.8
1	O	27	VAL	3.8
1	I	167	ARG	3.8
1	Q	164	TYR	3.8
1	N	111	LEU	3.8
1	P	164	TYR	3.8
1	S	217	ALA	3.8
1	G	105	ALA	3.8
1	D	219	GLN	3.8
1	Q	60	GLY	3.8
1	Q	148	THR	3.8
1	S	103	ASP	3.8
1	N	78	ALA	3.8
1	F	58	THR	3.8
1	D	110	THR	3.8
1	A	47	ALA	3.8
1	I	142	VAL	3.8
1	D	206	GLY	3.8
1	F	119	THR	3.8
1	M	109	SER	3.8
1	N	175	GLU	3.8
1	M	48	THR	3.7
1	N	180	GLU	3.7
1	Q	12	HIS	3.7
1	R	154	ARG	3.7
1	G	37	ILE	3.7
1	S	155	GLN	3.7
1	M	219	GLN	3.7
1	A	62	HIS	3.7
1	I	47	ALA	3.7
1	J	154	ARG	3.7
1	A	35	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
1	N	22	ALA	3.7
1	R	120	HIS	3.7
1	G	83	LEU	3.7
1	O	81	ASP	3.7
1	Q	28	GLU	3.7
1	D	178	SER	3.7
1	Q	137	GLY	3.7
1	C	182	LYS	3.7
1	N	176	GLN	3.7
1	C	166	ASP	3.7
1	I	69	LEU	3.7
1	H	164	TYR	3.7
1	C	110	THR	3.7
1	R	117	TRP	3.7
1	E	178	SER	3.7
1	A	74	ASN	3.6
1	D	215	MET	3.6
1	K	184	ALA	3.6
1	R	180	GLU	3.6
1	Q	182	LYS	3.6
1	D	163	ASP	3.6
1	M	146	SER	3.6
1	O	166	ASP	3.6
1	T	124	ILE	3.6
1	S	194	ALA	3.6
1	D	27	VAL	3.6
1	O	164	TYR	3.6
1	P	37	ILE	3.6
1	F	176	GLN	3.6
1	J	147	PRO	3.6
1	L	85	PRO	3.6
1	K	58	THR	3.6
1	R	203	LYS	3.6
1	E	114	GLN	3.6
1	M	196	PRO	3.6
1	Q	175	GLU	3.6
1	L	105	ALA	3.6
1	C	179	GLN	3.6
1	J	47	ALA	3.5
1	A	119	THR	3.5
1	A	208	GLY	3.5
1	A	209	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	R	46	GLY	3.5
1	R	63	GLN	3.5
1	G	149	SER	3.5
1	B	22	ALA	3.5
1	C	47	ALA	3.5
1	T	105	ALA	3.5
1	N	47	ALA	3.5
1	R	174	ALA	3.5
1	B	105	ALA	3.5
1	P	22	ALA	3.5
1	Q	118	MET	3.5
1	A	18	LEU	3.5
1	G	22	ALA	3.5
1	L	205	LEU	3.5
1	S	179	GLN	3.5
1	O	159	GLU	3.5
1	J	188	THR	3.5
1	D	81	ASP	3.5
1	E	167	ARG	3.5
1	F	34	PRO	3.5
1	S	80	TRP	3.5
1	T	157	PRO	3.5
1	T	182	LYS	3.5
1	P	103	ASP	3.4
1	R	153	ILE	3.4
1	N	167	ARG	3.4
1	E	137	GLY	3.4
1	M	46	GLY	3.4
1	G	116	GLY	3.4
1	O	73	ILE	3.4
1	A	103	ASP	3.4
1	H	121	ASN	3.4
1	Q	187	GLU	3.4
1	G	26	VAL	3.4
1	P	200	THR	3.4
1	H	217	ALA	3.4
1	I	31	ALA	3.4
1	F	49	PRO	3.4
1	G	205	LEU	3.4
1	T	127	GLY	3.4
1	M	167	ARG	3.4
1	T	38	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	137	GLY	3.4
1	C	218	CYS	3.4
1	F	22	ALA	3.3
1	J	59	VAL	3.3
1	A	218	CYS	3.3
1	H	58	THR	3.3
1	R	82	ARG	3.3
1	K	175	GLU	3.3
1	E	1	PRO	3.3
1	P	181	VAL	3.3
1	T	1	PRO	3.3
1	Q	34	PRO	3.3
1	R	169	TYR	3.3
1	Q	48	THR	3.3
1	M	169	TYR	3.3
1	D	105	ALA	3.3
1	P	209	ALA	3.3
1	G	199	LYS	3.3
1	D	143	ARG	3.3
1	O	191	VAL	3.3
1	K	83	LEU	3.3
1	O	104	ILE	3.3
1	G	194	ALA	3.3
1	E	35	GLU	3.3
