



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2017 – 02:35 PM EDT

PDB ID : 3CW1
Title : Crystal Structure of Human Spliceosomal U1 snRNP
Authors : Pomeranz Krummel, D.A.; Oubridge, C.; Leung, A.K.; Li, J.; Nagai, K.
Deposited on : unknown
Resolution : 5.49 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
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

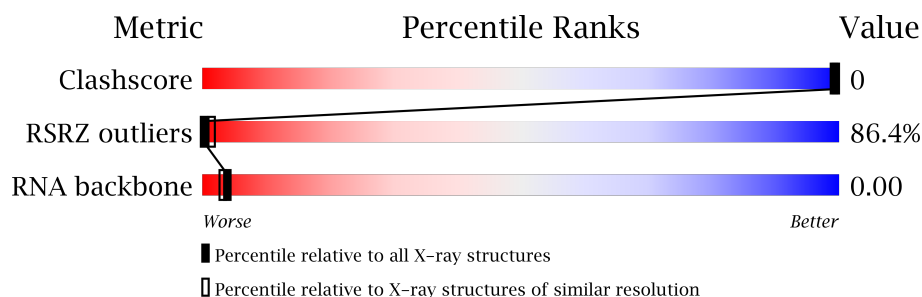
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.49 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))
Clashscore	112137	1021 (7.20-3.76)
RSRZ outliers	101464	1061 (7.20-3.70)
RNA backbone	2435	1049 (7.80-2.90)

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	V	138	<div> <div>99%</div> <div>100%</div> </div>
1	v	138	<div> <div>99%</div> <div>99%</div> </div>
1	w	138	<div> <div>99%</div> <div>100%</div> </div>
1	x	138	<div> <div>99%</div> <div>100%</div> </div>
2	D	126	<div> <div>51%</div> <div>60%</div> <div>40%</div> </div>
2	S	126	<div> <div>49%</div> <div>60%</div> <div>40%</div> </div>
2	T	126	<div> <div>51%</div> <div>60%</div> <div>40%</div> </div>
2	U	126	<div> <div>52%</div> <div>60%</div> <div>40%</div> </div>

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Mol	Chain	Length	Quality of chain
3	A	174	
3	H	174	
3	I	174	
3	J	174	
4	B	119	
4	M	119	
4	N	119	
4	O	119	
5	C	118	
5	P	118	
5	Q	118	
5	R	118	
6	1	86	
6	2	86	
6	F	86	
6	Z	86	
7	E	92	
7	W	92	
7	X	92	
7	Y	92	
8	3	76	
8	4	76	
8	5	76	
8	G	76	
9	6	216	

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Mol	Chain	Length	Quality of chain
9	7	216	<div> <div>46%</div> <div>56%</div> <div>44%</div> </div>
9	8	216	<div> <div>46%</div> <div>56%</div> <div>44%</div> </div>
9	K	216	<div> <div>46%</div> <div>55%</div> <div>44%</div> </div>
10	0	77	<div> <div>51%</div> <div>70%</div> <div>30%</div> </div>
10	9	77	<div> <div>61%</div> <div>75%</div> <div>25%</div> </div>
10	L	77	<div> <div>53%</div> <div>74%</div> <div>26%</div> </div>
10	l	77	<div> <div>57%</div> <div>75%</div> <div>25%</div> </div>

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 3365 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 RNA chain called U1 snRNA.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	V	138	Total P 138 138	0	0	138
1	v	138	Total P 138 138	0	0	138
1	w	138	Total P 138 138	0	0	138
1	x	138	Total P 138 138	0	0	138

- Molecule 2 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	D	76	Total C 76 76	0	0	76
2	S	76	Total C 76 76	0	0	76
2	T	76	Total C 76 76	0	0	76
2	U	76	Total C 76 76	0	0	76

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	66	CYS	SER	CONFLICT	UNP P62318
S	266	CYS	SER	CONFLICT	UNP P62318
T	466	CYS	SER	CONFLICT	UNP P62318
U	666	CYS	SER	CONFLICT	UNP P62318

- Molecule 3 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	A	64	Total C 64 64	0	0	64
3	H	64	Total C 64 64	0	0	64
3	I	63	Total C 63 63	0	0	63
3	J	63	Total C 63 63	0	0	63

- Molecule 4 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	B	77	Total C 77 77	0	0	77
4	M	77	Total C 77 77	0	0	77
4	N	76	Total C 76 76	0	0	76
4	O	77	Total C 77 77	0	0	77

- Molecule 5 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
5	C	88	Total C 88 88	0	0	88
5	P	86	Total C 86 86	0	0	86
5	Q	89	Total C 89 89	0	0	89
5	R	85	Total C 85 85	0	0	85

- Molecule 6 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
6	F	76	Total C 76 76	0	0	76
6	Z	70	Total C 70 70	0	0	70
6	1	75	Total C 75 75	0	0	75

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
6	2	76	Total C 76 76	0	0	76

- Molecule 7 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
7	E	75	Total C 75 75	0	0	75
7	W	75	Total C 75 75	0	0	75
7	X	75	Total C 75 75	0	0	75
7	Y	75	Total C 75 75	0	0	75

- Molecule 8 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
8	G	73	Total C 73 73	0	0	73
8	3	73	Total C 73 73	0	0	73
8	4	73	Total C 73 73	0	0	73
8	5	73	Total C 73 73	0	0	73

- Molecule 9 is a protein called U1 small nuclear ribonucleoprotein 70 kDa.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
9	K	120	Total C 120 120	0	0	120
9	6	120	Total C 120 120	0	0	120
9	7	120	Total C 120 120	0	0	120
9	8	120	Total C 120 120	0	0	120

- Molecule 10 is a protein called U1 small nuclear ribonucleoprotein C.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
10	L	57	Total C 57 57	0	0	57
10	9	58	Total C 58 58	0	0	58
10	0	54	Total C 54 54	0	0	54
10	1	58	Total C 58 58	0	0	58

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	39	CYS	GLN	CONFLICT	UNP P09234
9	239	CYS	GLN	CONFLICT	UNP P09234
0	439	CYS	GLN	CONFLICT	UNP P09234
1	639	CYS	GLN	CONFLICT	UNP P09234

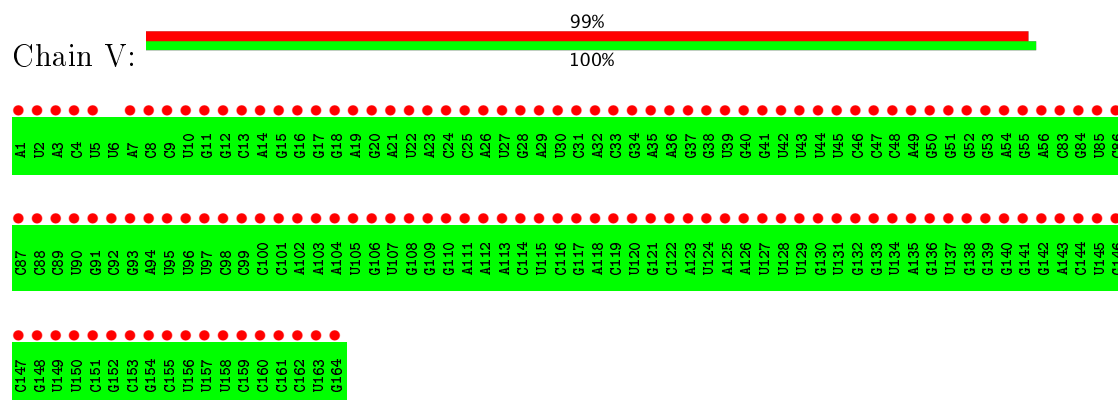
- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	0	1	Total Zn 1 1	0	0
11	1	1	Total Zn 1 1	0	0
11	9	1	Total Zn 1 1	0	0
11	L	1	Total Zn 1 1	0	0

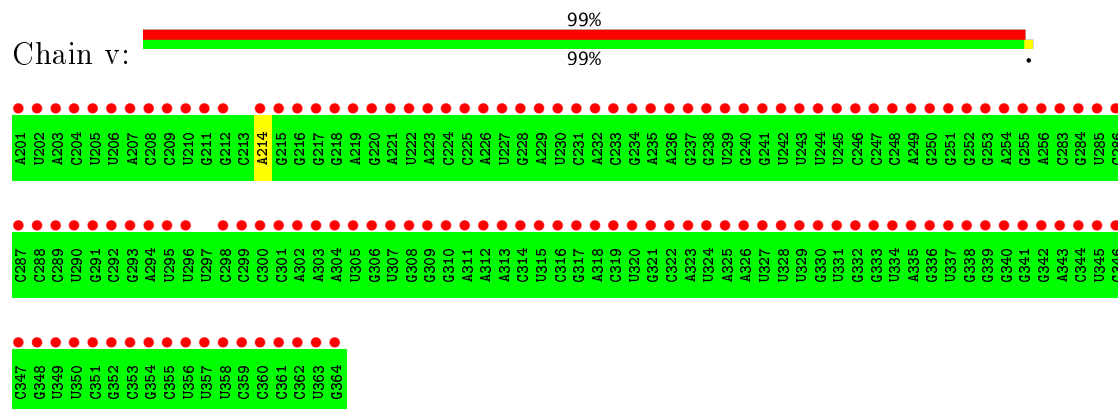
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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 ($\text{RSRZ} > 2$). 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.

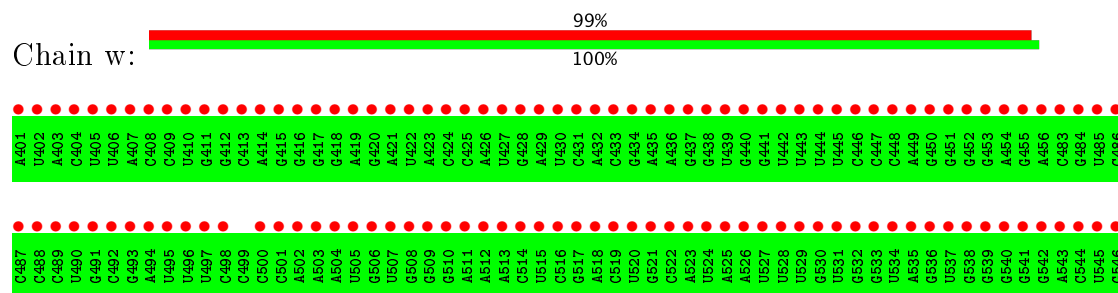
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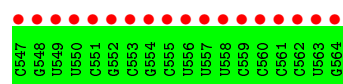


• Molecule 1: U1 snRNA

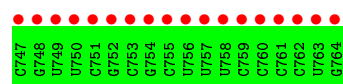
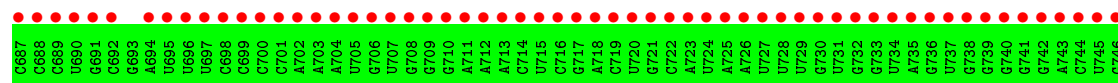
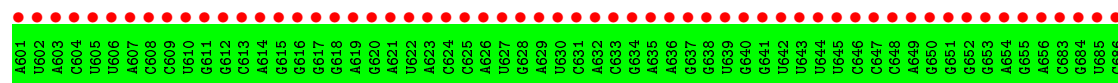


• Molecule 1: U1 snRNA

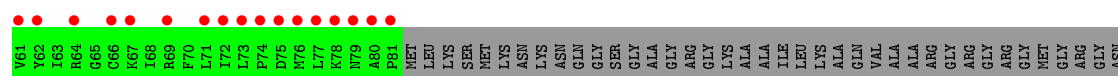
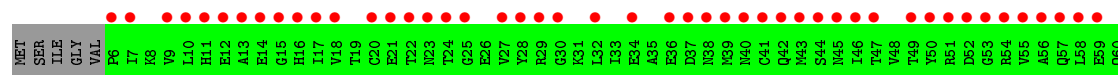




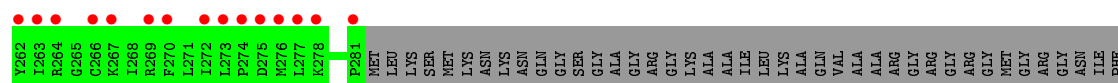
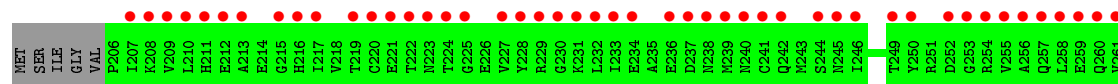
• Molecule 1: U1 snRNA



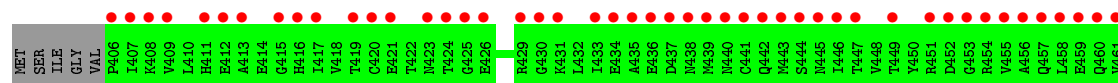
• Molecule 2: Small nuclear ribonucleoprotein Sm D3

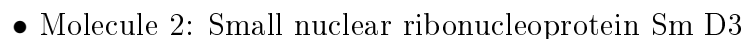


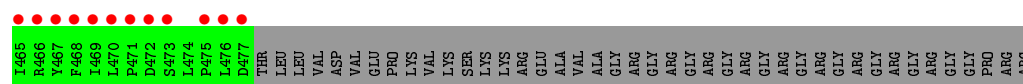
• Molecule 2: Small nuclear ribonucleoprotein Sm D3



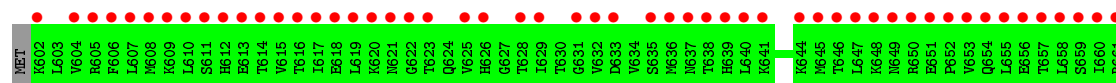
• Molecule 2: Small nuclear ribonucleoprotein Sm D3



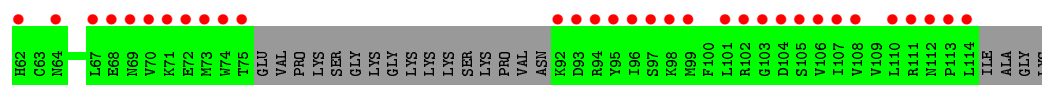
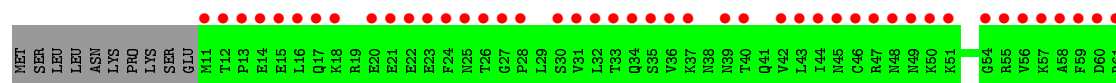
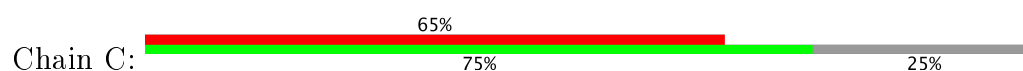




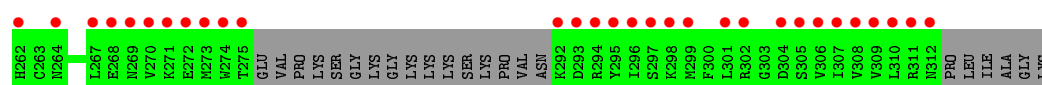
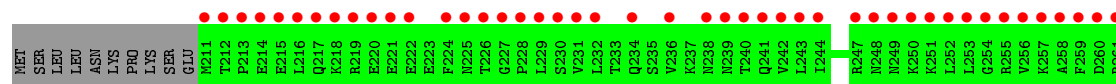
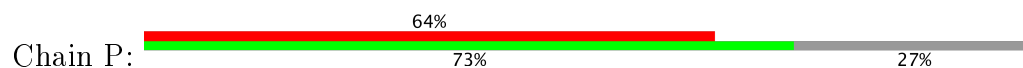
• Molecule 4: Small nuclear ribonucleoprotein Sm D1



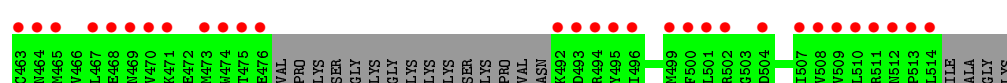
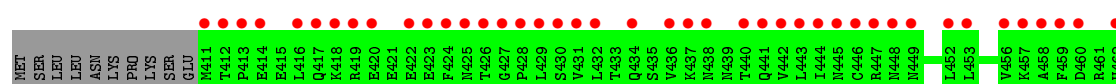
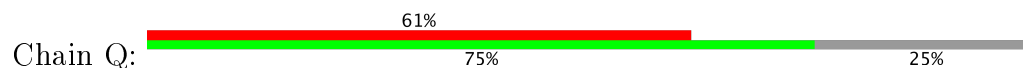
• Molecule 5: Small nuclear ribonucleoprotein Sm D2



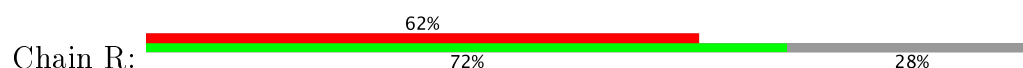
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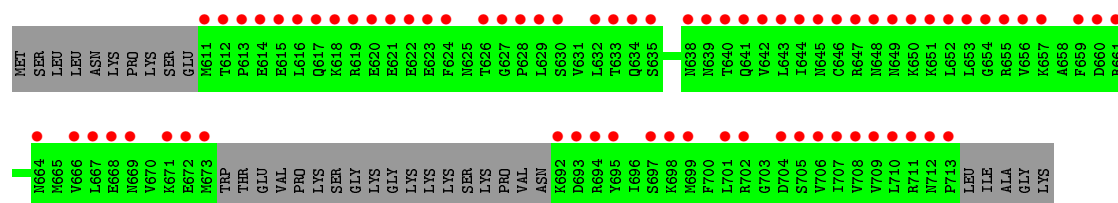


• Molecule 5: Small nuclear ribonucleoprotein Sm D2

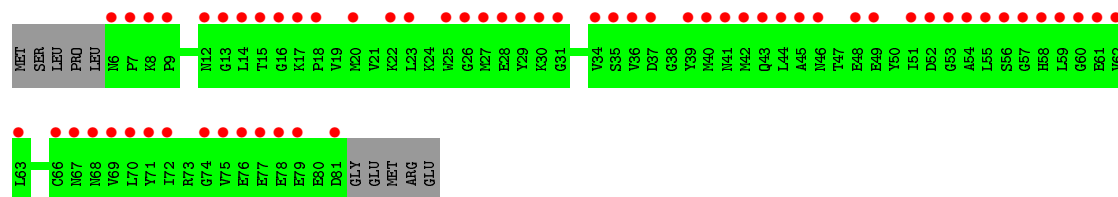
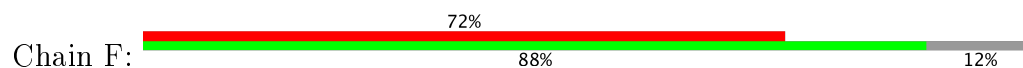


