



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:32 PM UTC

PDB ID : 3PGW / pdb_00003pgw
Title : Crystal structure of human U1 snRNP
Authors : Weber, G.; Trowitzsch, S.; Kastner, B.; Luehrmann, R.; Wahl, M.C.
Deposited on : 2010-11-02
Resolution : 4.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

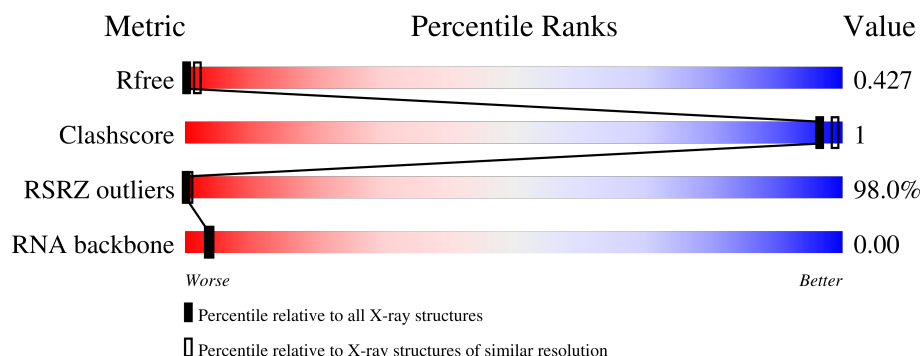
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1088 (4.90-3.90)
Clashscore	190562	1135 (4.90-3.90)
RSRZ outliers	180081	1084 (4.90-3.90)
RNA backbone	3983	1037 (5.60-3.10)

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

Mol	Chain	Length	Quality of chain
1	A	282	38% 38% 62%
1	P	282	39% 40% 60%
2	L	437	34% 34% 66%
2	S	437	34% 34% 66%
3	W	126	73% 73% 27%
3	Z	126	63% 63% 37%

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

2 Entry composition

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

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

- Molecule 1 is a protein called U1-A.

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

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

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

- Molecule 3 is a protein called Sm-D3.

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

- Molecule 4 is a protein called Sm B.

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

- Molecule 5 is a protein called Sm-D1.

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

- Molecule 6 is a protein called Sm-D2.

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

- Molecule 7 is a protein called Sm-F.

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

- Molecule 8 is a protein called Sm-E.

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

- Molecule 9 is a protein called Sm G.

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

- Molecule 10 is a RNA chain called U1 snRNA.

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

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

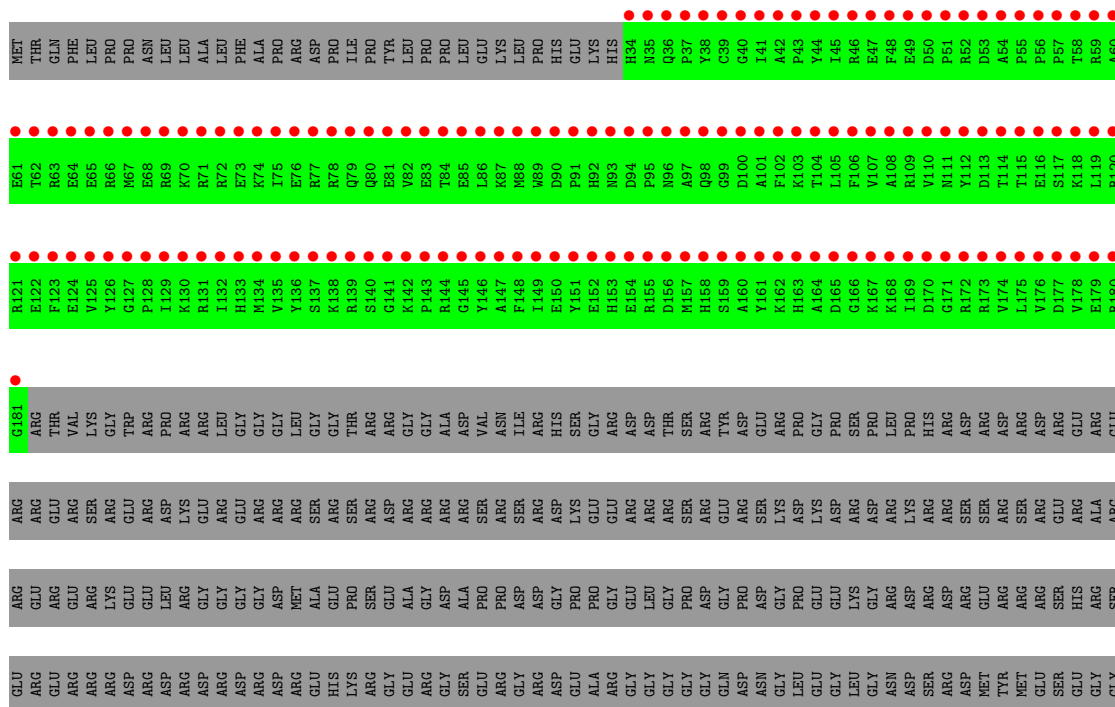
- Molecule 11 is a DNA chain called DNA 5'-D(*AP*GP*GP*TP*AP*AP*GP*TP*A)-3'.