1	K	155	GLN	3.3
1	J	57	ASN	3.2
1	B	145	TYR	3.2
1	F	144	MET	3.2
1	J	195	ASN	3.2
1	J	19	CYS	3.2
1	M	184	ALA	3.2
1	M	69	LEU	3.2
1	H	177	ALA	3.2
1	F	82	ARG	3.2
1	M	194	ALA	3.2
1	J	142	VAL	3.2
1	P	72	THR	3.2
1	O	201	ILE	3.2
1	D	137	GLY	3.2
1	G	84	HIS	3.2
1	M	147	PRO	3.2
1	B	150	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	E	219	GLN	3.2
1	D	167	ARG	3.2
1	S	121	ASN	3.2
1	H	153	ILE	3.2
1	E	49	PRO	3.2
1	F	118	MET	3.2
1	I	174	ALA	3.2
1	O	182	LYS	3.2
1	F	158	LYS	3.2
1	M	179	GLN	3.2
1	J	198	CYS	3.2
1	I	78	ALA	3.2
1	P	32	PHE	3.2
1	B	72	THR	3.2
1	O	168	PHE	3.2
1	D	109	SER	3.2
1	J	2	ILE	3.1
1	I	209	ALA	3.1
1	T	126	VAL	3.1
1	E	105	ALA	3.1
1	J	1	PRO	3.1
1	P	189	LEU	3.1
1	J	156	GLY	3.1
1	M	159	GLU	3.1
1	C	195	ASN	3.1
1	R	215	MET	3.1
1	A	49	PRO	3.1
1	K	28	GLU	3.1
1	S	142	VAL	3.1
1	D	193	ASN	3.1
1	K	174	ALA	3.1
1	M	204	ALA	3.1
1	L	109	SER	3.1
1	S	22	ALA	3.1
1	I	148	THR	3.1
1	S	196	PRO	3.1
1	L	78	ALA	3.1
1	O	63	GLN	3.1
1	M	107	THR	3.1
1	O	171	THR	3.1
1	S	195	ASN	3.1
1	H	114	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
1	H	174	ALA	3.1
1	N	215	MET	3.1
1	Q	142	VAL	3.0
1	Q	161	PHE	3.0
1	B	48	THR	3.0
1	N	68	MET	3.0
1	L	122	PRO	3.0
1	A	32	PHE	3.0
1	J	83	LEU	3.0
1	A	175	GLU	3.0
1	Q	165	VAL	3.0
1	G	73	ILE	3.0
1	E	63	GLN	3.0
1	A	72	THR	3.0
1	K	14	ALA	3.0
1	B	188	THR	3.0
1	F	106	GLY	3.0
1	A	12	HIS	3.0
1	O	31	ALA	2.9
1	A	82	ARG	2.9
1	O	62	HIS	2.9
1	S	219	GLN	2.9
1	S	166	ASP	2.9
1	K	166	ASP	2.9
1	O	110	THR	2.9
1	N	19	CYS	2.9
1	H	22	ALA	2.9
1	D	106	GLY	2.9
1	I	166	ASP	2.9
1	S	108	THR	2.9
1	M	203	LYS	2.9
1	G	101	GLY	2.9
1	C	85	PRO	2.9
1	N	205	LEU	2.9
1	O	85	PRO	2.9
1	G	174	ALA	2.9
1	Q	47	ALA	2.9
1	O	195	ASN	2.8
1	S	136	LEU	2.8
1	A	188	THR	2.8
1	P	155	GLN	2.8
1	H	117	TRP	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	68	MET	2.8
1	R	80	TRP	2.8
1	N	209	ALA	2.8
1	J	183	ASN	2.8
1	B	209	ALA	2.8
1	K	13	GLN	2.8
1	O	32	PHE	2.8
1	N	102	SER	2.8
1	F	73	ILE	2.8
1	J	179	GLN	2.8
1	P	2	ILE	2.8
1	K	25	LYS	2.8
1	P	78	ALA	2.8
1	Q	174	ALA	2.8
1	M	205	LEU	2.7
1	F	117	TRP	2.7
1	E	116	GLY	2.7
1	S	191	VAL	2.7
1	C	202	LEU	2.7
1	R	202	LEU	2.7
1	B	110	THR	2.7
1	D	124	ILE	2.7
1	J	174	ALA	2.7
1	B	194	ALA	2.7
1	A	69	LEU	2.7
1	J	85	PRO	2.7
1	C	103	ASP	2.7
1	C	104	ILE	2.7
1	A	77	ALA	2.7
1	S	78	ALA	2.7
1	G	62	HIS	2.7
1	G	60	GLY	2.7
1	O	165	VAL	2.7
1	Q	69	LEU	2.7
1	O	30	LYS	2.7
1	H	106	GLY	2.7
1	G	65	ALA	2.7