• Molecule 5: Small nuclear ribonucleoprotein Sm D2

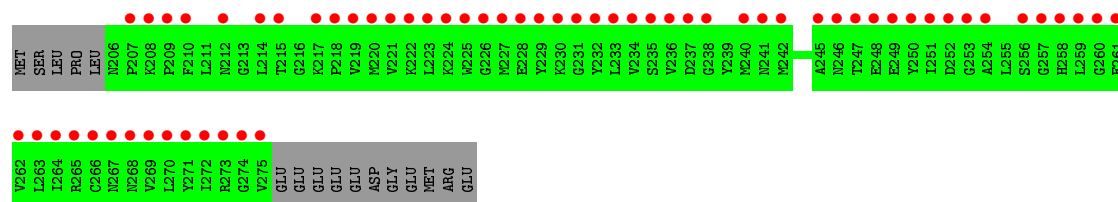
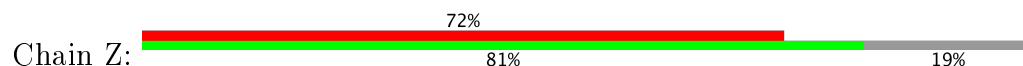




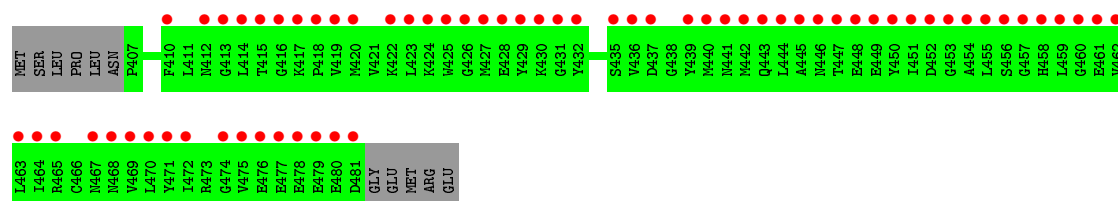
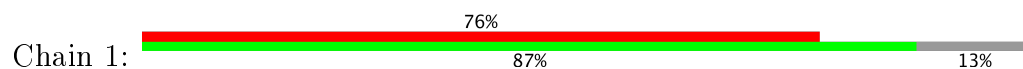
• Molecule 6: Small nuclear ribonucleoprotein F



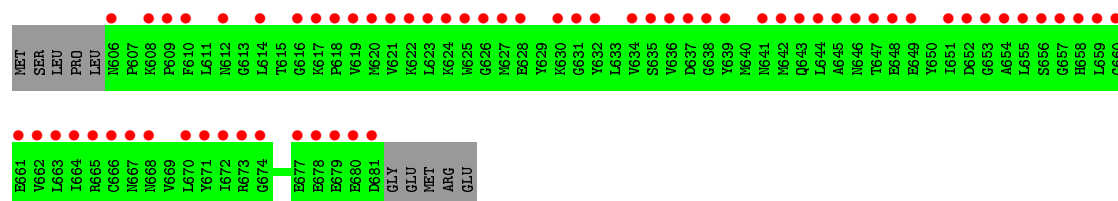
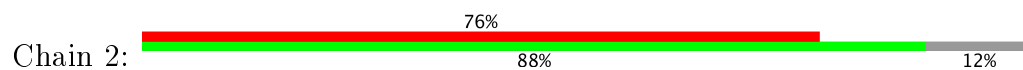
• Molecule 6: Small nuclear ribonucleoprotein F



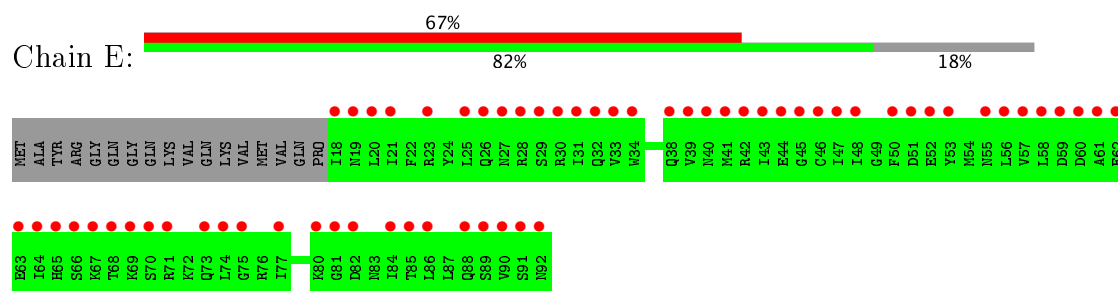
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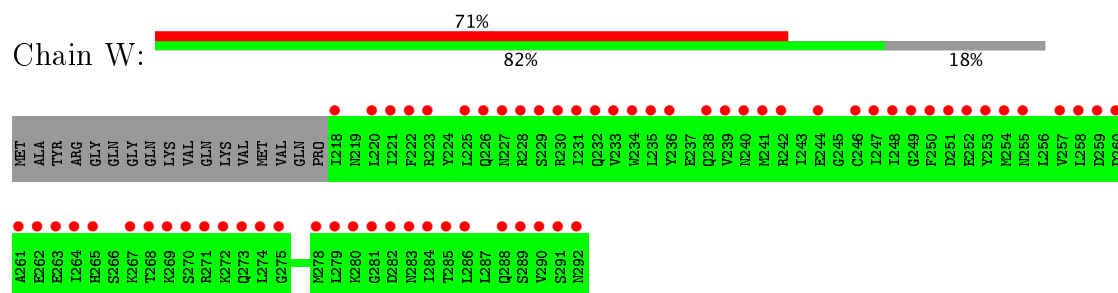
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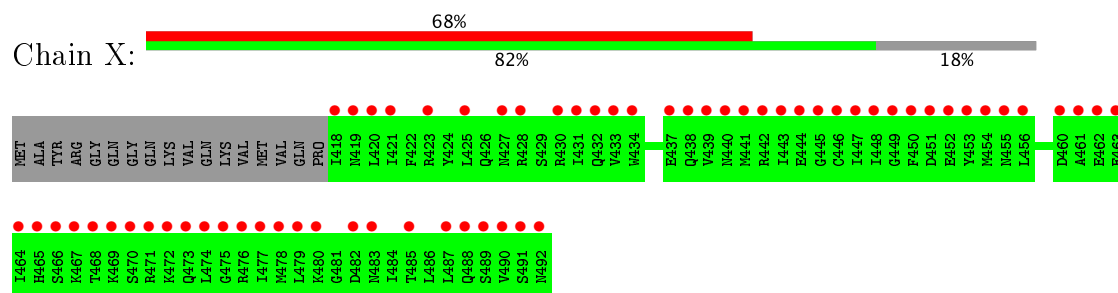
• Molecule 7: Small nuclear ribonucleoprotein E



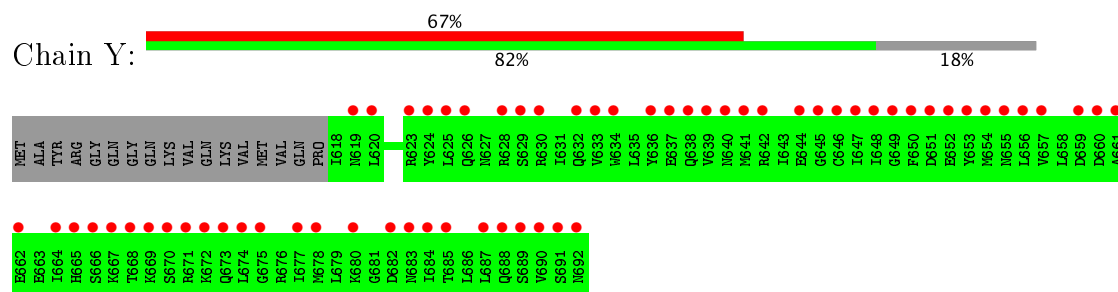
- Molecule 7: Small nuclear ribonucleoprotein E



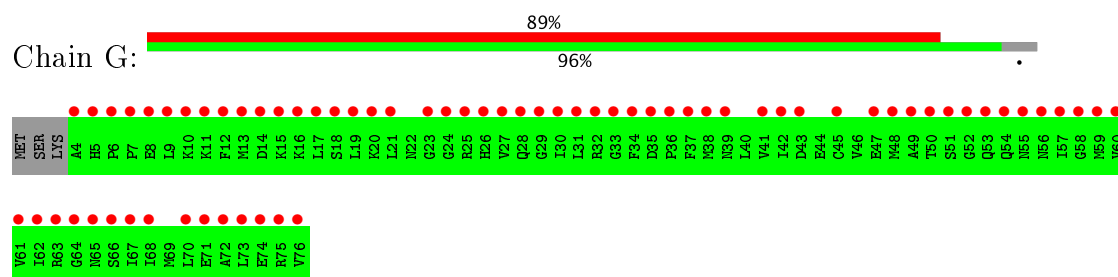
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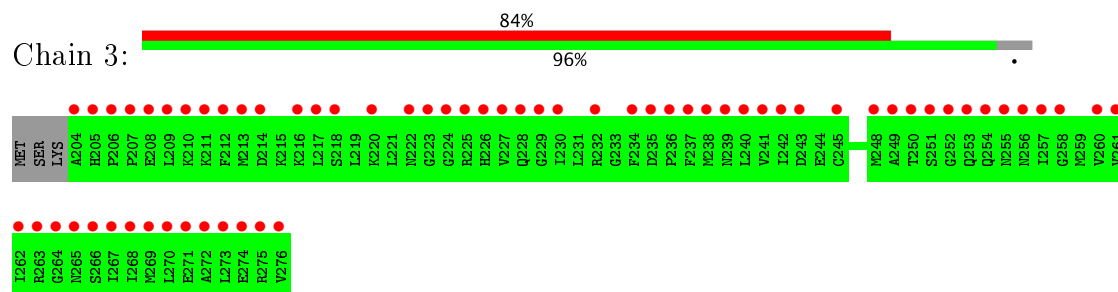
- Molecule 7: Small nuclear ribonucleoprotein E



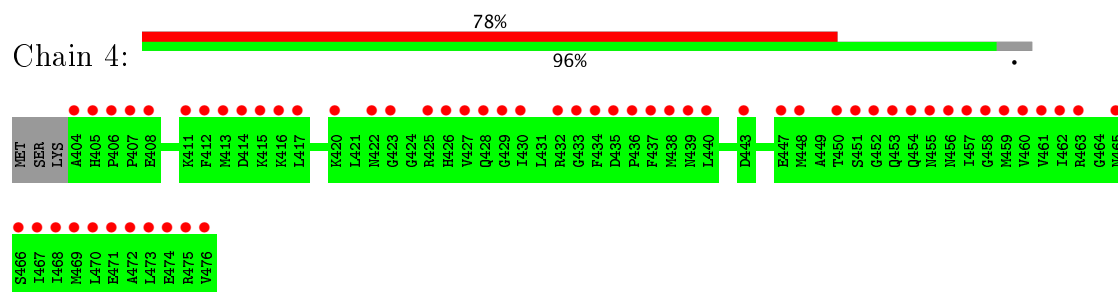
- Molecule 8: Small nuclear ribonucleoprotein G



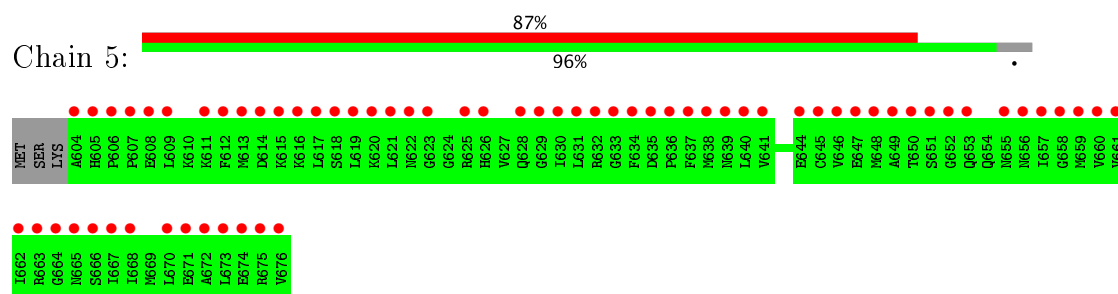
- Molecule 8: Small nuclear ribonucleoprotein G



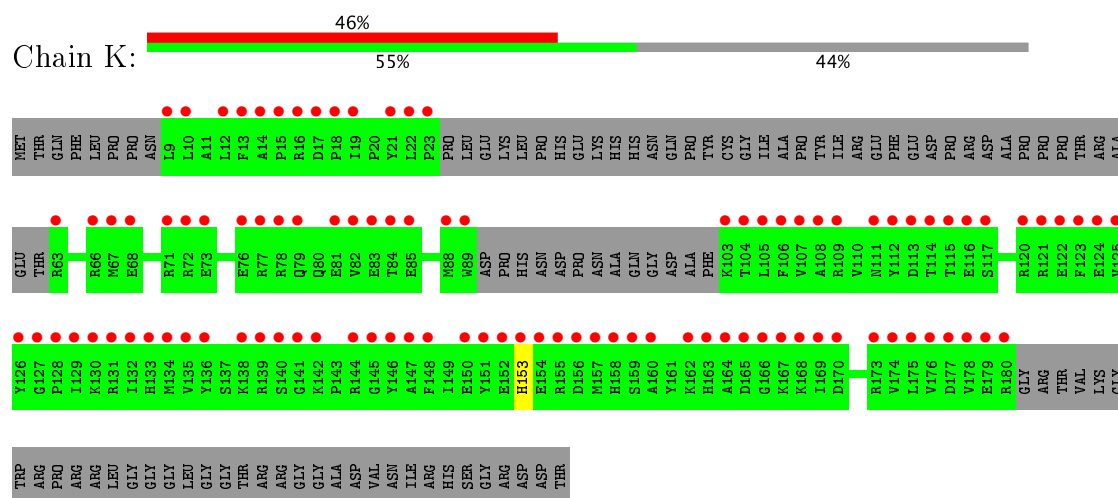
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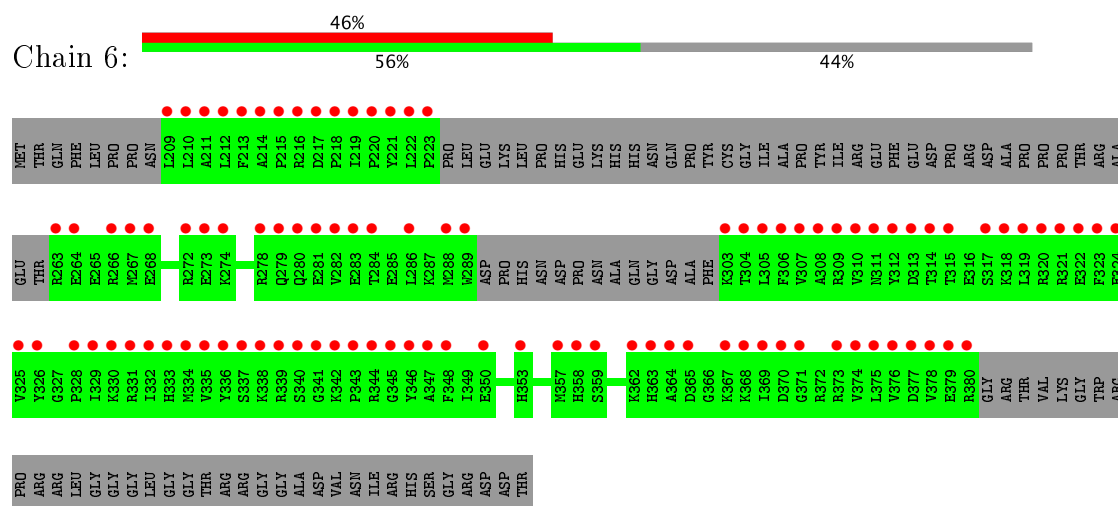
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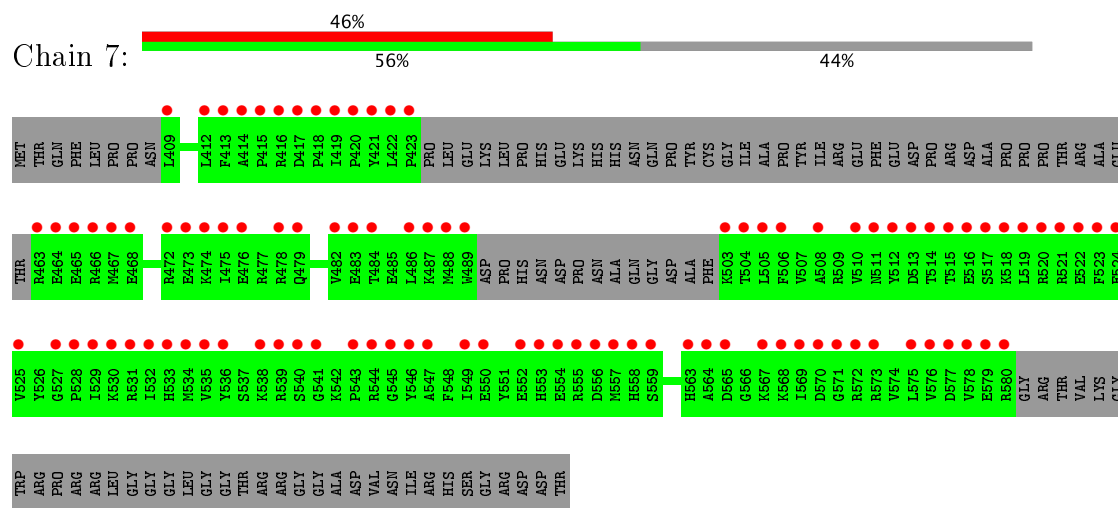
- Molecule 9: U1 small nuclear ribonucleoprotein 70 kDa