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

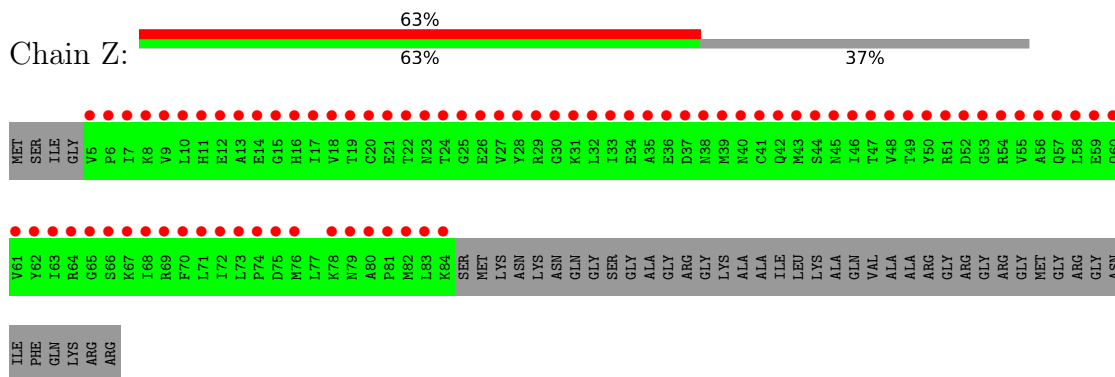
Chain S:

- Molecule 2: U1-70K

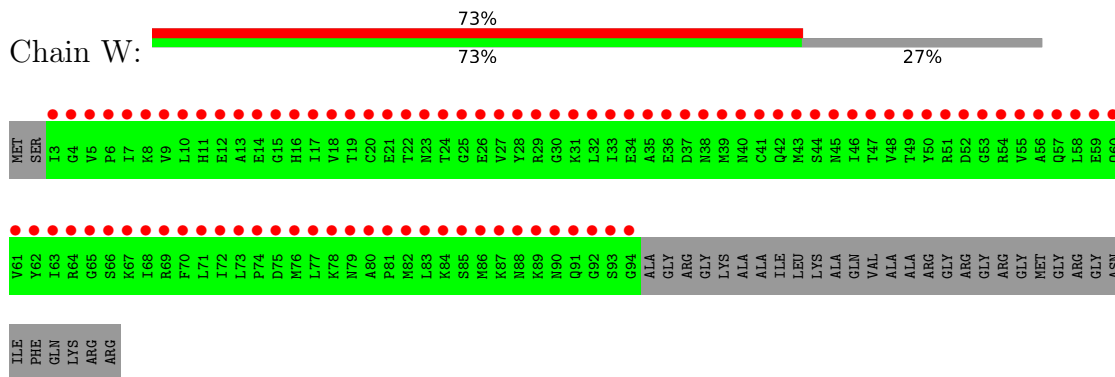
Chain L:



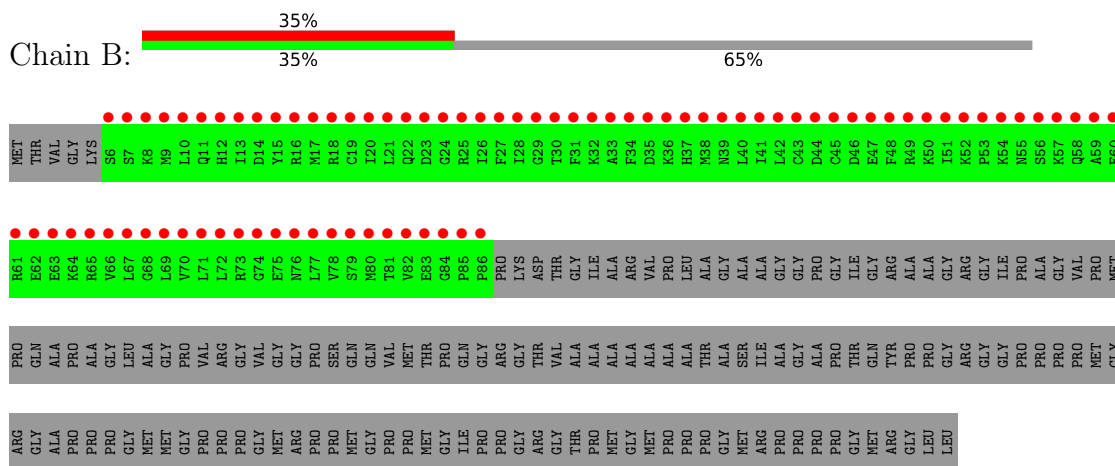
- Molecule 3: Sm-D3



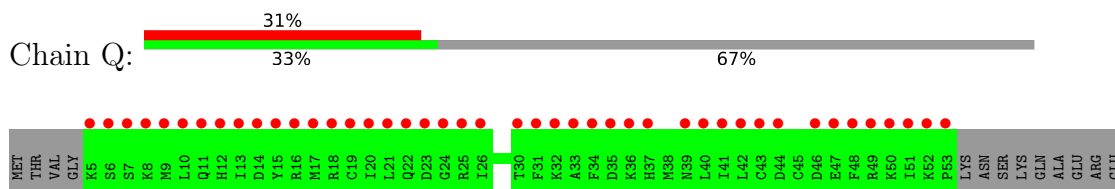
- Molecule 3: Sm-D3

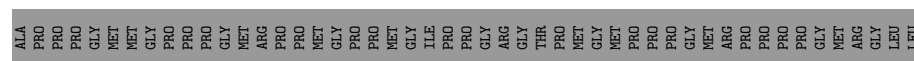


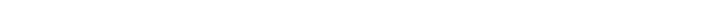
- Molecule 4: Sm B



- Molecule 4: Sm B



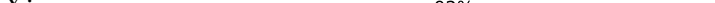


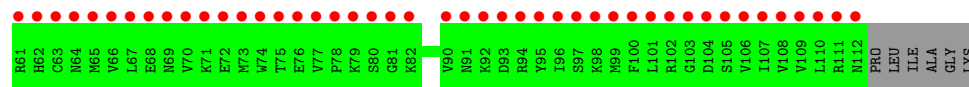
Chain X:  69% 71% 29%

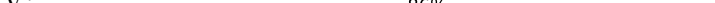


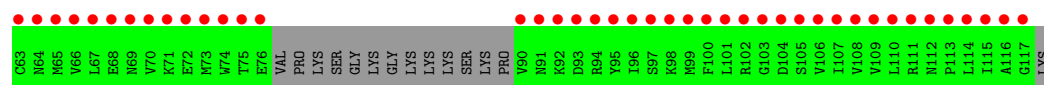
Chain U:  69% 71% 29%



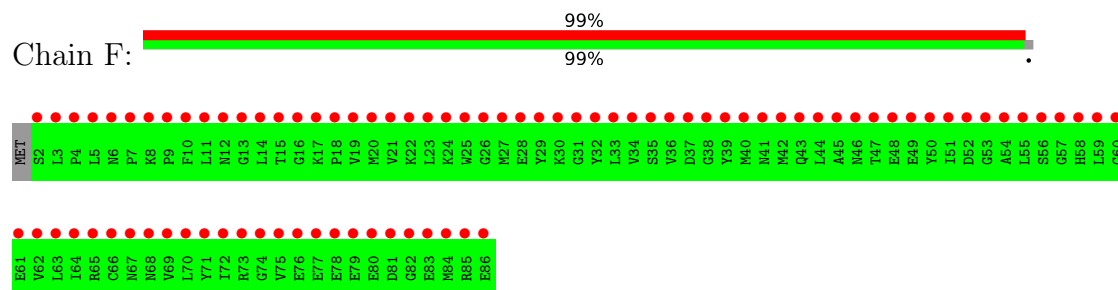
Chain Y:  87% 92% 6%



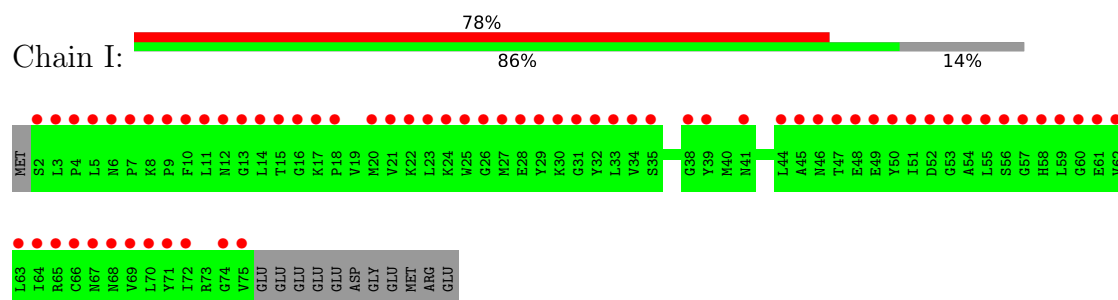
Chain V:  80% 86% 13%



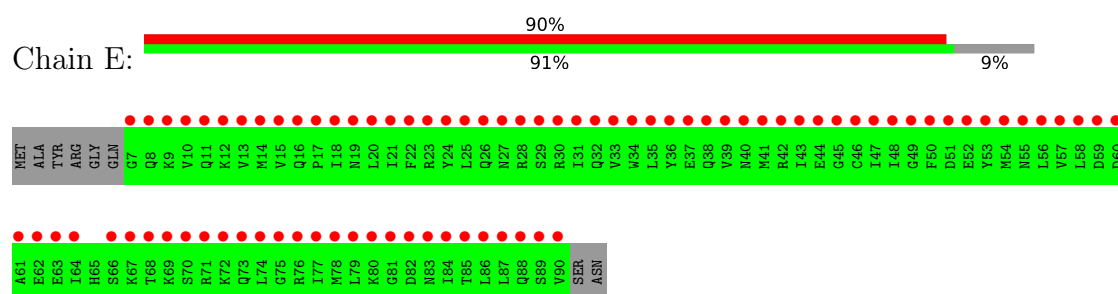
- Molecule 7: Sm-F



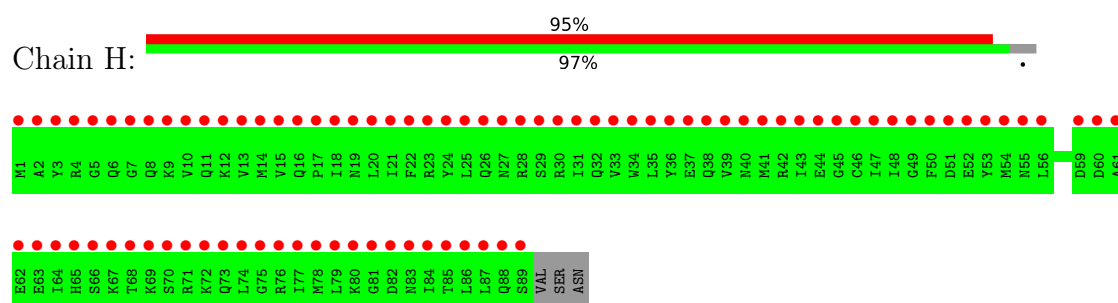
- Molecule 7: Sm-F