1	P	198	CYS	2.7
1	N	31	ALA	2.6
1	B	117	TRP	2.6
1	R	116	GLY	2.6
1	R	58	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	S	72	THR	2.6
1	G	68	MET	2.6
1	N	49	PRO	2.6
1	P	61	GLY	2.6
1	Q	84	HIS	2.6
1	R	168	PHE	2.6
1	M	148	THR	2.6
1	G	27	VAL	2.6
1	R	194	ALA	2.6
1	J	203	LYS	2.6
1	S	116	GLY	2.6
1	P	168	PHE	2.6
1	C	155	GLN	2.6
1	F	63	GLN	2.6
1	P	174	ALA	2.6
1	Q	150	ILE	2.6
1	N	54	THR	2.6
1	Q	214	MET	2.6
1	E	161	PHE	2.6
1	R	204	ALA	2.6
1	N	83	LEU	2.5
1	O	123	PRO	2.5
1	T	106	GLY	2.5
1	G	179	GLN	2.5
1	K	195	ASN	2.5
1	G	120	HIS	2.5
1	Q	30	LYS	2.5
1	M	155	GLN	2.5
1	C	212	GLU	2.5
1	E	184	ALA	2.5
1	I	205	LEU	2.5
1	F	81	ASP	2.5
1	T	35	GLU	2.5
1	D	201	ILE	2.5
1	E	165	VAL	2.5
1	J	182	LYS	2.5
1	Q	78	ALA	2.5
1	R	167	ARG	2.5
1	S	158	LYS	2.4
1	Q	218	CYS	2.4
1	G	198	CYS	2.4
1	A	149	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	L	203	LYS	2.4
1	O	205	LEU	2.4
1	M	85	PRO	2.4
1	J	157	PRO	2.4
1	Q	81	ASP	2.4
1	N	174	ALA	2.4
1	P	60	GLY	2.3
1	F	161	PHE	2.3
1	O	142	VAL	2.3
1	B	142	VAL	2.3
1	H	195	ASN	2.3
1	M	187	GLU	2.3
1	J	58	THR	2.3
1	A	19	CYS	2.3
1	S	153	ILE	2.3
1	J	117	TRP	2.3
1	I	119	THR	2.3
1	N	199	LYS	2.3
1	N	127	GLY	2.3
1	J	79	GLU	2.3
1	L	31	ALA	2.3
1	T	116	GLY	2.3
1	A	73	ILE	2.3
1	A	70	LYS	2.3
1	A	155	GLN	2.3
1	I	108	THR	2.3
1	I	30	LYS	2.3
1	S	46	GLY	2.3
1	P	197	ASP	2.3
1	H	178	SER	2.2
1	N	154	ARG	2.2
1	C	181	VAL	2.2
1	R	218	CYS	2.2
1	K	179	GLN	2.2
1	N	69	LEU	2.2
1	S	133	TRP	2.2
1	O	209	ALA	2.2
1	R	121	ASN	2.2
1	I	114	GLN	2.2
1	M	143	ARG	2.2
1	A	106	GLY	2.2
1	D	22	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	195	ASN	2.2
1	K	185	ALA	2.2
1	C	68	MET	2.2
1	D	195	ASN	2.2
1	B	78	ALA	2.2
1	M	47	ALA	2.2
1	D	182	LYS	2.2
1	E	202	LEU	2.1
1	K	26	VAL	2.1
1	I	155	GLN	2.1
1	N	138	LEU	2.1
1	O	194	ALA	2.1
1	J	84	HIS	2.1
1	S	14	ALA	2.1
1	Q	199	LYS	2.1
1	T	27	VAL	2.1
1	A	167	ARG	2.1
1	I	104	ILE	2.1
1	N	166	ASP	2.1
1	T	202	LEU	2.1
1	Q	124	ILE	2.1
1	T	165	VAL	2.1
1	B	178	SER	2.1
1	B	182	LYS	2.1
1	R	170	LYS	2.1
1	G	115	ILE	2.1
1	P	79	GLU	2.1
1	A	174	ALA	2.1
1	I	177	ALA	2.1
1	T	218	CYS	2.1
1	E	101	GLY	2.1
1	N	72	THR	2.0
1	P	69	LEU	2.0
1	D	142	VAL	2.0
1	T	200	THR	2.0
1	N	218	CYS	2.0
1	Q	121	ASN	2.0
1	L	149	SER	2.0
1	Q	2	ILE	2.0
1	K	164	TYR	2.0
1	A	215	MET	2.0
1	C	174	ALA	2.0

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

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.