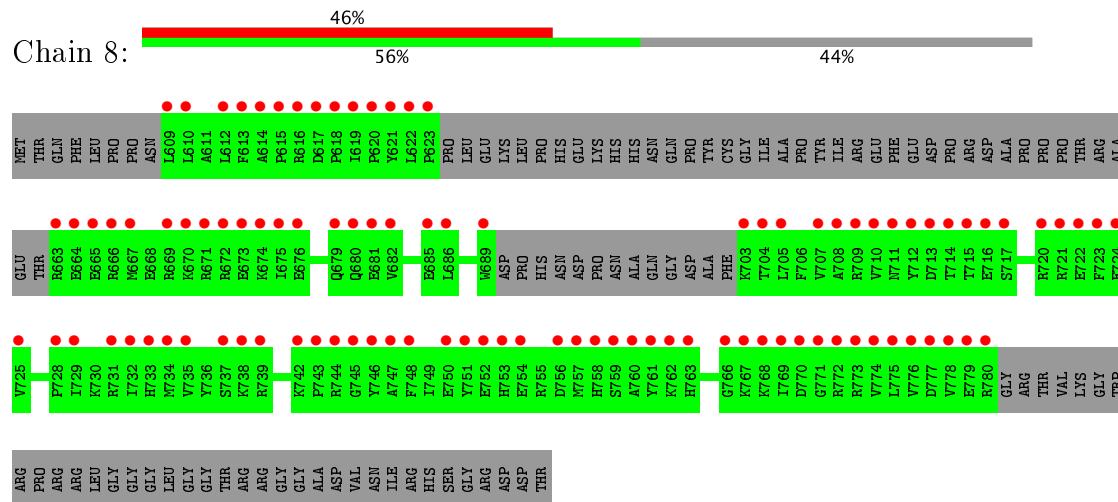
- Molecule 9: U1 small nuclear ribonucleoprotein 70 kDa



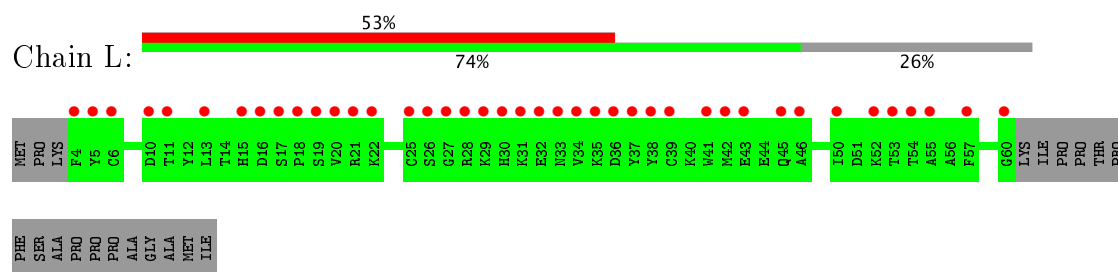
- Molecule 9: U1 small nuclear ribonucleoprotein 70 kDa



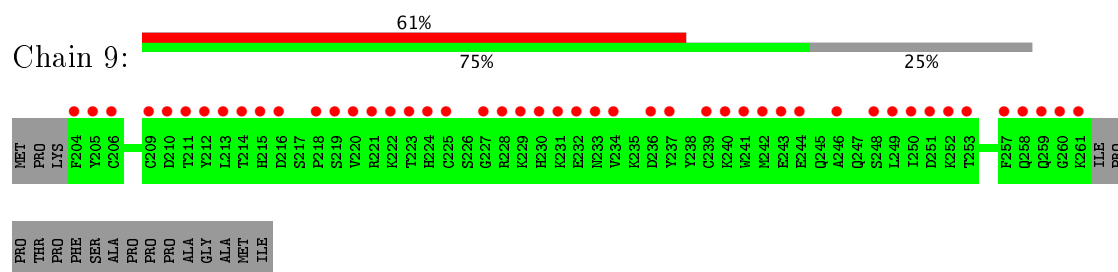
- Molecule 9: U1 small nuclear ribonucleoprotein 70 kDa



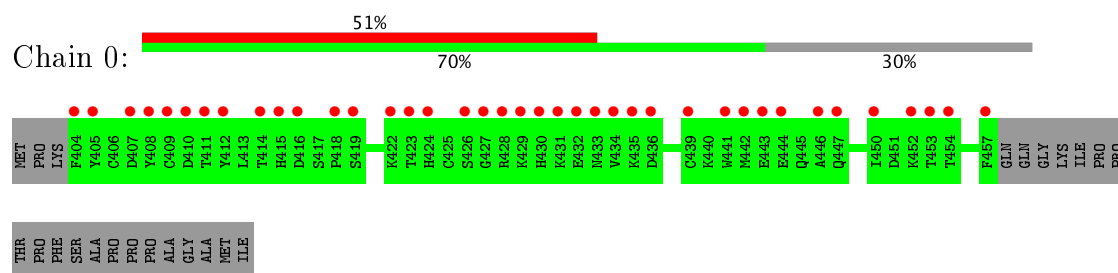
- Molecule 10: U1 small nuclear ribonucleoprotein C



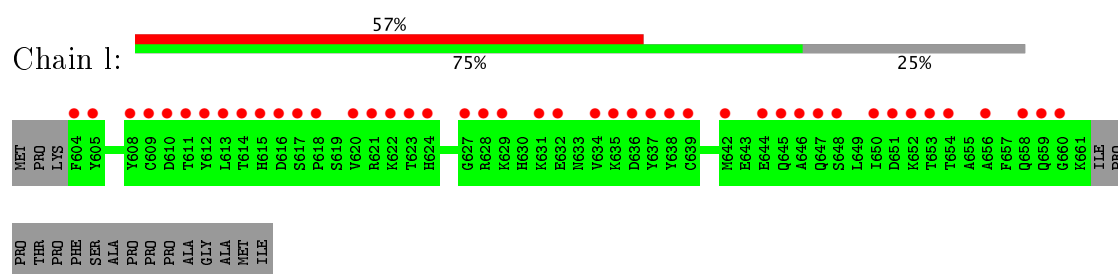
- Molecule 10: U1 small nuclear ribonucleoprotein C



- Molecule 10: U1 small nuclear ribonucleoprotein C



- Molecule 10: U1 small nuclear ribonucleoprotein C



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	126.47Å 127.08Å 152.02Å 95.42° 105.92° 101.80°	Depositor
Resolution (Å)	123.09 – 5.49 122.79 – 5.49	Depositor EDS
% Data completeness (in resolution range)	(Not available) (123.09-5.49) 93.9 (122.79-5.49)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.99 (at 5.42Å)	Xtriage
Refinement program		Depositor
R, R_{free}	(Not available) , (Not available) 0.497 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	251.7	Xtriage
Anisotropy	0.213	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.58 , -4.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.72	EDS
Total number of atoms	3365	wwPDB-VP
Average B, all atoms (Å ²)	231.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	V	138	0	0	0	0
1	v	138	0	0	0	1
1	w	138	0	0	0	0
1	x	138	0	0	0	0
2	D	76	0	0	0	0
2	S	76	0	0	0	0
2	T	76	0	0	0	0
2	U	76	0	0	0	0
3	A	64	0	0	0	0
3	H	64	0	0	0	0
3	I	63	0	0	0	0
3	J	63	0	0	0	0
4	B	77	0	0	0	0
4	M	77	0	0	0	0
4	N	76	0	0	0	0
4	O	77	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	88	0	0	0	0
5	P	86	0	0	0	0
5	Q	89	0	0	0	0
5	R	85	0	0	0	0
6	1	75	0	0	0	0
6	2	76	0	0	0	0
6	F	76	0	0	0	0
6	Z	70	0	0	0	0
7	E	75	0	0	0	0
7	W	75	0	0	0	0
7	X	75	0	0	0	0
7	Y	75	0	0	0	0
8	3	73	0	0	0	0
8	4	73	0	0	0	0
8	5	73	0	0	0	0
8	G	73	0	0	0	0
9	6	120	0	0	0	0
9	7	120	0	0	0	0
9	8	120	0	0	0	0
9	K	120	0	0	0	1
10	0	54	0	0	0	0
10	9	58	0	0	0	0
10	L	57	0	0	0	0
10	l	58	0	0	0	0
11	0	1	0	0	0	0
11	9	1	0	0	0	0
11	L	1	0	0	0	0
11	l	1	0	0	0	0
All	All	3365	0	0	0	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 0.

There are no clashes within the asymmetric unit.

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:v:214:A:P	9:K:153:HIS:CA[1_545]	2.05	0.15

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	V	0/138	-	-
1	v	0/138	-	-
1	w	0/138	-	-
1	x	0/138	-	-
All	All	0/552	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	V	138/138 (100%)	15.61	137 (99%) 0 0	232, 232, 232, 232	0
1	v	138/138 (100%)	16.24	136 (98%) 0 0	232, 232, 232, 232	0
1	w	138/138 (100%)	15.57	137 (99%) 0 0	232, 232, 232, 232	0
1	x	138/138 (100%)	15.06	137 (99%) 0 0	232, 232, 232, 232	0
2	D	76/126 (60%)	6.75	64 (84%) 0 1	232, 232, 232, 232	0
2	S	76/126 (60%)	6.89	62 (81%) 0 2	232, 232, 232, 232	0
2	T	76/126 (60%)	6.78	64 (84%) 0 1	232, 232, 232, 232	0
2	U	76/126 (60%)	6.32	66 (86%) 0 1	232, 232, 232, 232	0
3	A	64/174 (36%)	6.27	52 (81%) 0 2	232, 232, 232, 232	0
3	H	64/174 (36%)	6.26	55 (85%) 0 1	232, 232, 232, 232	0
3	I	63/174 (36%)	5.28	52 (82%) 0 2	232, 232, 232, 232	0
3	J	63/174 (36%)	5.93	49 (77%) 0 2	232, 232, 232, 232	0
4	B	77/119 (64%)	6.74	69 (89%) 0 1	232, 232, 232, 232	0
4	M	77/119 (64%)	5.62	67 (87%) 0 1	232, 232, 232, 232	0
4	N	76/119 (63%)	6.15	62 (81%) 0 2	232, 232, 232, 232	0
4	O	77/119 (64%)	5.94	66 (85%) 0 1	232, 232, 232, 232	0
5	C	88/118 (74%)	5.82	77 (87%) 0 1	232, 232, 232, 232	0
5	P	86/118 (72%)	6.04	75 (87%) 0 1	232, 232, 232, 232	0
5	Q	89/118 (75%)	5.77	72 (80%) 0 2	232, 232, 232, 232	0
5	R	85/118 (72%)	6.54	73 (85%) 0 1	232, 232, 232, 232	0
6	1	75/86 (87%)	6.66	65 (86%) 0 1	232, 232, 232, 232	0
6	2	76/86 (88%)	6.74	65 (85%) 0 1	232, 232, 232, 232	0
6	F	76/86 (88%)	6.40	62 (81%) 0 2	232, 232, 232, 232	0
6	Z	70/86 (81%)	5.99	62 (88%) 0 1	232, 232, 232, 232	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
7	E	75/92 (81%)	6.54	62 (82%) 0 2	232, 232, 232, 232	0
7	W	75/92 (81%)	5.86	65 (86%) 0 1	232, 232, 232, 232	0
7	X	75/92 (81%)	6.42	63 (84%) 0 1	232, 232, 232, 232	0
7	Y	75/92 (81%)	5.72	62 (82%) 0 2	232, 232, 232, 232	0
8	3	73/76 (96%)	5.92	64 (87%) 0 1	232, 232, 232, 232	0
8	4	73/76 (96%)	5.63	59 (80%) 0 2	232, 232, 232, 232	0
8	5	73/76 (96%)	6.49	66 (90%) 0 1	232, 232, 232, 232	0
8	G	73/76 (96%)	7.13	68 (93%) 0 1	232, 232, 232, 232	0
9	6	120/216 (55%)	6.23	99 (82%) 0 2	232, 232, 232, 232	0
9	7	120/216 (55%)	6.22	99 (82%) 0 2	232, 232, 232, 232	0
9	8	120/216 (55%)	5.78	99 (82%) 0 2	232, 232, 232, 232	0
9	K	120/216 (55%)	6.46	100 (83%) 0 1	232, 232, 232, 232	0
10	0	54/77 (70%)	5.86	39 (72%) 0 2	232, 232, 232, 232	0
10	9	58/77 (75%)	5.73	47 (81%) 0 2	232, 232, 232, 232	0
10	L	57/77 (74%)	5.37	41 (71%) 0 2	232, 232, 232, 232	0
10	l	58/77 (75%)	5.91	44 (75%) 0 2	232, 232, 232, 232	0
All	All	3361/4888 (68%)	7.73	2903 (86%) 0 1	232, 232, 232, 232	0

All (2903) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	V	56	A	51.6
1	w	489	C	49.8
1	V	110	G	49.4
1	v	342	G	48.8
1	w	564	G	48.8
1	V	7	A	48.2
1	V	12	G	46.1
1	V	109	G	43.0
1	w	532	G	42.8
1	x	721	G	42.3
1	v	364	G	40.5
1	x	751	C	39.7
1	V	161	C	39.3
1	V	23	A	39.2
1	v	346	G	38.5

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Mol	Chain	Res	Type	RSRZ
1	V	163	U	38.1
1	w	454	A	37.8
1	v	220	G	37.8
1	w	557	U	37.8
1	x	761	C	37.1
1	V	150	U	36.7
1	v	290	U	36.5
1	V	139	G	36.2
1	v	285	U	36.2
1	v	283	C	35.9
1	w	539	G	35.6
1	w	525	A	35.0
1	w	509	G	34.9
1	v	321	G	34.9
1	v	203	A	34.8
1	v	212	G	34.1
1	w	440	G	33.9
1	x	636	A	33.7
1	x	615	G	33.6
1	w	547	C	33.6
1	V	53	G	33.6
1	v	305	U	33.4
1	w	560	C	33.3
1	x	649	A	33.3
1	w	436	A	33.2
1	v	210	U	32.7
1	v	245	U	32.2
1	v	252	G	32.0
1	v	214	A	31.9
1	v	217	G	31.8
1	v	284	G	31.7
1	V	2	U	31.7
1	x	687	C	31.4
1	x	698	C	30.9
1	w	548	G	30.7
2	S	269	ARG	29.9
1	v	250	G	29.7
1	v	339	G	29.6
1	V	84	G	29.5
1	x	684	G	29.5
1	V	43	U	29.3
1	v	318	A	29.2

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Mol	Chain	Res	Type	RSRZ
1	x	759	C	28.9
1	v	295	U	28.9
1	x	730	G	28.9
1	x	691	G	28.6
1	V	113	A	28.2
1	w	531	U	27.9
7	X	466	SER	27.7
1	w	485	U	27.7
1	w	538	G	27.6
1	V	37	G	27.5
1	V	41	G	27.4
1	v	332	G	27.4
1	x	623	A	27.3
1	v	353	C	27.3
1	V	130	G	27.3
1	x	706	G	27.2
1	v	360	C	27.2
9	K	84	THR	27.2
9	K	72	ARG	27.0
1	v	362	C	26.9
1	V	133	G	26.9
1	v	326	A	26.9
1	V	106	G	26.7
5	R	649	ASN	26.6
1	V	132	G	26.6
1	V	49	A	26.5
4	N	431	GLY	26.3
1	V	47	C	26.2
1	x	729	U	26.2
1	x	696	U	26.0
1	w	425	C	26.0
1	x	740	G	26.0
1	w	510	G	25.8
1	x	723	A	25.8
1	v	317	G	25.6
1	v	225	C	25.6
1	v	237	G	25.5
1	w	501	C	25.4
1	w	441	G	25.4
1	v	227	U	25.4
1	v	294	A	25.4
1	v	347	C	25.1

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Mol	Chain	Res	Type	RSRZ
1	x	727	U	24.9
1	w	411	G	24.8
1	V	94	A	24.7
9	6	353	HIS	24.5
10	l	627	GLY	24.3
1	v	358	U	24.2
1	x	643	U	24.2
1	V	155	C	24.1
1	x	717	G	24.1
1	x	635	A	24.1
1	V	91	G	24.0
1	V	95	U	23.9
1	v	209	C	23.9
1	w	541	G	23.9
1	V	126	A	23.8
1	x	654	A	23.8
1	V	5	U	23.7
1	v	236	A	23.6
1	w	496	U	23.4
1	v	351	C	23.3
5	Q	437	LYS	23.1
1	x	614	A	23.1
5	R	645	ASN	23.1
1	w	408	C	23.0
3	A	77	LEU	23.0
2	S	272	ILE	23.0
1	w	444	U	22.9
1	v	240	G	22.8
5	R	629	LEU	22.7
1	w	428	G	22.6
1	v	229	A	22.6
1	V	55	G	22.5
1	V	30	U	22.5
1	v	253	G	22.4
1	x	648	C	22.4
8	3	235	ASP	22.4
1	w	520	U	22.3
1	v	302	A	22.2
1	x	731	U	22.2
1	x	626	A	22.2
1	w	507	U	22.1
1	x	656	A	22.0

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Mol	Chain	Res	Type	RSRZ
8	4	435	ASP	21.9
1	v	307	U	21.9
1	x	602	U	21.8
1	V	162	C	21.8
5	R	620	GLU	21.8
8	5	663	ARG	21.7
1	v	343	A	21.5
1	V	36	A	21.4
1	v	311	A	21.4
1	x	747	C	21.2
1	w	518	A	21.1
1	x	604	C	21.1
1	w	513	A	21.0
7	W	241	MET	21.0
7	E	41	MET	21.0
6	2	668	ASN	20.9
1	V	46	C	20.9
1	V	15	G	20.9
2	T	467	LYS	20.9
7	Y	661	ALA	20.9
1	w	423	A	20.9
6	Z	228	GLU	20.8
1	x	726	A	20.7
1	v	301	C	20.6
1	w	442	U	20.6
1	v	303	A	20.5
1	v	221	A	20.1
1	w	410	U	20.1
1	v	215	G	20.1
1	x	610	U	20.1
1	V	86	C	20.0
4	B	58	LEU	20.0
1	x	641	G	19.9
10	0	428	ARG	19.9
1	w	519	C	19.8
1	w	452	G	19.8
6	1	479	GLU	19.8
4	B	71	PRO	19.8
1	w	503	A	19.7
1	v	288	C	19.7
1	w	533	G	19.7
1	V	13	C	19.7

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Mol	Chain	Res	Type	RSRZ
1	V	115	U	19.7
10	9	233	ASN	19.7
7	X	440	ASN	19.6
8	G	74	GLU	19.6
1	V	137	U	19.6
1	x	694	A	19.5
1	V	118	A	19.5
1	x	703	A	19.5
6	F	48	GLU	19.5
6	2	622	LYS	19.4
1	x	686	C	19.2
1	V	108	G	19.2
1	v	287	C	19.1
9	K	116	GLU	19.1
6	1	447	THR	19.0
1	x	605	U	19.0
1	V	146	G	19.0
1	w	488	C	19.0
6	2	672	ILE	18.9
1	w	526	A	18.8
1	x	764	G	18.8
5	C	26	THR	18.7
1	x	650	G	18.6
4	N	446	THR	18.6
2	D	13	ALA	18.5
8	3	267	ILE	18.4
4	O	616	THR	18.4
2	U	646	ILE	18.3
9	6	311	ASN	18.3
1	x	612	G	18.2
1	v	232	A	18.2
1	w	551	C	18.2
7	E	61	ALA	18.2
9	6	350	GLU	18.1
10	9	224	HIS	18.1
1	x	638	G	18.1
1	w	494	A	18.1
1	w	416	G	18.1
1	w	429	A	18.1
1	x	711	A	18.0
1	v	352	G	18.0
1	x	619	A	17.9