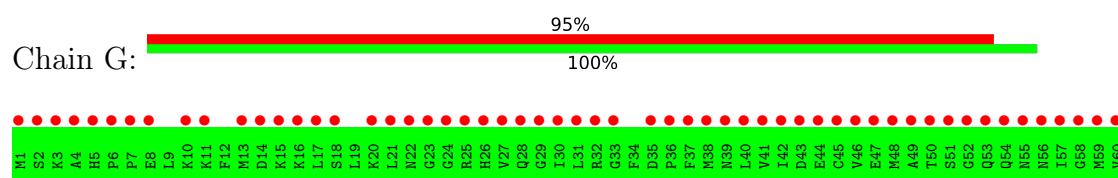
- Molecule 8: Sm-E

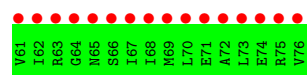


- Molecule 8: Sm-E

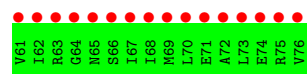
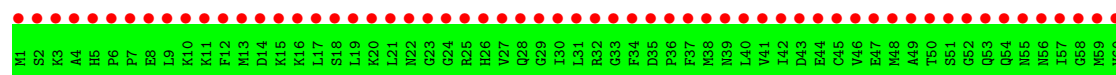


- Molecule 9: Sm G

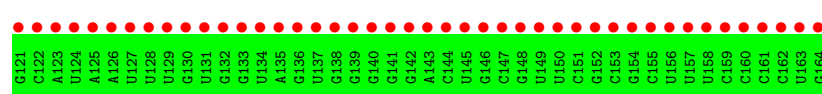
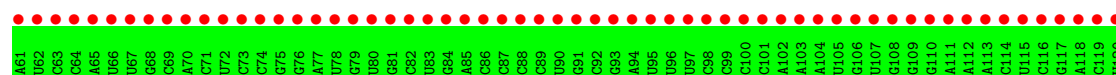
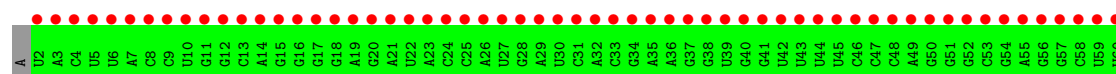




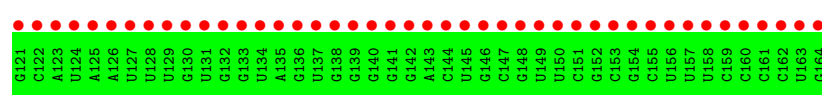
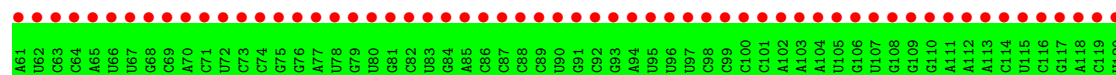
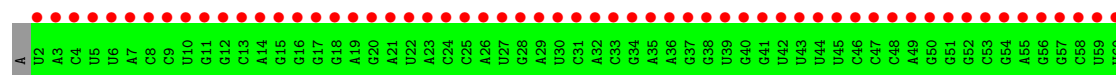
• Molecule 9: Sm G



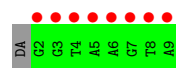
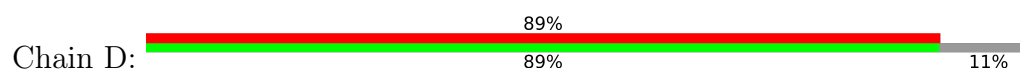
• Molecule 10: U1 snRNA



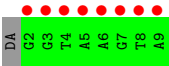
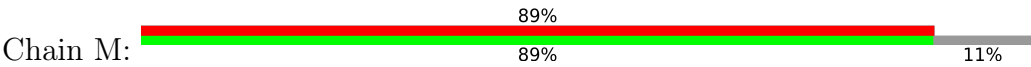
• Molecule 10: U1 snRNA