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Mol	Chain	Res	Type	RSRZ
9	8	620	PRO	17.8
10	0	407	ASP	17.8
6	F	28	GLU	17.8
1	x	753	C	17.8
9	7	479	GLN	17.8
1	w	516	C	17.8
3	H	284	GLY	17.8
7	X	445	GLY	17.7
1	x	607	A	17.6
1	v	330	G	17.6
1	v	202	U	17.6
1	V	27	U	17.6
1	V	103	A	17.6
1	v	322	C	17.6
1	w	536	G	17.5
1	V	100	C	17.5
2	T	420	CYS	17.4
1	V	127	U	17.4
9	7	467	MET	17.4
1	V	159	C	17.3
1	V	104	A	17.3
1	v	291	G	17.3
8	G	29	GLY	17.3
1	x	690	U	17.3
5	C	64	ASN	17.3
1	x	755	C	17.2
9	6	283	GLU	17.1
6	F	17	LYS	17.1
1	w	521	G	17.1
10	l	621	ARG	17.1
1	x	644	U	17.1
2	D	14	GLU	17.0
3	I	428	GLY	17.0
4	M	259	SER	17.0
1	x	688	C	16.9
5	C	27	GLY	16.9
1	w	545	U	16.8
1	w	549	U	16.8
1	w	491	G	16.8
5	P	307	ILE	16.8
1	V	54	A	16.7
1	x	622	U	16.7

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Mol	Chain	Res	Type	RSRZ
1	w	493	G	16.7
6	Z	222	LYS	16.7
1	x	685	U	16.6
9	7	573	ARG	16.6
6	1	451	ILE	16.6
1	v	310	G	16.6
1	v	238	G	16.6
1	V	105	U	16.5
1	x	653	G	16.5
1	x	627	U	16.5
3	J	630	THR	16.5
6	2	618	PRO	16.5
1	v	286	C	16.4
6	F	41	ASN	16.4
6	1	468	ASN	16.4
1	V	10	U	16.4
1	x	640	G	16.4
9	K	163	HIS	16.3
1	V	1	A	16.2
1	v	324	U	16.2
8	4	466	SER	16.2
1	V	85	U	16.1
1	w	498	C	16.0
9	K	152	GLU	16.0
1	v	336	G	15.9
1	w	517	G	15.9
9	7	538	LYS	15.9
8	G	71	GLU	15.9
1	v	223	A	15.8
10	0	427	GLY	15.8
1	x	709	G	15.8
5	P	241	GLN	15.8
1	w	438	G	15.8
1	V	98	C	15.7
1	w	422	U	15.7
9	7	468	GLU	15.7
7	X	490	VAL	15.7
9	K	128	PRO	15.7
10	L	25	CYS	15.7
4	M	254	GLN	15.7
1	w	490	U	15.6
9	6	328	PRO	15.6

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Mol	Chain	Res	Type	RSRZ
2	S	231	LYS	15.6
3	H	243	CYS	15.5
1	V	88	C	15.5
1	w	562	C	15.5
5	P	239	ASN	15.5
1	v	231	C	15.5
4	B	28	THR	15.5
1	V	128	U	15.4
2	U	653	GLY	15.4
3	I	481	THR	15.4
5	R	710	LEU	15.3
8	G	55	ASN	15.3
2	D	28	TYR	15.3
3	A	81	THR	15.3
1	x	732	G	15.3
2	T	439	MET	15.2
1	v	333	G	15.2
3	H	282	VAL	15.1
1	x	642	U	15.1
9	7	553	HIS	15.1
4	B	66	ARG	15.1
1	x	752	G	15.0
8	5	646	VAL	15.0
3	J	621	LEU	15.0
1	w	431	C	15.0
1	w	530	G	15.0
2	S	239	MET	14.9
1	V	83	C	14.9
1	x	624	C	14.9
8	G	70	LEU	14.9
1	w	414	A	14.9
6	1	416	GLY	14.9
1	v	211	G	14.9
1	V	111	A	14.9
1	w	435	A	14.8
1	w	556	U	14.8
6	1	475	VAL	14.8
7	E	29	SER	14.8
7	E	70	SER	14.8
1	V	24	C	14.8
10	l	616	ASP	14.8
10	L	52	LYS	14.7

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Mol	Chain	Res	Type	RSRZ
10	L	32	GLU	14.7
1	V	149	U	14.7
1	x	701	C	14.7
9	8	716	GLU	14.7
1	V	151	C	14.6
6	Z	217	LYS	14.6
1	w	522	C	14.6
4	B	31	GLY	14.5
8	G	49	ALA	14.5
1	v	331	U	14.5
2	U	638	ASN	14.5
7	W	263	GLU	14.5
5	R	615	GLU	14.5
1	v	335	A	14.5
1	x	655	G	14.4
7	W	251	ASP	14.4
6	F	72	ILE	14.4
1	w	512	A	14.4
10	l	632	GLU	14.4
5	R	698	LYS	14.3
1	V	131	U	14.3
8	5	645	CYS	14.3
1	V	97	U	14.3
1	V	160	C	14.3
1	w	403	A	14.3
1	x	744	C	14.2
9	7	564	ALA	14.2
2	S	230	GLY	14.2
6	2	641	ASN	14.2
2	U	640	ASN	14.2
3	A	76	ASN	14.2
8	5	637	PHE	14.1
7	Y	683	ASN	14.1
4	M	233	ASP	14.1
6	1	477	GLU	14.1
4	B	10	LEU	14.1
1	v	230	U	14.1
2	S	275	ASP	14.1
9	8	732	ILE	14.1
5	Q	420	GLU	14.1
1	w	439	U	14.1
4	N	459	SER	14.0

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Mol	Chain	Res	Type	RSRZ
8	5	634	PHE	14.0
3	J	672	LEU	14.0
4	O	633	ASP	14.0
9	7	478	ARG	14.0
1	x	645	U	14.0
4	B	21	ASN	13.9
9	6	346	TYR	13.9
4	O	654	GLN	13.9
9	K	177	ASP	13.9
4	B	40	LEU	13.9
1	x	630	U	13.9
1	x	754	G	13.9
9	7	484	THR	13.8
3	H	214	ASP	13.8
1	V	121	G	13.8
5	C	48	ASN	13.8
9	8	757	MET	13.8
8	4	416	LYS	13.8
2	S	217	ILE	13.8
5	Q	418	LYS	13.7
1	V	102	A	13.7
1	w	559	C	13.7
1	x	621	A	13.7
6	Z	226	GLY	13.7
4	N	415	VAL	13.7
1	w	508	G	13.7
1	w	453	G	13.7
6	F	67	ASN	13.7
9	7	483	GLU	13.6
1	V	9	C	13.6
1	w	506	G	13.6
1	x	741	G	13.6
7	E	46	CYS	13.6
1	v	355	C	13.6
1	V	19	A	13.6
2	T	445	ASN	13.5
1	x	702	A	13.5
4	O	670	LEU	13.5
1	w	546	G	13.5
6	1	418	PRO	13.5
2	T	431	LYS	13.5
9	6	358	HIS	13.4

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Mol	Chain	Res	Type	RSRZ
7	X	489	SER	13.4
7	E	85	THR	13.4
1	v	206	U	13.4
1	V	112	A	13.4
7	X	438	GLN	13.4
4	B	77	ASP	13.4
1	w	504	A	13.3
1	w	514	C	13.3
8	5	636	PRO	13.3
4	N	427	GLY	13.3
3	J	619	CYS	13.2
2	D	71	LEU	13.2
3	H	225	ARG	13.2
6	F	59	LEU	13.2
6	F	53	GLY	13.2
10	0	432	GLU	13.2
5	P	242	VAL	13.1
1	v	337	U	13.1
5	C	18	LYS	13.1
9	7	557	MET	13.1
2	D	40	ASN	13.1
2	T	444	SER	13.1
8	G	25	ARG	13.1
6	2	648	GLU	13.1
2	S	260	GLN	13.1
1	x	763	U	13.0
6	1	437	ASP	13.0
2	T	425	GLY	13.0
5	P	232	LEU	13.0
4	M	205	ARG	13.0
1	w	426	A	13.0
1	w	561	C	13.0
9	K	146	TYR	13.0
1	V	119	C	13.0
8	3	240	LEU	13.0
2	D	6	PRO	13.0
2	U	659	GLU	13.0
8	4	465	ASN	13.0
1	x	651	G	13.0
9	7	505	LEU	12.9
1	x	617	G	12.9
2	T	419	THR	12.9

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Mol	Chain	Res	Type	RSRZ
9	7	578	VAL	12.9
1	x	736	G	12.9
4	O	656	GLU	12.9
10	9	223	THR	12.9
8	5	658	GLY	12.9
9	6	357	MET	12.9
6	F	54	ALA	12.8
6	Z	221	VAL	12.8
1	w	450	G	12.8
5	Q	412	THR	12.8
3	H	228	ILE	12.8
4	N	433	ASP	12.8
6	2	651	ILE	12.8
1	V	125	A	12.8
5	P	251	LYS	12.8
7	E	74	LEU	12.8
4	N	451	GLU	12.8
8	3	216	LYS	12.8
6	1	427	MET	12.8
1	w	448	C	12.7
1	w	443	U	12.7
1	v	313	A	12.7
7	Y	685	THR	12.7
1	v	350	U	12.7
10	0	423	THR	12.7
9	K	111	ASN	12.7
10	L	28	ARG	12.7
1	V	144	C	12.6
1	x	700	C	12.6
2	D	72	ILE	12.6
4	O	667	TYR	12.6
1	w	487	C	12.6
2	D	12	GLU	12.6
2	U	610	LEU	12.6
6	2	667	ASN	12.5
10	l	623	THR	12.5
4	N	405	ARG	12.5
6	F	77	GLU	12.5
4	O	614	THR	12.5
2	S	236	GLU	12.5
1	V	152	G	12.5
1	w	505	U	12.5

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Mol	Chain	Res	Type	RSRZ
2	D	39	MET	12.5
5	R	653	LEU	12.5
3	H	233	ALA	12.4
8	G	65	ASN	12.4
2	S	257	GLN	12.4
10	9	228	ARG	12.4
6	2	627	MET	12.4
1	x	608	C	12.4
1	x	609	C	12.4
9	8	715	THR	12.4
6	1	445	ALA	12.3
7	Y	691	SER	12.3
10	l	631	LYS	12.3
9	7	413	PHE	12.3
2	T	474	PRO	12.3
6	F	74	GLY	12.3
8	5	671	GLU	12.3
4	B	27	GLY	12.3
3	I	485	PRO	12.3
3	A	83	GLU	12.2
8	G	10	LYS	12.2
5	R	655	ARG	12.2
6	1	446	ASN	12.2
1	v	344	C	12.2
1	x	625	C	12.2
4	M	224	GLN	12.1
5	R	628	PRO	12.1
9	8	775	LEU	12.1
9	6	214	ALA	12.1
4	B	59	SER	12.1
3	A	14	ASP	12.1
1	v	207	A	12.1
1	w	407	A	12.1
4	N	409	LYS	12.1
1	x	733	G	12.1
9	6	273	GLU	12.1
1	v	356	U	12.0
1	x	683	C	12.0
7	W	260	ASP	12.0
1	x	718	A	12.0
2	D	75	ASP	12.0
8	4	458	GLY	12.0

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Mol	Chain	Res	Type	RSRZ
1	v	315	U	12.0
2	S	229	ARG	12.0
5	Q	509	VAL	11.9
10	l	651	ASP	11.9
1	x	695	U	11.9
7	X	485	THR	11.9
9	7	415	PRO	11.9
1	x	606	U	11.9
7	X	474	LEU	11.9
1	w	401	A	11.9
8	G	39	ASN	11.9
9	6	374	VAL	11.9
2	T	434	GLU	11.9
3	J	643	CYS	11.9
7	E	88	GLN	11.9
1	w	420	G	11.9
1	V	96	U	11.9
7	E	30	ARG	11.9
2	S	212	GLU	11.8
1	x	713	A	11.8
2	T	469	ARG	11.8
5	P	225	ASN	11.8
9	6	379	GLU	11.8
9	K	129	ILE	11.8
2	U	674	PRO	11.8
1	v	314	C	11.8
1	x	697	U	11.8
6	Z	247	THR	11.8
1	v	234	G	11.8
9	6	272	ARG	11.8
6	F	20	MET	11.8
5	C	59	PHE	11.8
8	3	212	PHE	11.7
1	V	42	U	11.7
7	W	264	ILE	11.7
4	B	20	LYS	11.7
5	P	231	VAL	11.7
10	l	624	HIS	11.7
6	F	58	HIS	11.7
9	K	104	THR	11.7
2	S	277	LEU	11.7
9	7	539	ARG	11.7

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Mol	Chain	Res	Type	RSRZ
9	K	131	ARG	11.7
6	2	646	ASN	11.7
5	C	70	VAL	11.7
2	S	253	GLY	11.7
1	v	361	C	11.7
3	A	24	GLY	11.7
8	G	51	SER	11.7
1	w	424	C	11.7
5	C	68	GLU	11.6
7	Y	642	ARG	11.6
5	P	221	GLU	11.6
9	6	312	TYR	11.6
4	M	261	ARG	11.6
1	w	449	A	11.6
10	9	234	VAL	11.6
1	w	412	G	11.6
1	w	434	G	11.6
1	V	140	G	11.6
5	C	57	LYS	11.6
5	P	308	VAL	11.6
1	V	52	G	11.5
1	w	451	G	11.5
9	8	756	ASP	11.5
9	K	133	HIS	11.5
1	v	239	U	11.5
10	L	26	SER	11.5
8	G	58	GLY	11.5
6	1	480	GLU	11.5
3	A	13	ILE	11.5
5	R	664	ASN	11.5
8	G	67	ILE	11.4
3	H	275	GLU	11.4
6	F	35	SER	11.4
9	6	220	PRO	11.4
9	K	23	PRO	11.4
2	T	454	ARG	11.4
1	x	632	A	11.4
8	G	62	ILE	11.3
1	x	748	G	11.3
9	K	159	SER	11.3
7	W	240	ASN	11.3
6	2	678	GLU	11.3

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Mol	Chain	Res	Type	RSRZ
1	V	38	G	11.3
1	x	725	A	11.3
7	E	39	VAL	11.3
1	v	228	G	11.2
2	U	624	THR	11.2
4	O	644	LYS	11.2
1	x	620	G	11.2
1	x	637	G	11.2
7	E	42	ARG	11.2
8	G	47	GLU	11.2
2	T	466	CYS	11.2
3	H	268	GLY	11.2
6	Z	235	SER	11.2
1	v	323	A	11.2
1	w	430	U	11.2
9	6	370	ASP	11.1
9	6	279	GLN	11.1
4	N	471	PRO	11.1
1	V	25	C	11.1
6	2	664	ILE	11.1
3	A	35	ASP	11.1
1	v	296	U	11.1
7	E	92	ASN	11.1
8	3	260	VAL	11.1
9	K	113	ASP	11.1
3	A	34	PHE	11.1
7	X	476	ARG	11.0
3	I	431	LYS	11.0
1	V	135	A	11.0
1	v	242	U	11.0
1	w	497	U	11.0
2	D	69	ARG	11.0
8	5	650	THR	11.0
1	v	243	U	11.0
9	K	122	GLU	11.0
1	w	527	U	11.0
8	G	30	ILE	11.0
1	x	634	G	11.0
10	0	452	LYS	11.0
2	T	452	ASP	11.0
10	0	444	GLU	11.0
10	l	654	THR	10.9

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Mol	Chain	Res	Type	RSRZ
2	T	465	GLY	10.9
9	8	779	GLU	10.9
1	x	749	U	10.9
1	V	28	G	10.9
7	Y	665	HIS	10.9
7	E	58	LEU	10.9
8	G	72	ALA	10.9
9	8	728	PRO	10.9
1	v	251	G	10.9
2	U	612	GLU	10.9
5	Q	440	THR	10.9
4	B	48	LYS	10.9
5	R	622	GLU	10.9
5	P	264	ASN	10.8
8	3	265	ASN	10.8
2	T	424	THR	10.8
9	7	532	ILE	10.8
9	7	535	VAL	10.8
3	J	637	HIS	10.7
1	x	616	G	10.7
2	U	672	ILE	10.7
3	H	281	THR	10.7
1	x	628	G	10.7
5	C	17	GLN	10.7
4	O	659	SER	10.7
2	U	627	VAL	10.7
9	K	164	ALA	10.7
9	6	376	VAL	10.7
5	R	612	THR	10.7
4	B	60	ILE	10.7
3	H	276	ASN	10.7
3	I	446	GLU	10.7
8	3	250	THR	10.7
6	F	51	ILE	10.7
3	A	19	CYS	10.7
10	L	6	CYS	10.7
3	J	677	LEU	10.6
2	S	240	ASN	10.6
4	N	408	MET	10.6
7	X	492	ASN	10.6
7	W	288	GLN	10.6
3	I	410	GLN	10.6

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Mol	Chain	Res	Type	RSRZ
2	D	61	VAL	10.6
9	6	334	MET	10.6
6	2	635	SER	10.6
1	V	11	G	10.6
7	Y	653	TYR	10.6
9	6	362	LYS	10.6
7	W	282	ASP	10.6
2	S	242	GLN	10.6
1	v	354	G	10.5
7	Y	625	LEU	10.5
1	w	502	A	10.5
2	D	27	VAL	10.5
7	X	431	ILE	10.5
8	5	651	SER	10.5
8	5	622	ASN	10.5
1	V	157	U	10.5
7	X	488	GLN	10.5
2	S	238	ASN	10.5
6	2	652	ASP	10.5
7	X	452	GLU	10.5
9	8	712	TYR	10.5
10	0	443	GLU	10.4
2	D	45	ASN	10.4
2	S	223	ASN	10.4
5	R	646	CYS	10.4
8	5	614	ASP	10.4
4	O	651	GLU	10.4
9	8	665	GLU	10.4
6	1	476	GLU	10.4
5	Q	464	ASN	10.4
7	E	68	THR	10.4
5	C	32	LEU	10.4
5	Q	468	GLU	10.4
8	5	666	SER	10.4
9	8	761	TYR	10.4
4	N	416	THR	10.4
9	8	745	GLY	10.3
5	Q	473	MET	10.3
9	6	278	ARG	10.3
4	O	631	GLY	10.3
3	A	75	GLU	10.3
1	V	29	A	10.3

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Mol	Chain	Res	Type	RSRZ
3	H	230	THR	10.3
9	8	666	ARG	10.3
2	U	635	ALA	10.3
9	7	506	PHE	10.3
4	M	209	LYS	10.3
1	V	35	A	10.3
10	0	411	THR	10.3
2	T	468	ILE	10.3
8	G	57	ILE	10.3
10	L	27	GLY	10.3
3	I	413	ASP	10.3
5	C	40	THR	10.3
4	B	9	LYS	10.3
4	M	220	LYS	10.3
5	C	104	ASP	10.3
4	B	52	PRO	10.2
8	3	217	LEU	10.2
1	V	138	G	10.2
2	T	449	THR	10.2
7	X	454	MET	10.2
8	4	463	ARG	10.2
9	7	414	ALA	10.2
1	w	415	G	10.2
7	E	40	ASN	10.2
8	4	413	MET	10.2
5	P	214	GLU	10.2
2	U	652	ASP	10.2
1	V	17	G	10.2
7	W	233	VAL	10.2
2	D	62	TYR	10.2
7	Y	664	ILE	10.2
1	v	249	A	10.1
8	3	251	SER	10.1
2	T	406	PRO	10.1
1	x	633	C	10.1
10	9	250	ILE	10.1
6	2	654	ALA	10.1
10	0	418	PRO	10.1
8	3	213	MET	10.1
1	w	524	U	10.1
2	U	654	ARG	10.1
2	T	426	GLU	10.1

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Mol	Chain	Res	Type	RSRZ
3	A	12	HIS	10.1
6	F	9	PRO	10.1
9	8	742	LYS	10.1
2	D	42	GLN	10.1
10	9	260	GLY	10.1
6	F	55	LEU	10.0
2	D	25	GLY	10.0
4	N	447	LEU	10.0
5	R	647	ARG	10.0
1	V	31	C	10.0
1	V	90	U	10.0
2	S	245	ASN	10.0
9	8	748	PHE	10.0
9	K	108	ALA	10.0
2	D	49	THR	10.0
6	Z	270	LEU	10.0
8	5	623	GLY	10.0
9	8	759	SER	10.0
1	w	406	U	10.0
10	0	424	HIS	10.0
9	K	165	ASP	9.9
4	O	650	ARG	9.9
1	w	446	C	9.9
3	H	265	ARG	9.9
1	x	715	U	9.9
7	Y	660	ASP	9.9
9	6	367	LYS	9.9
10	0	453	THR	9.9
10	l	605	TYR	9.9
8	4	454	GLN	9.9
1	x	722	C	9.9
9	K	145	GLY	9.9
4	N	441	LYS	9.9
8	4	451	SER	9.9
1	V	124	U	9.9
1	x	710	G	9.9
6	2	662	VAL	9.9
7	W	272	LYS	9.9
10	9	210	ASP	9.9
1	v	304	A	9.8
8	G	54	GLN	9.8
5	P	301	LEU	9.8

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Mol	Chain	Res	Type	RSRZ
3	A	7	SER	9.8
7	E	19	ASN	9.8
7	E	44	GLU	9.8
1	w	537	U	9.8
1	w	419	A	9.8
4	B	78	THR	9.8
4	N	473	SER	9.8
8	3	254	GLN	9.8
2	S	262	TYR	9.8
2	T	416	HIS	9.8
2	T	437	ASP	9.8
6	F	15	THR	9.8
9	8	750	GLU	9.8
4	B	15	VAL	9.8
6	1	464	ILE	9.7
5	C	12	THR	9.7
2	S	224	THR	9.7
7	E	28	ARG	9.7
1	v	235	A	9.7
1	w	555	C	9.7
1	v	340	G	9.7
7	X	447	ILE	9.7
1	w	540	G	9.7
9	K	140	SER	9.7
10	0	442	MET	9.7
3	A	84	GLY	9.7
10	L	38	TYR	9.7
9	6	221	TYR	9.7
9	8	753	HIS	9.7
2	U	637	ASP	9.7
7	E	47	ILE	9.6
9	K	173	ARG	9.6
5	P	240	THR	9.6
7	E	50	PHE	9.6
7	E	45	GLY	9.6
7	X	453	TYR	9.6
7	Y	654	MET	9.6
10	L	43	GLU	9.6
4	O	646	THR	9.6
7	W	267	LYS	9.6
6	F	71	TYR	9.6
5	R	711	ARG	9.6

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Mol	Chain	Res	Type	RSRZ
8	4	460	VAL	9.6
2	U	628	TYR	9.6
8	3	270	LEU	9.6
1	x	712	A	9.6
5	R	613	PRO	9.5
9	6	333	HIS	9.5
5	Q	424	PHE	9.5
1	v	205	U	9.5
1	v	224	C	9.5
1	v	218	G	9.5
3	I	445	ASP	9.5
6	2	642	MET	9.5
1	x	601	A	9.5
6	F	45	ALA	9.5
2	S	208	LYS	9.5
1	w	404	C	9.5
4	B	72	ASP	9.5
4	B	8	MET	9.5
9	K	115	THR	9.5
7	Y	640	ASN	9.5
6	2	606	ASN	9.5
9	K	120	ARG	9.5
9	8	615	PRO	9.5
10	l	650	ILE	9.5
8	5	674	GLU	9.4
10	9	216	ASP	9.4
5	Q	513	PRO	9.4
3	A	36	LYS	9.4
4	B	75	PRO	9.4
8	5	605	HIS	9.4
7	W	259	ASP	9.4
10	9	218	PRO	9.4
9	7	523	PHE	9.4
4	O	606	PHE	9.4
2	S	213	ALA	9.4
7	W	239	VAL	9.4
2	D	24	THR	9.4
2	S	276	MET	9.4
9	7	417	ASP	9.4
9	8	724	GLU	9.4
8	5	639	ASN	9.4
4	N	462	GLY	9.4

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Mol	Chain	Res	Type	RSRZ
6	1	449	GLU	9.4
2	D	67	LYS	9.4
8	5	675	ARG	9.4
1	x	750	U	9.3
9	8	705	LEU	9.3
5	Q	496	ILE	9.3
6	2	619	VAL	9.3
9	6	373	ARG	9.3
4	M	211	SER	9.3
1	x	692	C	9.3
1	v	292	C	9.3
1	x	631	C	9.3
5	P	257	LYS	9.3
1	x	699	C	9.3
6	1	441	ASN	9.3
3	J	671	LEU	9.3
9	6	364	ALA	9.3
2	T	435	ALA	9.3
6	Z	246	ASN	9.3
7	W	228	ARG	9.3
6	F	76	GLU	9.3
5	C	33	THR	9.3
5	Q	500	PHE	9.2
6	1	429	TYR	9.2
6	2	656	SER	9.2
8	5	612	PHE	9.2
7	Y	666	SER	9.2
10	L	4	PHE	9.2
4	O	605	ARG	9.2
10	9	231	LYS	9.2
1	w	544	C	9.2
5	R	619	ARG	9.2
10	l	611	THR	9.2
8	G	73	LEU	9.2
5	Q	453	LEU	9.2
3	J	675	GLU	9.2
3	I	477	LEU	9.2
3	J	676	ASN	9.2
4	B	17	ILE	9.2
4	O	637	ASN	9.2
4	B	4	VAL	9.2
8	G	34	PHE	9.1

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Mol	Chain	Res	Type	RSRZ
8	3	236	PRO	9.1
9	6	363	HIS	9.1
2	T	436	GLU	9.1
1	x	705	U	9.1
2	S	207	ILE	9.1
6	Z	214	LEU	9.1
3	I	484	GLY	9.1
1	V	44	U	9.1
7	E	73	GLN	9.1
9	8	619	ILE	9.1
1	w	500	C	9.1
4	B	63	ASN	9.1
10	0	431	LYS	9.1
5	R	614	GLU	9.1
9	8	778	VAL	9.1
8	3	225	ARG	9.1
9	K	151	TYR	9.1
3	J	628	ILE	9.1
6	Z	251	ILE	9.1
10	l	637	TYR	9.1
4	N	470	LEU	9.1
9	7	567	LYS	9.1
5	Q	495	TYR	9.1
5	Q	494	ARG	9.1
9	8	746	TYR	9.1
9	6	218	PRO	9.0
3	J	611	GLN	9.0
2	D	50	TYR	9.0
6	2	647	THR	9.0
9	K	85	GLU	9.0
5	R	639	ASN	9.0
7	X	467	LYS	9.0
9	6	216	ARG	9.0
6	F	18	PRO	9.0
3	J	620	ILE	9.0
6	1	452	ASP	9.0
2	S	273	LEU	9.0
3	I	429	THR	9.0
2	T	438	ASN	9.0
9	6	331	ARG	9.0
2	D	53	GLY	9.0
5	C	42	VAL	9.0

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Mol	Chain	Res	Type	RSRZ
1	v	328	U	9.0
5	P	295	TYR	9.0
8	5	667	ILE	9.0
2	D	38	ASN	9.0
1	V	123	A	8.9
1	w	511	A	8.9
7	Y	623	ARG	8.9
7	Y	672	LYS	8.9
9	K	153	HIS	8.9
8	4	436	PRO	8.9
8	G	23	GLY	8.9
1	v	201	A	8.9
3	J	622	GLN	8.9
5	C	74	TRP	8.9
7	W	270	SER	8.9
9	7	552	GLU	8.9
6	Z	265	ARG	8.9
8	5	632	ARG	8.9
10	1	622	LYS	8.9
9	8	776	VAL	8.9
8	5	665	ASN	8.9
6	2	628	GLU	8.9
8	3	257	ILE	8.9
3	H	239	ASN	8.9
9	6	365	ASP	8.9
2	D	22	THR	8.9
7	X	464	ILE	8.9
9	8	773	ARG	8.9
10	L	19	SER	8.9
5	Q	458	ALA	8.8
7	W	286	LEU	8.8
8	5	604	ALA	8.8
2	U	634	GLU	8.8
3	A	67	LEU	8.8
8	4	432	ARG	8.8
6	Z	227	MET	8.8
8	4	450	THR	8.8
9	K	157	MET	8.8
9	7	422	LEU	8.8
3	H	266	VAL	8.8
8	4	457	ILE	8.8
10	L	46	ALA	8.8

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Mol	Chain	Res	Type	RSRZ
6	2	621	VAL	8.8
6	F	8	LYS	8.8
5	P	260	ASP	8.8
1	V	122	C	8.8
2	D	73	LEU	8.7
1	w	445	U	8.7
3	J	607	SER	8.7
10	0	434	VAL	8.7
4	B	74	LEU	8.7
3	J	631	PHE	8.7
9	K	123	PHE	8.7
3	A	43	CYS	8.7
1	V	87	C	8.7
4	N	453	VAL	8.7
9	6	217	ASP	8.7
4	O	649	ASN	8.7
2	T	417	ILE	8.7
4	M	260	ILE	8.7
9	K	135	VAL	8.7
9	6	222	LEU	8.7
2	T	407	ILE	8.7
4	N	466	ARG	8.7
6	F	56	SER	8.7
10	L	33	ASN	8.7
1	x	762	C	8.7
10	9	258	GLN	8.7
7	X	423	ARG	8.6
7	W	273	GLN	8.6
9	K	67	MET	8.6
5	C	102	ARG	8.6
7	X	473	GLN	8.6
10	l	636	ASP	8.6
8	3	204	ALA	8.6
8	5	619	LEU	8.6
3	I	438	ASN	8.6
5	P	248	ASN	8.6
5	P	311	ARG	8.6
2	D	77	LEU	8.6
2	D	80	ALA	8.6
3	H	207	SER	8.6
3	J	686	PRO	8.6
6	2	658	HIS	8.6

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Mol	Chain	Res	Type	RSRZ
1	x	708	G	8.6
4	B	50	ARG	8.5
3	H	223	ASP	8.5
2	U	657	GLN	8.5
1	v	327	U	8.5
10	0	410	ASP	8.5
9	7	420	PRO	8.5
3	H	229	GLY	8.5
7	E	52	GLU	8.5
8	G	7	PRO	8.5
9	K	76	GLU	8.5
2	D	9	VAL	8.5
6	2	655	LEU	8.5
1	x	611	G	8.5
7	W	247	ILE	8.5
9	8	767	LYS	8.5
6	2	681	ASP	8.5
10	9	257	PHE	8.5
1	w	484	G	8.5
9	6	344	ARG	8.5
3	I	432	ALA	8.5
9	8	713	ASP	8.5
10	9	239	CYS	8.5
5	C	99	MET	8.5
10	9	242	MET	8.5
1	v	233	C	8.4
1	V	20	G	8.4
9	8	621	TYR	8.4
9	7	489	TRP	8.4
3	A	8	LYS	8.4
3	J	678	VAL	8.4
3	J	667	LEU	8.4
3	H	272	LEU	8.4
1	V	142	G	8.4
4	O	609	LYS	8.4
1	w	534	U	8.4
5	P	227	GLY	8.4
5	R	694	ARG	8.4
9	8	754	GLU	8.4
1	v	204	C	8.4
8	4	428	GLN	8.4
1	V	114	C	8.4

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Mol	Chain	Res	Type	RSRZ
5	P	305	SER	8.4
9	7	547	ALA	8.4
1	x	618	G	8.4
2	S	255	VAL	8.3
2	T	477	LEU	8.3
4	M	271	PRO	8.3
1	x	739	G	8.3
8	3	208	GLU	8.3
8	5	629	GLY	8.3
4	M	215	VAL	8.3
2	D	81	PRO	8.3
7	X	465	HIS	8.3
7	W	232	GLN	8.3
6	Z	241	ASN	8.3
10	L	10	ASP	8.3
10	L	36	ASP	8.3
5	C	23	GLU	8.3
7	E	82	ASP	8.3
7	Y	688	GLN	8.3
9	K	144	ARG	8.3
9	7	569	ILE	8.3
8	G	11	LYS	8.3
7	X	482	ASP	8.3
4	N	430	THR	8.3
2	S	210	LEU	8.3
5	Q	449	ASN	8.3
9	6	375	LEU	8.3
4	O	611	SER	8.3
8	5	655	ASN	8.3
3	J	684	GLY	8.3
5	C	58	ALA	8.3
4	M	237	ASN	8.3
1	w	528	U	8.3
6	2	617	LYS	8.3
7	Y	656	LEU	8.3
8	5	659	MET	8.2
7	Y	680	LYS	8.2
6	2	644	LEU	8.2
9	6	329	ILE	8.2
6	Z	224	LYS	8.2
9	7	568	LYS	8.2
6	F	68	ASN	8.2

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Mol	Chain	Res	Type	RSRZ
6	Z	262	VAL	8.2
9	7	550	GLU	8.2
1	w	486	C	8.2
7	X	428	ARG	8.2
8	G	26	HIS	8.2
6	Z	257	GLY	8.2
6	1	417	LYS	8.2
8	G	16	LYS	8.2
9	8	771	GLY	8.2
4	M	258	LEU	8.2
5	P	247	ARG	8.2
10	9	211	THR	8.2
8	3	274	GLU	8.2
4	M	208	MET	8.2
1	v	208	C	8.1
1	v	338	G	8.1
5	R	704	ASP	8.1
6	1	457	GLY	8.1
7	X	430	ARG	8.1
1	V	3	A	8.1
6	Z	248	GLU	8.1
9	7	558	HIS	8.1
4	N	437	ASN	8.1
7	W	248	ILE	8.1
3	A	87	PRO	8.1
6	1	455	LEU	8.1
4	O	638	THR	8.1
9	7	536	TYR	8.1
7	W	236	TYR	8.1
9	6	267	MET	8.1
10	L	11	THR	8.1
1	x	728	U	8.1
9	8	680	GLN	8.1
9	7	515	THR	8.1
1	v	244	U	8.1
8	G	13	MET	8.1
3	I	407	LYS	8.0
5	C	44	ILE	8.0
10	l	614	THR	8.0
10	0	435	LYS	8.0
6	1	428	GLU	8.0
9	6	325	VAL	8.0

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Mol	Chain	Res	Type	RSRZ
8	4	470	LEU	8.0
3	I	421	GLN	8.0
2	S	267	LYS	8.0
1	w	495	U	8.0
10	l	638	TYR	8.0
6	F	43	GLN	8.0
2	S	234	GLU	8.0
2	U	642	GLN	8.0
9	6	317	SER	8.0
5	P	216	LEU	8.0
5	R	648	ASN	8.0
5	R	660	ASP	8.0
1	V	148	G	8.0
4	B	51	GLU	8.0
2	U	615	GLY	8.0
9	8	616	ARG	8.0
1	v	319	C	8.0
3	J	626	ILE	8.0
9	K	16	ARG	8.0
7	Y	637	GLU	8.0
8	5	660	VAL	8.0
7	E	91	SER	8.0
10	L	42	MET	8.0
5	Q	459	PHE	8.0
1	x	757	U	8.0
3	J	617	MET	8.0
8	4	405	HIS	7.9
9	K	18	PRO	7.9
4	O	610	LEU	7.9
2	D	59	GLU	7.9
3	J	681	THR	7.9
9	7	563	HIS	7.9
9	8	729	ILE	7.9
8	4	407	PRO	7.9
9	6	268	GLU	7.9
8	4	411	LYS	7.9
6	1	465	ARG	7.9
7	Y	671	ARG	7.9
6	2	680	GLU	7.9
9	6	330	LYS	7.9
2	D	52	ASP	7.9
2	U	669	ARG	7.9

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Mol	Chain	Res	Type	RSRZ
3	H	224	GLY	7.9
8	G	4	ALA	7.9
2	S	221	GLU	7.8
6	1	442	MET	7.8
6	1	470	LEU	7.8
3	A	41	ILE	7.8
10	0	433	ASN	7.8
3	A	11	GLN	7.8
5	R	640	THR	7.8
3	H	267	LEU	7.8
3	H	274	GLY	7.8
1	v	254	A	7.8
9	K	142	LYS	7.8
5	R	661	ARG	7.8
5	Q	457	LYS	7.8
6	1	474	GLY	7.8
8	G	56	ASN	7.8
5	P	275	THR	7.8
7	E	66	SER	7.8
1	v	289	C	7.8
1	x	716	C	7.8
1	x	707	U	7.8
4	O	675	PRO	7.8
2	U	677	LEU	7.8
4	B	54	GLN	7.8
10	L	29	LYS	7.8
6	F	30	LYS	7.8
8	4	430	ILE	7.7
7	Y	684	ILE	7.7
2	T	442	GLN	7.7
3	A	17	MET	7.7
4	B	2	LYS	7.7
9	6	345	GLY	7.7
5	C	43	LEU	7.7
8	G	18	SER	7.7
5	R	695	TYR	7.7
2	U	643	MET	7.7
6	Z	240	MET	7.7
8	G	48	MET	7.7
9	7	474	LYS	7.7
9	7	416	ARG	7.7
3	H	213	ILE	7.7