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	358.42Å 88.22Å 150.90Å 90.00° 111.88° 90.00°	Depositor
Resolution (Å)	100.00 – 4.40 100.00 – 4.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (100.00-4.40) 99.4 (100.00-4.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 4.47Å)	Xtriage
Refinement program	PHENIX, CNS 1.3	Depositor
R, R_{free}	0.299 , 0.348 0.437 , 0.427	Depositor DCC
R_{free} test set	1404 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	222.6	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	12.66 , 999.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.037 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.58	EDS
Total number of atoms	2058	wwPDB-VP
Average B, all atoms (Å ²)	255.0	wwPDB-VP

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

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

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

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

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

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

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

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

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

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	108/282 (38%)	12.33	108 (100%) 0 0	135, 201, 306, 344	0
1	P	113/282 (40%)	13.54	110 (97%) 0 0	135, 202, 310, 344	0
2	L	148/437 (33%)	12.33	148 (100%) 0 0	189, 268, 352, 389	0
2	S	150/437 (34%)	11.37	149 (99%) 0 0	185, 269, 352, 390	0
3	W	92/126 (73%)	12.71	92 (100%) 0 0	153, 228, 354, 392	0
3	Z	80/126 (63%)	12.44	79 (98%) 0 0	152, 225, 260, 292	0
4	B	81/231 (35%)	10.78	81 (100%) 0 0	160, 250, 322, 350	0
4	Q	76/231 (32%)	8.50	71 (93%) 0 1	159, 232, 298, 350	0
5	U	85/119 (71%)	10.83	82 (96%) 0 0	151, 223, 260, 359	0
5	X	85/119 (71%)	12.25	82 (96%) 0 0	153, 222, 259, 363	0
6	V	103/118 (87%)	10.43	94 (91%) 0 1	149, 234, 295, 321	0
6	Y	104/118 (88%)	12.44	103 (99%) 0 0	150, 233, 300, 490	0
7	F	85/86 (98%)	13.66	85 (100%) 0 0	150, 224, 303, 373	0
7	I	74/86 (86%)	10.62	67 (90%) 0 1	151, 217, 265, 283	0
8	E	84/92 (91%)	10.68	83 (98%) 0 0	184, 243, 359, 423	0
8	H	89/92 (96%)	11.07	87 (97%) 0 0	181, 246, 362, 385	0
9	G	76/76 (100%)	10.24	72 (94%) 0 0	179, 237, 302, 315	0
9	J	76/76 (100%)	9.98	76 (100%) 0 0	180, 241, 307, 363	0
10	N	163/164 (99%)	12.76	163 (100%) 0 0	182, 295, 494, 557	0
10	R	163/164 (99%)	12.64	163 (100%) 0 0	183, 289, 494, 557	0
11	D	8/9 (88%)	15.56	8 (100%) 0 0	431, 501, 523, 526	0
11	M	8/9 (88%)	14.40	8 (100%) 0 0	431, 500, 522, 525	0
All	All	2051/3480 (58%)	11.78	2011 (98%) 0 0	135, 242, 379, 557	0

All (2011) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	X	23	THR	69.8
3	W	85	SER	68.3
1	P	51	MET	61.6
1	P	46	SER	56.8
1	A	53	GLY	49.0
8	H	27	ASN	48.0
7	I	16	GLY	47.9
1	A	46	SER	45.9
1	P	48	SER	45.5
8	E	49	GLY	44.9
1	P	47	ARG	44.5
3	Z	84	LYS	44.2
5	X	47	LEU	44.2
1	P	53	GLY	43.0
1	P	17	LEU	42.6
7	F	18	PRO	40.7
5	X	46	THR	40.1
1	A	18	ASN	39.5
4	B	46	ASP	39.2
7	F	32	TYR	37.5
1	P	52	ARG	37.4
2	S	167	LYS	37.2
7	F	33	LEU	37.2
1	A	51	MET	37.2
5	X	43	VAL	37.1
1	A	52	ARG	36.3
1	A	26	LEU	36.2
5	X	45	MET	35.9
3	W	86	MET	35.6
1	A	48	SER	35.6
3	W	91	GLN	34.4
2	S	81	GLU	34.1
3	W	81	PRO	33.8
2	L	53	ASP	33.5
9	G	72	ALA	32.9
5	U	53	VAL	32.8
1	P	23	LYS	32.6
8	H	11	GLN	32.6
5	X	21	ASN	32.4
5	X	24	GLN	32.3
2	S	144	ARG	32.0
10	N	75	G	31.9
3	W	49	THR	31.9

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Mol	Chain	Res	Type	RSRZ
5	X	57	THR	31.3
8	E	48	ILE	31.3
1	P	18	ASN	31.1
3	W	79	ASN	31.0
7	F	79	GLU	30.8
2	S	80	GLN	30.6
2	S	84	THR	30.5
6	Y	30	SER	30.5
8	E	29	SER	30.5
6	Y	74	TRP	30.1
1	P	25	GLU	30.0
1	A	107	LYS	29.9
2	S	143	PRO	29.8
7	I	12	ASN	29.7
2	S	46	ARG	29.6
1	A	79	ASP	29.5
1	A	19	GLU	29.3
1	P	21	ILE	29.3
2	S	168	LYS	29.0
8	H	7	GLY	28.6
6	V	25	ASN	28.6
1	P	16	ASN	28.5
7	I	11	LEU	28.2
6	Y	75	THR	28.0
7	I	2	SER	28.0
6	Y	22	GLU	28.0
1	A	78	TYR	27.7
6	Y	16	LEU	27.7
3	W	89	LYS	27.7
4	Q	48	PHE	27.6
3	W	93	SER	27.5
7	F	6	ASN	27.5
5	U	6	PHE	27.5
1	P	19	GLU	27.5
2	L	46	ARG	27.4
1	P	78	TYR	27.4
4	Q	87	PRO	27.2
7	F	77	GLU	27.2
6	Y	26	THR	27.1
6	Y	112	ASN	27.1
5	X	44	LYS	26.8
5	X	25	VAL	26.8