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Mol	Chain	Res	Type	RSRZ
1	x	743	A	7.7
3	A	85	PRO	7.7
2	U	676	MET	7.6
4	N	440	LEU	7.6
10	9	215	HIS	7.6
7	W	226	GLN	7.6
5	R	656	VAL	7.6
1	V	4	C	7.6
3	J	636	LYS	7.6
7	E	84	ILE	7.6
9	K	158	HIS	7.6
4	B	47	LEU	7.6
6	Z	245	ALA	7.6
8	3	252	GLY	7.6
8	G	50	THR	7.6
1	V	153	C	7.6
2	U	681	PRO	7.6
5	P	243	LEU	7.6
9	K	139	ARG	7.6
1	V	16	G	7.6
5	R	705	SER	7.6
7	E	51	ASP	7.6
1	w	402	U	7.6
1	w	413	C	7.6
9	8	739	ARG	7.6
3	A	29	GLY	7.6
4	B	53	VAL	7.6
3	A	73	ARG	7.6
5	C	75	THR	7.6
8	5	653	GLN	7.5
9	K	166	GLY	7.5
9	8	738	LYS	7.5
2	D	57	GLN	7.5
4	B	38	THR	7.5
2	U	651	ARG	7.5
1	w	554	G	7.5
6	2	609	PRO	7.5
9	K	78	ARG	7.5
9	7	549	ILE	7.5
3	A	30	THR	7.5
8	4	414	ASP	7.5
4	N	452	PRO	7.5

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Mol	Chain	Res	Type	RSRZ
9	7	514	THR	7.5
6	1	444	LEU	7.5
7	E	80	LYS	7.5
10	L	54	THR	7.5
1	w	405	U	7.5
6	F	6	ASN	7.5
6	1	458	HIS	7.5
2	U	623	ASN	7.5
8	G	59	MET	7.5
9	8	769	ILE	7.5
5	Q	443	LEU	7.5
7	X	472	LYS	7.5
1	V	18	G	7.5
9	K	147	ALA	7.5
4	N	420	LYS	7.5
1	V	141	G	7.5
4	O	677	ASP	7.5
6	1	454	ALA	7.5
6	2	661	GLU	7.5
5	P	309	VAL	7.4
1	V	48	C	7.4
8	4	455	ASN	7.4
6	2	639	TYR	7.4
9	K	117	SER	7.4
2	U	675	ASP	7.4
9	K	19	ILE	7.4
9	K	167	LYS	7.4
1	x	629	A	7.4
6	1	453	GLY	7.4
10	9	237	TYR	7.4
4	N	448	LYS	7.4
2	D	29	ARG	7.4
3	A	66	VAL	7.4
3	I	427	ILE	7.4
6	Z	253	GLY	7.4
5	Q	456	VAL	7.4
4	B	61	ARG	7.4
10	0	457	PHE	7.4
3	J	685	PRO	7.4
10	9	240	LYS	7.4
2	S	216	HIS	7.4
8	3	258	GLY	7.4

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Mol	Chain	Res	Type	RSRZ
10	9	236	ASP	7.4
9	8	722	GLU	7.4
4	M	253	VAL	7.3
5	P	256	VAL	7.3
2	U	607	ILE	7.3
5	R	616	LEU	7.3
3	I	482	VAL	7.3
3	A	46	ASP	7.3
9	6	281	GLU	7.3
4	M	263	ASN	7.3
9	8	703	LYS	7.3
8	4	420	LYS	7.3
7	Y	633	VAL	7.3
7	X	471	ARG	7.3
9	6	310	VAL	7.3
1	w	550	U	7.3
8	G	12	PHE	7.3
6	Z	231	GLY	7.3
1	x	689	C	7.3
5	Q	467	LEU	7.3
2	D	21	GLU	7.3
1	V	154	G	7.3
1	w	515	U	7.3
8	3	232	ARG	7.3
8	3	275	ARG	7.3
4	N	439	HIS	7.3
1	V	117	G	7.3
3	H	211	GLN	7.3
7	W	283	ASN	7.3
5	Q	422	GLU	7.2
5	C	107	ILE	7.2
5	C	71	LYS	7.2
2	T	458	LEU	7.2
10	0	450	ILE	7.2
2	U	636	GLU	7.2
9	6	213	PHE	7.2
7	W	284	ILE	7.2
9	6	332	ILE	7.2
5	C	114	LEU	7.2
9	8	772	ARG	7.2
7	Y	690	VAL	7.2
3	I	420	LEU	7.2

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Mol	Chain	Res	Type	RSRZ
6	Z	258	HIS	7.2
3	J	646	ASP	7.2
7	X	455	ASN	7.2
9	7	473	GLU	7.2
2	D	17	ILE	7.2
3	I	467	LEU	7.2
8	G	45	CYS	7.2
9	8	743	PRO	7.2
4	M	250	ARG	7.2
10	l	635	LYS	7.2
5	C	113	PRO	7.1
5	P	211	MET	7.1
2	D	15	GLY	7.1
8	3	214	ASP	7.1
9	8	689	TRP	7.1
5	Q	413	PRO	7.1
2	U	625	GLY	7.1
9	8	686	LEU	7.1
9	7	504	THR	7.1
8	3	266	SER	7.1
5	P	296	ILE	7.1
7	Y	668	THR	7.1
10	l	618	PRO	7.1
3	J	633	ALA	7.1
9	K	169	ILE	7.1
5	R	638	ASN	7.1
4	O	632	VAL	7.1
8	5	670	LEU	7.1
9	7	418	PRO	7.1
9	6	378	VAL	7.1
2	T	478	LYS	7.0
9	6	324	GLU	7.0
9	7	423	PRO	7.0
9	K	14	ALA	7.0
9	7	511	ASN	7.0
10	9	212	TYR	7.0
1	w	432	A	7.0
6	Z	208	LYS	7.0
9	7	513	ASP	7.0
4	N	460	ILE	7.0
7	Y	692	ASN	7.0
6	2	659	LEU	7.0

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Mol	Chain	Res	Type	RSRZ
5	Q	504	ASP	7.0
4	B	49	ASN	7.0
1	V	32	A	7.0
4	O	608	MET	7.0
5	Q	427	GLY	7.0
10	I	629	LYS	7.0
6	F	39	TYR	7.0
8	4	404	ALA	7.0
5	Q	474	TRP	7.0
10	L	60	GLY	7.0
9	6	314	THR	7.0
9	7	531	ARG	7.0
5	Q	492	LYS	7.0
1	v	256	A	7.0
4	M	272	ASP	7.0
6	Z	264	ILE	7.0
1	w	433	C	7.0
10	9	244	GLU	7.0
6	F	75	VAL	6.9
1	V	21	A	6.9
10	L	30	HIS	6.9
4	O	660	ILE	6.9
8	G	35	ASP	6.9
10	9	209	CYS	6.9
6	1	435	SER	6.9
7	W	234	TRP	6.9
5	Q	460	ASP	6.9
4	M	278	THR	6.9
4	M	231	GLY	6.9
8	3	248	MET	6.9
6	1	481	ASP	6.9
7	E	90	VAL	6.9
8	3	230	ILE	6.9
9	8	613	PHE	6.9
9	8	725	VAL	6.9
6	1	467	ASN	6.9
5	Q	514	LEU	6.9
9	6	219	ILE	6.9
7	Y	636	TYR	6.9
5	P	220	GLU	6.9
5	P	212	THR	6.9
7	W	253	TYR	6.9

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Mol	Chain	Res	Type	RSRZ
4	O	648	LYS	6.9
8	4	474	GLU	6.9
3	I	424	ARG	6.9
5	P	304	ASP	6.9
6	2	625	TRP	6.9
6	2	624	LYS	6.9
4	O	658	LEU	6.9
3	H	285	PRO	6.8
6	1	412	ASN	6.8
5	Q	510	LEU	6.8
2	S	250	TYR	6.8
4	M	257	THR	6.8
5	Q	417	GLN	6.8
5	P	270	VAL	6.8
7	Y	650	PHE	6.8
2	D	78	LYS	6.8
10	0	412	TYR	6.8
5	R	657	LYS	6.8
9	7	487	LYS	6.8
4	N	432	VAL	6.8
5	P	215	GLU	6.8
7	Y	619	ASN	6.8
1	x	742	G	6.8
6	2	610	PHE	6.8
3	J	614	ASP	6.8
5	Q	432	LEU	6.8
7	X	451	ASP	6.8
9	6	215	PRO	6.8
9	K	170	ASP	6.8
9	K	21	TYR	6.8
2	T	429	ARG	6.8
6	F	60	GLY	6.8
5	C	106	VAL	6.8
9	K	83	GLU	6.8
4	O	669	ILE	6.8
5	P	219	ARG	6.7
9	K	174	VAL	6.7
9	8	780	ARG	6.7
3	J	644	ASP	6.7
5	Q	507	ILE	6.7
1	V	34	G	6.7
4	M	275	PRO	6.7

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Mol	Chain	Res	Type	RSRZ
9	8	675	ILE	6.7
4	B	5	ARG	6.7
2	T	411	HIS	6.7
5	R	632	LEU	6.7
4	O	625	VAL	6.7
5	P	306	VAL	6.7
2	U	630	GLY	6.7
4	B	73	SER	6.7
4	O	671	PRO	6.7
9	6	308	ALA	6.7
1	w	456	A	6.7
6	Z	271	TYR	6.7
7	X	470	SER	6.7
1	v	222	U	6.7
5	P	249	ASN	6.7
5	R	669	ASN	6.7
9	6	307	VAL	6.7
5	C	96	ILE	6.6
10	l	653	THR	6.6
3	J	683	GLU	6.6
5	P	271	LYS	6.6
7	W	223	ARG	6.6
1	V	134	U	6.6
1	V	143	A	6.6
10	l	615	HIS	6.6
9	7	522	GLU	6.6
7	W	244	GLU	6.6
10	l	659	GLN	6.6
3	J	635	ASP	6.6
2	T	460	GLN	6.6
7	X	483	ASN	6.6
4	M	206	PHE	6.6
2	U	639	MET	6.6
6	1	430	LYS	6.6
2	D	74	PRO	6.6
9	7	580	ARG	6.6
4	M	238	THR	6.6
10	L	21	ARG	6.6
7	Y	670	SER	6.6
2	D	79	ASN	6.6
6	F	14	LEU	6.5
1	x	760	C	6.5

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Mol	Chain	Res	Type	RSRZ
9	6	340	SER	6.5
9	7	520	ARG	6.5
1	V	39	U	6.5
9	8	617	ASP	6.5
5	C	30	SER	6.5
9	7	525	VAL	6.5
7	Y	659	ASP	6.5
2	U	663	ILE	6.5
9	8	671	ARG	6.5
2	U	679	ASN	6.5
5	Q	446	CYS	6.5
2	T	481	PRO	6.5
1	x	737	U	6.5
4	M	202	LYS	6.5
8	4	440	LEU	6.5
8	3	229	GLY	6.5
1	w	409	C	6.5
9	8	623	PRO	6.5
2	S	254	ARG	6.5
6	1	448	GLU	6.5
8	4	468	ILE	6.5
7	W	227	ASN	6.5
8	4	461	VAL	6.5
1	V	164	G	6.5
4	M	252	PRO	6.5
9	7	545	GLY	6.4
1	V	129	U	6.4
6	2	630	LYS	6.4
6	2	673	ARG	6.4
3	A	25	ARG	6.4
9	8	721	ARG	6.4
1	v	219	A	6.4
9	7	554	GLU	6.4
7	X	478	MET	6.4
7	W	290	VAL	6.4
4	N	410	LEU	6.4
5	R	650	LYS	6.4
3	H	244	ASP	6.4
3	I	471	LEU	6.4
4	N	469	ILE	6.4
5	Q	438	ASN	6.4
4	O	615	VAL	6.4

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Mol	Chain	Res	Type	RSRZ
5	Q	428	PRO	6.4
1	v	241	G	6.4
1	v	357	U	6.4
7	X	475	GLY	6.4
8	3	242	ILE	6.4
6	F	52	ASP	6.4
8	5	626	HIS	6.4
3	A	15	TYR	6.4
5	R	699	MET	6.4
3	H	287	PRO	6.4
3	J	634	PHE	6.4
3	H	212	HIS	6.4
10	l	608	TYR	6.4
5	Q	411	MET	6.4
1	v	312	A	6.4
1	w	417	G	6.3
6	Z	225	TRP	6.3
7	X	448	ILE	6.3
8	5	633	GLY	6.3
9	8	614	ALA	6.3
7	E	21	ILE	6.3
10	9	222	LYS	6.3
5	P	294	ARG	6.3
8	3	222	ASN	6.3
9	6	313	ASP	6.3
2	U	664	ARG	6.3
9	K	141	GLY	6.3
9	8	622	LEU	6.3
3	J	670	VAL	6.3
5	Q	447	ARG	6.3
9	8	760	ALA	6.3
7	Y	689	SER	6.3
6	F	22	LYS	6.3
7	Y	632	GLN	6.3
2	D	66	CYS	6.3
5	R	666	VAL	6.3
1	v	248	C	6.3
8	4	475	ARG	6.3
8	5	635	ASP	6.3
1	x	652	G	6.3
5	Q	414	GLU	6.3
2	S	209	VAL	6.3

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Mol	Chain	Res	Type	RSRZ
8	5	613	MET	6.3
9	8	717	SER	6.3
6	1	472	ILE	6.3
3	H	221	LEU	6.3
2	D	16	HIS	6.3
9	K	150	GLU	6.3
7	Y	630	ARG	6.3
5	Q	423	GLU	6.3
1	w	427	U	6.3
2	S	278	LYS	6.3
7	X	420	LEU	6.3
9	6	335	VAL	6.3
4	M	228	THR	6.2
5	Q	476	GLU	6.2
7	E	18	ILE	6.2
5	C	101	LEU	6.2
5	Q	416	LEU	6.2
3	A	78	VAL	6.2
9	K	168	LYS	6.2
9	7	544	ARG	6.2
1	w	563	U	6.2
5	P	274	TRP	6.2
1	x	646	C	6.2
4	M	213	GLU	6.2
6	Z	218	PRO	6.2
7	X	487	LEU	6.2
7	Y	648	ILE	6.2
10	l	617	SER	6.2
9	6	323	PHE	6.2
7	Y	639	VAL	6.2
3	J	613	ILE	6.2
5	R	621	GLU	6.2
6	Z	219	VAL	6.2
7	E	67	LYS	6.2
5	P	252	LEU	6.2
3	H	278	VAL	6.2
5	C	55	ARG	6.2
1	v	348	G	6.2
1	v	298	C	6.2
5	C	15	GLU	6.2
8	4	423	GLY	6.2
5	R	709	VAL	6.1

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Mol	Chain	Res	Type	RSRZ
10	0	415	HIS	6.1
3	A	71	LEU	6.1
9	8	768	LYS	6.1
5	C	20	GLU	6.1
7	W	252	GLU	6.1
7	W	261	ALA	6.1
1	w	483	C	6.1
9	7	546	TYR	6.1
10	9	219	SER	6.1
6	2	653	GLY	6.1
9	8	618	PRO	6.1
1	V	99	C	6.1
2	S	264	ARG	6.1
3	I	418	CYS	6.1
9	K	136	TYR	6.1
8	4	434	PHE	6.1
9	7	419	ILE	6.1
2	T	409	VAL	6.0
10	0	436	ASP	6.0
6	2	679	GLU	6.0
9	8	762	LYS	6.0
4	M	227	GLY	6.0
7	E	20	LEU	6.0
1	V	8	C	6.0
5	P	238	ASN	6.0
5	Q	442	VAL	6.0
7	Y	646	CYS	6.0
10	0	405	TYR	6.0
2	D	58	LEU	6.0
9	K	125	VAL	6.0
7	X	462	GLU	6.0
10	L	5	TYR	6.0
10	9	230	HIS	6.0
1	V	101	C	6.0
1	x	720	U	6.0
3	A	38	MET	6.0
6	1	440	MET	6.0
9	7	412	LEU	6.0
9	8	670	LYS	6.0
2	U	616	HIS	6.0
5	C	105	SER	6.0
9	6	380	ARG	6.0

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Mol	Chain	Res	Type	RSRZ
4	O	678	THR	6.0
4	N	412	HIS	6.0
7	E	33	VAL	6.0
1	v	325	A	5.9
9	K	176	VAL	5.9
4	N	404	VAL	5.9
7	Y	620	LEU	5.9
1	v	255	G	5.9
8	5	652	GLY	5.9
3	I	475	GLU	5.9
5	Q	445	ASN	5.9
1	w	535	A	5.9
4	B	3	LEU	5.9
8	3	253	GLN	5.9
10	L	35	LYS	5.9
1	v	216	G	5.9
6	2	643	GLN	5.9
9	7	530	LYS	5.9
10	9	259	GLN	5.9
3	I	465	ARG	5.9
4	M	222	GLY	5.9
4	M	273	SER	5.9
2	T	441	CYS	5.9
5	Q	426	THR	5.9
2	T	413	ALA	5.9
5	C	97	SER	5.9
4	M	232	VAL	5.9
2	T	451	ARG	5.9
3	H	286	PRO	5.9
3	A	31	PHE	5.9
8	3	207	PRO	5.9
2	U	608	LYS	5.9
4	N	418	GLU	5.9
3	A	23	ASP	5.8
8	G	66	SER	5.8
9	7	565	ASP	5.8
4	M	225	VAL	5.8
8	G	19	LEU	5.8
7	E	89	SER	5.8
1	v	226	A	5.8
8	3	255	ASN	5.8
7	E	55	ASN	5.8

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Mol	Chain	Res	Type	RSRZ
3	H	236	LYS	5.8
8	3	218	SER	5.8
4	O	657	THR	5.8
9	6	223	PRO	5.8
10	l	609	CYS	5.8
2	T	464	ARG	5.8
1	w	552	G	5.8
1	x	758	U	5.8
5	C	47	ARG	5.8
4	M	210	LEU	5.8
9	K	81	GLU	5.8
8	3	211	LYS	5.8
5	P	299	MET	5.8
6	F	31	GLY	5.8
7	E	56	LEU	5.8
9	8	704	THR	5.8
7	W	250	PHE	5.8
4	N	426	HIS	5.8
8	5	661	VAL	5.7
10	l	620	VAL	5.7
8	4	453	GLN	5.7
2	T	473	LEU	5.7
9	K	68	GLU	5.7
2	D	7	ILE	5.7
7	X	444	GLU	5.7
6	Z	236	VAL	5.7
1	x	738	G	5.7
9	K	79	GLN	5.7
5	R	618	LYS	5.7
5	C	28	PRO	5.7
9	8	720	ARG	5.7
2	D	41	CYS	5.7
2	T	470	PHE	5.7
4	M	269	ILE	5.7
2	T	455	VAL	5.7
9	7	517	SER	5.7
4	N	450	ARG	5.7
5	Q	469	ASN	5.7
4	M	239	HIS	5.7
8	G	75	ARG	5.7
2	T	475	ASP	5.7
3	H	277	LEU	5.7

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Mol	Chain	Res	Type	RSRZ
2	S	266	CYS	5.7
4	O	663	ASN	5.7
7	E	86	LEU	5.7
5	P	262	HIS	5.6
6	F	63	LEU	5.6
7	W	229	SER	5.6
6	Z	223	LEU	5.6
8	G	53	GLN	5.6
9	6	305	LEU	5.6
9	7	527	GLY	5.6
9	7	579	GLU	5.6
7	X	480	LYS	5.6
2	U	673	LEU	5.6
3	H	231	PHE	5.6
9	K	77	ARG	5.6
4	O	664	ASN	5.6
6	Z	252	ASP	5.6
9	7	529	ILE	5.6
9	7	510	VAL	5.6
1	v	308	G	5.6
10	L	22	LYS	5.6
9	K	22	LEU	5.6
8	G	63	ARG	5.6
7	Y	641	MET	5.6
1	w	553	C	5.6
4	B	12	HIS	5.6
4	B	56	GLU	5.6
6	F	26	GLY	5.6
6	F	78	GLU	5.6
7	W	278	MET	5.6
6	2	666	CYS	5.6
7	W	242	ARG	5.6
8	G	33	GLY	5.6
2	D	20	CYS	5.5
5	P	269	ASN	5.5
7	Y	651	ASP	5.5
9	7	421	TYR	5.5
9	K	73	GLU	5.5
6	Z	268	ASN	5.5
9	7	533	HIS	5.5
3	J	623	ASP	5.5
8	5	657	ILE	5.5

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Mol	Chain	Res	Type	RSRZ
1	w	437	G	5.5
9	7	534	MET	5.5
8	G	24	GLY	5.5
6	2	612	ASN	5.5
4	M	242	ALA	5.5
7	E	62	GLU	5.5
5	P	298	LYS	5.5
5	R	712	ASN	5.5
6	F	46	ASN	5.5
2	S	252	ASP	5.5
1	v	299	C	5.5
5	P	213	PRO	5.5
6	2	670	LEU	5.5
1	V	107	U	5.5
4	B	55	LEU	5.5
7	Y	652	GLU	5.5
8	G	15	LYS	5.5
4	N	411	SER	5.5
4	M	212	HIS	5.5
9	K	66	ARG	5.5
1	v	329	U	5.4
7	E	31	ILE	5.4
2	U	613	ALA	5.4
2	D	30	GLY	5.4
6	Z	237	ASP	5.4
2	D	54	ARG	5.4
7	W	220	LEU	5.4
9	K	179	GLU	5.4
7	W	291	SER	5.4
2	S	211	HIS	5.4
1	V	147	C	5.4
4	M	241	LYS	5.4
6	Z	232	TYR	5.4
5	R	611	MET	5.4
5	Q	501	LEU	5.4
9	K	126	TYR	5.4
9	7	488	MET	5.4
3	A	10	LEU	5.4
9	K	13	PHE	5.4
5	P	297	SER	5.4
8	G	52	GLY	5.4
5	C	11	MET	5.4

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Mol	Chain	Res	Type	RSRZ
6	1	450	TYR	5.4
1	V	51	G	5.3
9	K	160	ALA	5.3
3	H	279	SER	5.3
4	B	46	THR	5.3
10	0	430	HIS	5.3
7	X	427	ASN	5.3
6	2	626	GLY	5.3
4	M	267	TYR	5.3
10	0	416	ASP	5.3
4	N	477	ASP	5.3
5	Q	436	VAL	5.3
5	R	673	MET	5.3
5	C	37	LYS	5.3
2	U	620	CYS	5.3
10	L	45	GLN	5.3
1	x	724	U	5.3
1	v	300	C	5.3
9	8	685	GLU	5.3
1	V	156	U	5.3
8	G	32	ARG	5.3
2	T	412	GLU	5.3
7	E	32	GLN	5.3
10	L	37	TYR	5.3
5	R	701	LEU	5.3
3	J	629	GLY	5.2
4	M	218	GLU	5.3
9	7	571	GLY	5.2
2	U	609	VAL	5.2
10	l	610	ASP	5.2
2	T	480	ALA	5.2
2	U	666	CYS	5.2
3	J	608	LYS	5.2
1	v	306	G	5.2
6	Z	254	ALA	5.2
8	5	656	ASN	5.2
7	Y	624	TYR	5.2
6	Z	212	ASN	5.2
8	G	41	VAL	5.2
10	0	429	LYS	5.2
8	4	425	ARG	5.2
2	T	463	ILE	5.2

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Mol	Chain	Res	Type	RSRZ
1	w	543	A	5.2
1	v	309	G	5.2
2	S	256	ALA	5.2
2	U	680	ALA	5.2
7	X	433	VAL	5.2
4	N	414	THR	5.2
2	S	227	VAL	5.2
4	N	455	LEU	5.2
8	G	64	GLY	5.2
8	4	476	VAL	5.2
4	O	668	PHE	5.2
3	A	22	GLN	5.2
6	F	36	VAL	5.2
7	W	274	LEU	5.2
9	7	577	ASP	5.2
7	E	60	ASP	5.2
2	U	650	TYR	5.2
9	K	162	LYS	5.2
7	E	69	LYS	5.1
9	7	524	GLU	5.1
4	N	421	ASN	5.1
4	B	6	PHE	5.1
7	W	262	GLU	5.1
5	R	713	PRO	5.1
9	K	109	ARG	5.1
1	x	603	A	5.1
10	0	454	THR	5.1
2	T	462	TYR	5.1
4	M	244	LYS	5.1
8	4	417	LEU	5.1
5	C	72	GLU	5.1
6	Z	263	LEU	5.1
1	V	120	U	5.1
7	E	38	GLN	5.1
7	E	64	ILE	5.1
7	X	463	GLU	5.1
1	V	33	C	5.1
5	Q	475	THR	5.1
4	O	602	LYS	5.1
6	2	637	ASP	5.1
8	3	243	ASP	5.1
9	K	71	ARG	5.1

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Mol	Chain	Res	Type	RSRZ
3	J	665	ARG	5.1
5	Q	511	ARG	5.1
1	V	92	C	5.1
4	B	13	GLU	5.1
3	I	436	HIS	5.1
1	v	349	U	5.1
4	B	36	MET	5.1
9	6	304	THR	5.1
4	M	221	ASN	5.0
5	C	31	VAL	5.0
3	H	246	ASP	5.0
8	5	616	LYS	5.0
2	D	55	VAL	5.0
1	V	40	G	5.0
1	x	704	A	5.0
9	7	482	VAL	5.0
3	A	37	HIS	5.0
10	0	408	TYR	5.0
4	M	268	PHE	5.0
5	P	312	ASN	5.0
5	R	627	GLY	5.0
10	L	20	VAL	5.0
7	X	441	MET	5.0
4	O	666	ARG	5.0
2	S	241	CYS	5.0
9	K	132	ILE	5.0
4	N	428	THR	5.0
2	S	228	TYR	5.0
3	I	487	PRO	5.0
4	N	454	GLN	5.0
8	G	27	VAL	5.0
2	S	249	THR	5.0
8	4	427	VAL	5.0
3	H	241	ILE	5.0
2	T	453	GLY	5.0
4	B	11	SER	5.0
4	O	612	HIS	5.0
9	K	107	VAL	5.0
4	N	475	PRO	5.0
6	Z	269	VAL	5.0
3	I	476	ASN	5.0
8	G	37	PHE	5.0

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Mol	Chain	Res	Type	RSRZ
9	K	127	GLY	4.9
8	3	241	VAL	4.9
9	8	733	HIS	4.9
6	Z	273	ARG	4.9
6	1	426	GLY	4.9
2	S	263	ILE	4.9
6	F	34	VAL	4.9
8	5	668	ILE	4.9
9	K	114	THR	4.9
2	T	423	ASN	4.9
8	5	647	GLU	4.9
6	Z	250	TYR	4.9
4	O	626	HIS	4.9
2	T	433	ILE	4.9
6	1	431	GLY	4.9
6	1	432	TYR	4.9
3	I	443	ASP	4.9
7	W	279	LEU	4.9
7	X	434	TRP	4.9
7	Y	647	ILE	4.9
10	l	644	GLU	4.9
4	M	214	THR	4.9
4	N	419	LEU	4.9
9	6	315	THR	4.9
9	7	475	ILE	4.9
6	2	614	LEU	4.9
4	B	30	THR	4.9
8	3	228	GLN	4.9
3	I	480	MET	4.9
3	I	486	PRO	4.9
9	8	758	HIS	4.9
5	C	50	LYS	4.9
9	8	679	GLN	4.9
9	8	747	ALA	4.8
5	C	25	ASN	4.8
2	T	443	MET	4.8
10	9	220	VAL	4.8
5	R	642	VAL	4.8
5	P	302	ARG	4.8
1	w	492	C	4.8
2	D	10	LEU	4.8
10	L	16	ASP	4.8

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Mol	Chain	Res	Type	RSRZ
5	P	267	LEU	4.8
5	C	36	VAL	4.8
5	R	707	ILE	4.8
6	F	69	VAL	4.8
9	K	180	ARG	4.8
8	4	437	PHE	4.8
9	K	106	PHE	4.8
10	l	634	VAL	4.8
4	B	39	HIS	4.8
6	1	424	LYS	4.8
4	O	628	THR	4.8
4	M	247	LEU	4.8
8	4	433	GLY	4.8
7	W	246	CYS	4.8
5	C	49	ASN	4.8
6	1	420	MET	4.8
9	6	212	LEU	4.8
3	I	411	HIS	4.8
1	x	756	U	4.8
8	4	438	MET	4.8
1	v	363	U	4.8
2	S	220	CYS	4.8
7	E	23	ARG	4.8
9	7	466	ARG	4.8
2	U	617	ILE	4.8
1	w	523	A	4.8
2	S	219	THR	4.7
6	Z	274	GLY	4.8
8	5	664	GLY	4.8
3	I	419	ILE	4.7
8	5	608	GLU	4.7
10	9	232	GLU	4.7
2	U	667	LYS	4.7
8	5	615	LYS	4.7
8	5	625	ARG	4.7
7	W	271	ARG	4.7
7	E	59	ASP	4.7
10	9	252	LYS	4.7
2	S	246	ILE	4.7
1	V	50	G	4.7
2	U	649	THR	4.7
5	P	222	GLU	4.7

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Mol	Chain	Res	Type	RSRZ
10	L	31	LYS	4.7
5	R	643	LEU	4.7
7	X	479	LEU	4.7
3	I	414	TYR	4.7
9	6	336	TYR	4.7
7	X	491	SER	4.7
1	x	647	C	4.7
7	Y	682	ASP	4.7
8	5	662	ILE	4.7
3	H	238	MET	4.7
3	J	632	LYS	4.7
4	B	76	LEU	4.6
7	W	268	THR	4.6
9	K	88	MET	4.6
5	Q	448	ASN	4.6
4	N	457	THR	4.6
9	6	377	ASP	4.6
4	M	276	LEU	4.6
7	E	71	ARG	4.6
7	X	443	ILE	4.6
2	U	662	TYR	4.6
3	A	27	PHE	4.6
9	6	280	GLN	4.6
5	Q	508	VAL	4.6
9	8	723	PHE	4.6
9	K	103	LYS	4.6
5	R	708	VAL	4.6
9	6	339	ARG	4.6
9	8	674	LYS	4.6
6	Z	272	ILE	4.6
5	C	54	GLY	4.6
2	U	631	LYS	4.6
4	O	639	HIS	4.6
1	v	341	G	4.6
8	3	249	ALA	4.6
9	7	572	ARG	4.6
8	5	672	ALA	4.5
4	N	424	GLN	4.5
9	7	409	LEU	4.5
8	5	640	LEU	4.5
7	X	456	LEU	4.5
3	I	422	ASP	4.5

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Mol	Chain	Res	Type	RSRZ
3	I	442	CYS	4.5
4	O	629	ILE	4.5
2	T	457	GLN	4.5
8	3	237	PHE	4.5
9	7	575	LEU	4.5
1	V	22	U	4.5
4	N	463	ASN	4.5
2	D	37	ASP	4.5
5	Q	493	ASP	4.5
1	w	418	G	4.5
1	v	345	U	4.5
9	6	342	LYS	4.5
9	7	559	SER	4.5
2	U	645	ASN	4.5
4	M	223	THR	4.5
8	3	264	GLY	4.5
10	0	419	SER	4.5
8	3	276	VAL	4.5
4	N	402	LYS	4.5
1	V	145	U	4.4
1	v	316	C	4.4
6	F	79	GLU	4.4
1	v	246	C	4.4
6	2	663	LEU	4.4
9	8	735	VAL	4.4
9	K	155	ARG	4.4
7	Y	673	GLN	4.4
8	G	76	VAL	4.4
5	P	229	LEU	4.4
9	6	341	GLY	4.4
8	4	415	LYS	4.4
5	C	13	PRO	4.4
6	1	461	GLU	4.4
8	4	406	PRO	4.4
9	6	209	LEU	4.4
4	B	44	LYS	4.4
6	F	42	MET	4.4
3	H	283	GLU	4.4
9	8	752	GLU	4.4
10	L	39	CYS	4.4
2	U	644	SER	4.4
4	B	29	ILE	4.4

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Mol	Chain	Res	Type	RSRZ
8	3	256	ASN	4.4
7	E	53	TYR	4.4
4	N	422	GLY	4.4
4	O	676	LEU	4.4
6	Z	234	VAL	4.4
9	K	112	TYR	4.4
9	6	369	ILE	4.4
7	Y	629	SER	4.4
1	V	116	C	4.4
6	1	439	TYR	4.4
9	8	664	GLU	4.4
4	O	635	SER	4.4
9	8	777	ASP	4.4
5	C	56	VAL	4.3
3	A	20	ILE	4.3
7	Y	678	MET	4.3
3	A	33	ALA	4.3
7	W	292	ASN	4.3
8	G	36	PRO	4.3
9	8	714	THR	4.3
6	1	478	GLU	4.3
6	2	623	LEU	4.3
3	A	72	LEU	4.3
7	E	63	GLU	4.3
4	O	621	ASN	4.3
1	V	136	G	4.3
10	9	205	TYR	4.3
1	V	89	C	4.3
1	w	421	A	4.3
6	F	66	CYS	4.3
8	3	224	GLY	4.3
4	O	645	MET	4.3
8	3	262	ILE	4.3
8	4	443	ASP	4.3
6	Z	209	PRO	4.3
8	4	467	ILE	4.3
9	7	576	VAL	4.3
9	6	264	GLU	4.3
5	Q	470	VAL	4.3
7	W	230	ARG	4.3
10	0	441	TRP	4.3
9	7	543	PRO	4.3

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Mol	Chain	Res	Type	RSRZ
8	3	261	VAL	4.3
1	x	714	C	4.2
5	P	217	GLN	4.2
9	6	319	LEU	4.2
10	0	414	THR	4.2
9	K	121	ARG	4.2
9	7	512	TYR	4.2
7	Y	677	ILE	4.2
1	w	447	C	4.2
4	O	673	SER	4.2
2	U	619	THR	4.2
10	l	660	GLY	4.2
4	O	607	LEU	4.2
5	C	103	GLY	4.2
7	W	258	LEU	4.2
9	8	609	LEU	4.2
2	D	11	HIS	4.2
7	X	469	LYS	4.2
5	C	62	HIS	4.2
6	Z	267	ASN	4.2
7	X	477	ILE	4.2
8	4	426	HIS	4.2
7	W	238	GLN	4.2
5	R	693	ASP	4.2
7	W	255	ASN	4.2
9	K	63	ARG	4.2
5	R	630	SER	4.2
9	8	708	ALA	4.2
3	A	65	ARG	4.2
7	X	439	VAL	4.2
5	Q	425	ASN	4.1
8	4	473	LEU	4.1
10	l	613	LEU	4.1
4	N	436	MET	4.1
7	W	235	LEU	4.1
2	U	671	LEU	4.1
9	K	89	TRP	4.1
3	H	218	ARG	4.1
9	K	15	PRO	4.1
9	6	263	ARG	4.1
9	8	766	GLY	4.1
9	8	676	GLU	4.1

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Mol	Chain	Res	Type	RSRZ
9	8	681	GLU	4.1
5	Q	441	GLN	4.1
5	C	73	MET	4.1
5	Q	444	ILE	4.1
8	5	649	ALA	4.1
5	Q	499	MET	4.1
5	C	112	ASN	4.1
3	I	433	PHE	4.1
1	V	93	G	4.1
8	4	408	GLU	4.1
9	7	519	LEU	4.1
5	R	671	LYS	4.1
8	4	422	ASN	4.1
10	L	41	TRP	4.0
2	T	447	THR	4.0
9	6	338	LYS	4.0
3	I	408	MET	4.0
3	A	28	ILE	4.0
10	9	261	LYS	4.0
6	F	57	GLY	4.0
9	K	130	LYS	4.0
9	8	663	ARG	4.0
5	P	224	PHE	4.0
5	Q	452	LEU	4.0
8	G	31	LEU	4.0
4	M	240	LEU	4.0
2	U	606	PRO	4.0
8	4	429	GLY	4.0
9	6	343	PRO	4.0
1	v	247	C	4.0
10	l	604	PHE	4.0
1	V	26	A	4.0
7	E	43	ILE	4.0
5	C	108	VAL	4.0
6	F	61	GLU	4.0
6	F	70	LEU	4.0
4	M	216	THR	4.0
7	X	418	ILE	4.0
9	8	710	VAL	4.0
5	P	272	GLU	4.0
1	x	734	U	4.0
4	N	456	GLU	4.0