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Mol	Chain	Res	Type	RSRZ
6	Y	78	PRO	26.7
2	S	166	GLY	26.6
3	W	80	ALA	26.6
7	I	34	VAL	26.4
3	Z	28	TYR	26.3
9	J	14	ASP	26.3
3	Z	81	PRO	26.3
1	P	22	LYS	26.3
2	S	90	ASP	26.2
5	X	22	GLY	26.2
7	I	4	PRO	26.1
2	L	49	GLU	26.0
8	E	50	PHE	25.9
3	W	50	TYR	25.8
9	J	2	SER	25.7
8	E	27	ASN	25.6
7	I	18	PRO	25.5
3	Z	26	GLU	25.4
3	W	92	GLY	25.3
8	E	10	VAL	25.2
7	F	35	SER	25.2
7	I	17	LYS	25.1
6	V	24	PHE	25.0
2	S	173	ARG	25.0
4	Q	66	VAL	24.9
2	L	140	SER	24.8
3	Z	27	VAL	24.7
8	H	16	GLN	24.7
3	Z	19	THR	24.6
1	A	47	ARG	24.5
7	F	85	ARG	24.5
8	H	3	TYR	24.5
6	Y	18	LYS	24.5
3	W	76	MET	24.5
5	U	52	PRO	24.4
1	P	80	LYS	24.4
6	V	91	ASN	24.3
6	V	20	GLU	24.3
6	Y	15	GLU	24.2
1	A	25	GLU	24.2
7	F	80	GLU	24.2
4	Q	85	PRO	24.2

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Mol	Chain	Res	Type	RSRZ
6	Y	17	GLN	24.1
8	H	30	ARG	24.0
1	P	24	ASP	24.0
6	V	60	ASP	24.0
11	D	5	DA	24.0
7	F	10	PHE	23.9
6	Y	19	ARG	23.7
8	E	66	SER	23.7
4	B	14	ASP	23.7
7	F	7	PRO	23.7
3	W	4	GLY	23.7
2	S	137	SER	23.6
1	P	104	ARG	23.5
2	L	76	GLU	23.3
9	G	71	GLU	23.3
6	V	38	ASN	23.2
4	Q	65	ARG	23.2
3	Z	46	ILE	23.2
8	H	14	MET	23.1
1	A	105	ASP	23.1
7	F	76	GLU	23.0
2	S	50	ASP	23.0
6	V	12	THR	23.0
9	G	2	SER	23.0
7	F	15	THR	22.9
2	L	81	GLU	22.9
3	Z	79	ASN	22.9
3	W	57	GLN	22.9
2	L	89	TRP	22.8
7	I	46	ASN	22.8
9	J	36	PRO	22.7
6	Y	24	PHE	22.7
2	S	79	GLN	22.7
6	Y	76	GLU	22.7
2	S	113	ASP	22.7
4	B	65	ARG	22.6
7	F	74	GLY	22.6
6	V	33	THR	22.6
7	F	4	PRO	22.6
2	S	43	PRO	22.6
3	W	83	LEU	22.6
8	E	8	GLN	22.6

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Mol	Chain	Res	Type	RSRZ
1	P	79	ASP	22.5
3	Z	59	GLU	22.5
7	I	45	ALA	22.5
2	S	85	GLU	22.4
9	J	49	ALA	22.4
2	S	89	TRP	22.4
3	Z	83	LEU	22.3
1	P	26	LEU	22.3
2	L	90	ASP	22.3
3	W	82	MET	22.3
5	U	73	SER	22.3
2	S	83	GLU	22.3
8	E	30	ARG	22.3
9	G	26	HIS	22.2
9	G	48	MET	22.2
5	U	77	ASP	22.1
3	W	47	THR	22.1
2	S	78	ARG	22.1
6	V	75	THR	22.1
9	G	25	ARG	22.0
7	I	38	GLY	22.0
1	A	23	LYS	22.0
1	A	21	ILE	22.0
6	V	30	SER	22.0
4	B	47	GLU	21.9
5	U	46	THR	21.9
7	F	45	ALA	21.9
5	U	48	LYS	21.9
2	S	51	PRO	21.8
7	F	5	LEU	21.8
6	Y	25	ASN	21.8
7	F	11	LEU	21.8
3	W	75	ASP	21.7
2	L	85	GLU	21.7
2	L	84	THR	21.7
9	J	35	ASP	21.5
1	P	106	ARG	21.5
7	F	61	GLU	21.4
6	Y	29	LEU	21.4
5	X	48	LYS	21.4
8	E	51	ASP	21.4
3	Z	45	ASN	21.3