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Mol	Chain	Res	Type	RSRZ
2	S	274	PRO	3.9
2	T	440	ASN	3.9
6	1	471	TYR	3.9
5	C	94	ARG	3.9
10	9	251	ASP	3.9
9	7	528	PRO	3.9
1	w	558	U	3.9
9	K	175	LEU	3.9
9	6	322	GLU	3.9
6	F	81	ASP	3.9
8	3	245	CYS	3.9
2	D	46	ILE	3.9
4	B	69	ILE	3.9
5	R	667	LEU	3.9
1	w	542	G	3.9
10	9	204	PHE	3.9
2	S	261	VAL	3.9
7	E	75	GLY	3.9
7	W	280	LYS	3.9
1	w	529	U	3.9
9	6	326	TYR	3.9
4	O	604	VAL	3.9
2	D	44	SER	3.9
9	K	9	LEU	3.9
1	V	45	U	3.9
3	I	479	SER	3.9
4	M	255	LEU	3.9
4	O	623	THR	3.8
10	l	628	ARG	3.8
3	H	217	MET	3.8
4	O	640	LEU	3.8
8	G	38	MET	3.8
2	S	244	SER	3.8
1	v	293	G	3.8
8	3	238	MET	3.8
9	6	306	PHE	3.8
6	2	632	TYR	3.8
7	X	442	ARG	3.8
7	Y	628	ARG	3.8
4	O	655	LEU	3.8
6	2	608	LYS	3.8
7	Y	674	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
5	Q	512	ASN	3.8
4	B	16	THR	3.8
8	3	220	LYS	3.8
5	R	706	VAL	3.8
2	U	660	GLN	3.8
9	6	210	LEU	3.8
1	x	639	U	3.8
7	W	289	SER	3.8
2	S	225	GLY	3.8
7	X	419	ASN	3.8
2	U	656	ALA	3.7
10	0	426	SER	3.7
2	U	633	ILE	3.7
4	M	236	MET	3.7
2	T	459	GLU	3.7
4	M	264	ASN	3.7
2	D	18	VAL	3.7
4	O	653	VAL	3.7
7	Y	645	GLY	3.7
8	5	638	MET	3.7
8	G	8	GLU	3.7
8	3	239	ASN	3.7
8	3	223	GLY	3.7
7	E	48	ILE	3.7
10	0	422	LYS	3.7
5	R	623	GLU	3.7
6	2	674	GLY	3.7
9	8	673	GLU	3.7
9	8	682	VAL	3.7
5	P	255	ARG	3.7
5	P	261	ARG	3.7
7	E	81	GLY	3.7
10	0	404	PHE	3.7
6	F	16	GLY	3.7
5	R	635	SER	3.7
1	w	455	G	3.7
6	Z	249	GLU	3.7
4	O	636	MET	3.7
8	G	9	LEU	3.7
2	U	641	CYS	3.7
6	2	677	GLU	3.7
2	T	430	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
6	2	645	ALA	3.7
10	l	656	ALA	3.7
1	x	745	U	3.7
6	Z	242	MET	3.7
4	M	226	HIS	3.7
7	W	218	ILE	3.7
4	M	243	VAL	3.6
8	4	447	GLU	3.6
3	I	430	PHE	3.6
3	J	666	VAL	3.6
10	0	446	ALA	3.6
5	C	60	ASP	3.6
9	7	516	GLU	3.6
3	H	210	LEU	3.6
5	Q	419	ARG	3.6
6	2	671	TYR	3.6
9	6	309	ARG	3.6
6	Z	233	LEU	3.6
8	5	611	LYS	3.6
8	5	630	ILE	3.6
7	Y	675	GLY	3.6
8	G	28	GLN	3.6
8	G	68	ILE	3.6
7	W	225	LEU	3.6
10	l	648	SER	3.6
9	8	711	ASN	3.6
1	v	334	U	3.6
7	X	421	ILE	3.6
8	4	439	ASN	3.6
6	Z	256	SER	3.6
6	Z	275	VAL	3.6
4	B	42	ALA	3.6
3	A	82	VAL	3.6
3	I	412	ILE	3.6
3	H	208	LYS	3.5
10	9	246	ALA	3.5
3	H	280	MET	3.5
5	C	69	ASN	3.5
3	J	639	ASN	3.5
10	L	18	PRO	3.5
1	x	719	C	3.5
10	l	612	TYR	3.5

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Mol	Chain	Res	Type	RSRZ
4	O	652	PRO	3.5
2	U	629	ARG	3.5
3	I	425	ILE	3.5
6	1	425	TRP	3.5
3	H	219	CYS	3.5
2	D	32	LEU	3.5
4	N	476	LEU	3.5
4	M	277	ASP	3.5
10	9	253	THR	3.5
6	F	27	MET	3.5
6	2	665	ARG	3.5
3	H	209	MET	3.5
3	I	478	VAL	3.5
5	C	110	LEU	3.5
9	7	540	SER	3.5
5	R	641	GLN	3.5
1	V	158	U	3.4
10	9	229	LYS	3.4
2	S	232	LEU	3.4
8	4	456	ASN	3.4
8	3	209	LEU	3.4
7	W	221	ILE	3.4
2	D	34	GLU	3.4
8	G	60	VAL	3.4
5	Q	463	CYS	3.4
10	L	15	HIS	3.4
7	Y	644	GLU	3.4
2	S	237	ASP	3.4
2	D	23	ASN	3.4
3	H	273	ARG	3.4
5	C	21	GLU	3.4
3	J	609	MET	3.4
3	A	18	ARG	3.4
1	v	359	C	3.4
9	7	555	ARG	3.4
4	O	613	GLU	3.4
4	M	207	LEU	3.4
5	P	228	PRO	3.4
5	R	633	THR	3.4
7	E	65	HIS	3.4
2	D	76	MET	3.4
3	I	439	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
7	Y	687	LEU	3.4
10	L	53	THR	3.4
3	H	226	ILE	3.4
4	M	229	ILE	3.4
5	R	672	GLU	3.4
6	Z	210	PHE	3.4
6	Z	215	THR	3.4
2	T	456	ALA	3.3
5	P	236	VAL	3.3
7	E	26	GLN	3.3
9	K	10	LEU	3.3
8	3	263	ARG	3.3
6	1	469	VAL	3.3
7	W	257	VAL	3.3
8	3	268	ILE	3.3
4	O	641	LYS	3.3
5	C	35	SER	3.3
8	5	617	LEU	3.3
9	7	570	ASP	3.3
5	Q	431	VAL	3.3
7	E	27	ASN	3.3
3	H	215	TYR	3.3
9	8	734	MET	3.3
6	F	25	TRP	3.3
6	1	443	GLN	3.3
10	L	34	VAL	3.3
10	L	50	ILE	3.3
5	R	652	LEU	3.3
6	2	649	GLU	3.3
5	Q	502	ARG	3.3
6	F	49	GLU	3.3
6	Z	261	GLU	3.3
7	X	437	GLU	3.3
8	5	607	PRO	3.3
10	L	55	ALA	3.3
9	6	289	TRP	3.3
6	Z	220	MET	3.3
7	X	460	ASP	3.3
1	v	320	U	3.2
8	3	210	LYS	3.2
2	U	621	GLU	3.2
4	N	403	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
8	3	273	LEU	3.2
2	T	408	LYS	3.2
3	H	269	LEU	3.2
5	P	226	THR	3.2
8	5	648	MET	3.2
6	F	13	GLY	3.2
3	J	610	LEU	3.2
5	R	668	GLU	3.2
8	3	272	ALA	3.2
3	I	440	ILE	3.2
9	7	503	LYS	3.2
5	R	654	GLY	3.2
3	I	473	ARG	3.2
3	I	483	GLU	3.2
5	P	254	GLY	3.2
7	X	432	GLN	3.2
9	6	286	LEU	3.2
9	8	744	ARG	3.2
9	6	284	THR	3.2
6	1	419	VAL	3.2
5	P	253	LEU	3.2
8	G	17	LEU	3.2
8	4	452	GLY	3.2
2	D	47	THR	3.2
6	F	23	LEU	3.2
5	R	624	PHE	3.2
9	7	508	ALA	3.2
10	9	221	ARG	3.2
5	R	697	SER	3.2
6	F	44	LEU	3.2
6	2	631	GLY	3.1
6	F	37	ASP	3.1
4	N	434	VAL	3.1
4	N	449	ASN	3.1
4	N	468	PHE	3.1
3	A	86	PRO	3.1
9	6	211	ALA	3.1
3	J	640	LEU	3.1
4	O	647	LEU	3.1
5	P	273	MET	3.1
10	l	652	LYS	3.1
7	Y	657	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
8	3	269	MET	3.1
4	B	67	TYR	3.1
5	P	234	GLN	3.1
8	3	227	VAL	3.1
5	R	644	ILE	3.1
9	K	138	LYS	3.1
2	S	281	PRO	3.1
5	P	293	ASP	3.1
3	I	435	LYS	3.1
4	B	24	GLN	3.1
5	R	702	ARG	3.1
4	B	22	GLY	3.1
8	3	226	HIS	3.1
10	9	227	GLY	3.1
7	W	231	ILE	3.1
9	8	770	ASP	3.1
10	9	243	GLU	3.0
9	8	709	ARG	3.0
7	E	34	TRP	3.0
7	W	222	PHE	3.0
4	N	465	ILE	3.0
8	5	676	VAL	3.0
4	B	26	HIS	3.0
6	Z	229	TYR	3.0
2	S	233	ILE	3.0
8	4	472	ALA	3.0
6	1	415	THR	3.0
8	4	412	PHE	3.0
6	1	422	LYS	3.0
8	4	459	MET	3.0
5	P	310	LEU	3.0
5	C	24	PHE	3.0
6	Z	238	GLY	3.0
10	9	225	CYS	3.0
8	5	644	GLU	3.0
9	7	521	ARG	3.0
10	0	409	CYS	3.0
8	4	471	GLU	3.0
8	5	621	LEU	3.0
2	S	258	LEU	2.9
9	7	463	ARG	2.9
4	B	70	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
10	9	206	CYS	2.9
8	5	618	SER	2.9
5	R	692	LYS	2.9
7	Y	655	ASN	2.9
9	6	303	LYS	2.9
10	l	639	CYS	2.9
5	P	259	PHE	2.9
5	C	98	LYS	2.9
2	T	415	GLY	2.9
5	C	22	GLU	2.9
9	6	320	ARG	2.9
4	O	661	ARG	2.9
8	3	234	PHE	2.9
6	2	638	GLY	2.9
9	K	12	LEU	2.9
8	G	20	LYS	2.9
7	X	468	THR	2.9
3	J	679	SER	2.9
4	O	617	ILE	2.9
2	S	259	GLU	2.9
6	Z	230	LYS	2.9
6	1	456	SER	2.9
5	C	14	GLU	2.9
3	J	612	HIS	2.9
6	1	436	VAL	2.8
5	C	46	CYS	2.8
5	P	292	LYS	2.8
4	M	203	LEU	2.8
6	2	620	MET	2.8
9	6	288	MET	2.8
9	6	368	LYS	2.8
9	K	154	GLU	2.8
8	3	205	HIS	2.8
6	Z	260	GLY	2.8
10	l	642	MET	2.8
6	Z	259	LEU	2.8
7	Y	667	LYS	2.8
4	N	413	GLU	2.8
6	Z	207	PRO	2.8
8	5	641	VAL	2.8
5	C	16	LEU	2.8
10	9	214	THR	2.8

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Mol	Chain	Res	Type	RSRZ
9	8	774	VAL	2.8
3	J	674	GLY	2.8
4	O	618	GLU	2.8
4	B	7	LEU	2.8
9	K	82	VAL	2.8
3	I	434	ASP	2.8
9	8	672	ARG	2.8
2	U	670	PHE	2.7
2	D	64	ARG	2.7
9	K	134	MET	2.7
1	x	613	C	2.7
9	6	282	VAL	2.7
9	7	556	ASP	2.7
4	B	23	THR	2.7
8	5	609	LEU	2.7
7	Y	649	GLY	2.7
5	C	61	ARG	2.7
4	O	619	LEU	2.7
9	7	518	LYS	2.7
5	Q	465	MET	2.7
5	R	617	GLN	2.7
7	Y	626	GLN	2.7
9	8	707	VAL	2.7
8	4	462	ILE	2.7
4	M	234	VAL	2.7
4	M	249	ASN	2.7
5	C	39	ASN	2.7
6	F	7	PRO	2.7
3	I	472	LEU	2.7
7	Y	662	GLU	2.7
8	G	14	ASP	2.7
5	R	659	PHE	2.7
9	K	178	VAL	2.7
5	C	111	ARG	2.7
6	1	459	LEU	2.7
6	2	634	VAL	2.7
10	l	646	ALA	2.7
9	K	105	LEU	2.7
5	C	95	TYR	2.7
4	B	41	LYS	2.6
9	K	17	ASP	2.6
9	K	124	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
4	N	472	ASP	2.6
9	K	148	PHE	2.6
6	F	62	VAL	2.6
7	E	77	ILE	2.6
9	6	371	GLY	2.6
6	1	423	LEU	2.6
10	1	645	GLN	2.6
6	2	657	GLY	2.6
4	B	57	THR	2.6
4	N	467	TYR	2.6
5	P	244	ILE	2.6
4	B	25	VAL	2.6
5	P	268	GLU	2.6
10	9	248	SER	2.6
10	9	249	LEU	2.6
9	7	465	GLU	2.6
4	B	32	VAL	2.6
9	6	337	SER	2.6
9	6	318	LYS	2.6
10	L	17	SER	2.6
7	X	425	LEU	2.6
4	M	251	GLU	2.6
10	0	439	CYS	2.6
9	8	610	LEU	2.6
2	D	36	GLU	2.6
5	Q	434	GLN	2.5
9	8	667	MET	2.5
2	T	446	ILE	2.5
4	M	266	ARG	2.5
10	L	13	LEU	2.5
9	7	472	ARG	2.5
6	1	413	GLY	2.5
6	1	462	VAL	2.5
2	T	421	GLU	2.5
8	5	628	GLN	2.5
9	8	612	LEU	2.5
7	W	281	GLY	2.5
3	A	9	MET	2.5
8	3	271	GLU	2.5
2	D	51	ARG	2.5
3	J	618	ARG	2.5
5	P	258	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
9	8	751	TYR	2.5
3	A	21	LEU	2.5
5	C	45	ASN	2.5
10	9	241	TRP	2.5
9	7	486	LEU	2.5
4	O	620	LYS	2.5
9	7	476	GLU	2.5
10	9	213	LEU	2.5
10	L	57	PHE	2.5
8	4	469	MET	2.4
2	U	614	GLU	2.4
5	R	626	THR	2.4
8	G	6	PRO	2.4
10	I	647	GLN	2.4
8	5	631	LEU	2.4
2	D	43	MET	2.4
4	M	217	ILE	2.4
8	4	448	MET	2.4
4	N	464	ASN	2.4
3	A	70	VAL	2.4
7	X	449	GLY	2.4
6	1	414	LEU	2.4
5	C	51	LYS	2.4
7	X	446	CYS	2.4
7	E	25	LEU	2.4
6	F	29	TYR	2.4
3	H	216	ARG	2.4
9	6	321	ARG	2.4
4	B	37	ASN	2.4
6	F	40	MET	2.4
2	T	476	MET	2.4
5	C	92	LYS	2.4
4	B	68	PHE	2.4
1	x	746	G	2.4
2	U	678	LYS	2.3
6	1	410	PHE	2.3
3	H	234	PHE	2.3
3	J	682	VAL	2.3
7	W	285	THR	2.3
5	C	93	ASP	2.3
9	K	156	ASP	2.3
2	U	661	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
7	W	275	GLY	2.3
8	G	43	ASP	2.3
7	Y	638	GLN	2.3
10	0	447	GLN	2.3
4	O	622	GLY	2.3
5	Q	462	HIS	2.3
10	l	658	GLN	2.3
6	2	660	GLY	2.3
2	S	270	PHE	2.3
8	5	673	LEU	2.2
6	1	460	GLY	2.2
7	E	57	VAL	2.2
8	3	206	PRO	2.2
3	I	470	VAL	2.2
8	G	42	ILE	2.2
9	6	266	ARG	2.2
3	H	270	VAL	2.2
3	I	409	LEU	2.2
8	5	606	PRO	2.2
5	P	250	LYS	2.2
2	D	56	ALA	2.2
2	S	222	THR	2.2
9	6	274	LYS	2.2
5	R	651	LYS	2.2
9	7	541	GLY	2.2
3	H	235	ASP	2.2
1	V	14	A	2.2
4	N	461	ARG	2.2
1	x	735	A	2.2
8	G	5	HIS	2.2
7	W	249	GLY	2.2
4	M	204	VAL	2.1
8	G	61	VAL	2.1
3	I	474	GLY	2.1
3	A	26	ILE	2.1
4	B	34	VAL	2.1
8	5	620	LYS	2.1
7	X	461	ALA	2.1
7	X	450	PHE	2.1
5	P	230	SER	2.1
5	Q	429	LEU	2.1
5	R	634	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
5	P	218	LYS	2.1
7	Y	634	TRP	2.1
2	T	461	VAL	2.1
6	Z	266	CYS	2.1
7	W	254	MET	2.1
4	B	14	THR	2.1
6	F	12	ASN	2.1
9	7	464	GLU	2.1
2	U	655	VAL	2.1
9	8	731	ARG	2.1
8	G	21	LEU	2.1
9	6	348	PHE	2.1
7	W	269	LYS	2.1
6	2	616	GLY	2.1
9	8	763	HIS	2.1
3	A	44	ASP	2.0
4	M	262	GLY	2.0
5	C	34	GLN	2.0
5	Q	471	LYS	2.0
9	6	359	SER	2.0
9	8	737	SER	2.0
6	2	636	VAL	2.0
4	B	64	ASN	2.0
5	C	67	LEU	2.0
3	H	237	HIS	2.0
9	6	347	ALA	2.0
2	S	215	GLY	2.0
9	8	669	ARG	2.0
6	1	463	LEU	2.0
5	Q	430	SER	2.0
7	Y	669	LYS	2.0
7	W	265	HIS	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
11	ZN	9	278	1/1	0.22	0.95	-	231,231,231,231	0
11	ZN	L	78	1/1	-0.10	0.74	-	231,231,231,231	0
11	ZN	1	678	1/1	-0.02	0.78	-	231,231,231,231	0
11	ZN	0	478	1/1	0.25	2.12	-	231,231,231,231	0

6.5 Other polymers [i](#)

There are no such residues in this entry.