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Mol	Chain	Res	Type	RSRZ
3	Z	76	MET	21.3
9	G	18	SER	21.3
3	Z	49	THR	21.2
6	V	23	GLU	21.1
11	M	9	DA	21.0
5	X	84	GLU	20.9
5	U	5	ARG	20.9
2	L	47	GLU	20.9
8	H	6	GLN	20.9
2	L	56	PRO	20.8
8	E	7	GLY	20.8
6	Y	93	ASP	20.8
6	Y	73	MET	20.8
1	A	109	GLU	20.7
2	L	73	GLU	20.7
7	F	34	VAL	20.7
8	H	26	GLN	20.7
1	A	24	ASP	20.7
1	P	105	ASP	20.7
3	Z	75	ASP	20.6
7	I	15	THR	20.6
1	A	108	ARG	20.5
5	U	74	LEU	20.5
2	S	136	TYR	20.5
7	F	36	VAL	20.5
2	L	79	GLN	20.5
1	P	28	LYS	20.4
4	B	49	ARG	20.4
5	X	50	ARG	20.4
4	B	44	ASP	20.4
4	B	60	GLU	20.4
5	U	76	LEU	20.4
9	J	54	GLN	20.4
2	L	77	ARG	20.4
3	Z	50	TYR	20.3
4	Q	6	SER	20.3
9	G	23	GLY	20.3
2	S	93	ASN	20.2
2	S	42	ALA	20.2
7	I	74	GLY	20.2
4	Q	36	LYS	20.2
10	R	48	C	20.2

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Mol	Chain	Res	Type	RSRZ
9	J	13	MET	20.2
6	V	58	ALA	20.2
2	S	135	VAL	20.1
1	P	107	LYS	20.1
3	Z	30	GLY	20.0
3	Z	29	ARG	20.0
9	G	55	ASN	20.0
6	V	21	GLU	20.0
5	U	50	ARG	20.0
7	F	17	LYS	20.0
6	Y	91	ASN	19.9
8	E	13	VAL	19.9
3	Z	20	CYS	19.9
2	L	153	HIS	19.9
1	A	106	ARG	19.9
8	H	4	ARG	19.8
4	Q	5	LYS	19.8
8	H	17	PRO	19.8
2	S	172	ARG	19.8
4	B	83	GLU	19.8
3	W	88	ASN	19.7
3	W	94	GLY	19.7
2	L	80	GLN	19.7
2	S	87	LYS	19.6
9	G	54	GLN	19.6
1	P	109	GLU	19.6
8	H	8	GLN	19.6
10	R	49	A	19.5
5	X	49	ASN	19.4
1	P	102	VAL	19.4
3	W	84	LYS	19.3
3	Z	47	THR	19.3
9	G	73	LEU	19.3
2	L	91	PRO	19.3
1	A	22	LYS	19.3
2	L	50	ASP	19.3
4	Q	89	ASP	19.3
3	W	77	LEU	19.2
4	B	58	GLN	19.2
7	F	14	LEU	19.2
3	W	56	ALA	19.2
4	B	68	GLY	19.2

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Mol	Chain	Res	Type	RSRZ
8	H	10	VAL	19.2
7	F	12	ASN	19.1
6	V	36	VAL	19.1
1	P	50	LYS	19.1
6	V	57	LYS	19.1
6	V	13	PRO	19.1
2	L	128	PRO	19.0
2	L	138	LYS	19.0
2	L	35	ASN	19.0
5	U	51	GLU	19.0
2	L	72	ARG	19.0
6	Y	27	GLY	19.0
6	V	14	GLU	19.0
2	S	171	GLY	18.9
9	J	10	LYS	18.9
8	H	5	GLY	18.9
4	B	59	ALA	18.9
6	Y	11	MET	18.8
6	V	61	ARG	18.8
4	Q	88	LYS	18.8
2	L	88	MET	18.8
4	Q	84	GLY	18.7
4	B	67	LEU	18.7
2	L	74	LYS	18.7
5	U	80	LEU	18.7
5	U	75	PRO	18.7
5	U	54	GLN	18.6
5	X	52	PRO	18.6
9	G	49	ALA	18.6
4	B	48	PHE	18.5
9	J	7	PRO	18.5
8	E	76	ARG	18.5
2	L	139	ARG	18.5
7	F	86	GLU	18.5
5	X	56	GLU	18.5
6	Y	12	THR	18.5
3	W	90	ASN	18.4
1	A	80	LYS	18.4
2	L	75	ILE	18.4
5	X	51	GLU	18.4
2	L	155	ARG	18.4
2	L	36	GLN	18.4

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Mol	Chain	Res	Type	RSRZ
9	J	6	PRO	18.4
2	S	88	MET	18.3
9	G	74	GLU	18.3
8	H	29	SER	18.3
2	S	140	SER	18.3
6	Y	111	ARG	18.3
1	P	110	LYS	18.3
2	L	68	GLU	18.2
2	L	141	GLY	18.2
5	X	42	ALA	18.2
5	U	78	THR	18.2
2	S	112	TYR	18.2
4	B	15	TYR	18.2
8	H	13	VAL	18.1
9	J	32	ARG	18.1
2	L	57	PRO	18.1
9	J	50	THR	18.0
3	W	55	VAL	18.0
9	J	11	LYS	18.0
5	U	1	MET	18.0
2	L	78	ARG	18.0
10	R	123	A	18.0
2	S	82	VAL	18.0
2	S	125	VAL	17.9
4	B	86	PRO	17.9
6	V	7	PRO	17.9
1	A	54	GLN	17.9
9	G	24	GLY	17.9
3	Z	48	VAL	17.8
5	U	3	LEU	17.8
9	J	53	GLN	17.8
10	R	33	C	17.7
5	U	82	ASP	17.7
8	H	68	THR	17.7
1	A	110	LYS	17.7
5	U	10	LEU	17.7
5	X	54	GLN	17.7
2	S	47	GLU	17.7
8	H	12	LYS	17.7
10	R	75	G	17.7
2	L	83	GLU	17.7
8	H	31	ILE	17.7

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Mol	Chain	Res	Type	RSRZ
7	I	54	ALA	17.6
11	D	2	DG	17.5
11	D	4	DT	17.5
10	R	18	G	17.5
7	F	16	GLY	17.5
8	H	15	VAL	17.5
1	P	101	PHE	17.5
2	S	183	THR	17.5
8	E	68	THR	17.5
6	Y	14	GLU	17.5
1	P	49	LEU	17.5
10	N	117	G	17.4
1	A	28	LYS	17.4
4	B	66	VAL	17.4
6	Y	77	VAL	17.4
4	Q	90	THR	17.4
2	L	52	ARG	17.4
2	S	34	HIS	17.4
8	E	40	ASN	17.4
9	J	3	LYS	17.3
7	I	10	PHE	17.3
5	X	53	VAL	17.3
1	P	54	GLN	17.2
8	E	12	LYS	17.2
5	U	81	VAL	17.1
1	P	108	ARG	17.1
5	U	79	LEU	17.1
5	U	49	ASN	17.1
3	Z	52	ASP	17.1
9	J	51	SER	17.1
6	V	112	ASN	17.0
11	D	3	DG	17.0
5	X	55	LEU	17.0
10	N	66	U	17.0
6	V	17	GLN	17.0
4	B	85	PRO	17.0
2	L	62	THR	17.0
1	P	111	ARG	17.0
2	L	54	ALA	17.0
7	F	2	SER	17.0
8	H	25	LEU	16.9
8	E	60	ASP	16.9

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Mol	Chain	Res	Type	RSRZ
4	B	62	GLU	16.9
4	B	84	GLY	16.9
7	F	9	PRO	16.9
2	L	64	GLU	16.9
7	F	43	GLN	16.9
9	J	55	ASN	16.9
7	I	75	VAL	16.9
4	Q	86	PRO	16.8
9	J	48	MET	16.8
10	R	104	A	16.8
6	V	92	LYS	16.8
7	F	8	LYS	16.8
1	P	100	THR	16.8
5	U	9	LYS	16.7
10	N	119	C	16.7
9	G	53	GLN	16.7
6	V	37	LYS	16.7
4	B	57	LYS	16.7
8	H	24	TYR	16.7
3	Z	53	GLY	16.7
2	L	65	GLU	16.7
5	U	84	GLU	16.7
7	F	60	GLY	16.7
2	L	61	GLU	16.7
8	H	2	ALA	16.7
1	P	20	LYS	16.6
3	Z	51	ARG	16.6
8	E	67	LYS	16.6
9	G	50	THR	16.6
5	U	83	VAL	16.6
1	P	99	GLY	16.5
2	L	58	THR	16.5
7	I	52	ASP	16.5
2	L	69	ARG	16.5
5	X	1	MET	16.4
8	H	9	LYS	16.4
2	L	82	VAL	16.4
8	E	9	LYS	16.4
10	N	84	G	16.4
7	F	13	GLY	16.3
9	J	52	GLY	16.3
8	E	17	PRO	16.3

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Mol	Chain	Res	Type	RSRZ
2	S	142	LYS	16.3
2	S	134	MET	16.3
9	G	51	SER	16.3
8	E	28	ARG	16.3
9	J	76	VAL	16.3
8	E	25	LEU	16.2
6	Y	33	THR	16.2
2	L	181	GLY	16.2
3	W	53	GLY	16.2
2	L	71	ARG	16.1
7	I	32	TYR	16.1
3	W	52	ASP	16.1
1	P	113	PRO	16.1
8	E	31	ILE	16.1
8	E	24	TYR	16.1
3	Z	57	GLN	16.1
6	Y	94	ARG	16.1
10	N	50	G	16.0
2	S	182	ARG	16.0
6	Y	9	SER	16.0
10	N	118	A	16.0
10	N	116	C	16.0
6	Y	90	VAL	16.0
10	N	74	C	15.9
1	A	17	LEU	15.9
10	N	161	C	15.9
1	A	6	THR	15.9
2	L	154	GLU	15.8
10	R	126	A	15.8
10	N	6	U	15.8
10	R	34	G	15.8
2	S	86	LEU	15.8
1	A	111	ARG	15.8
3	Z	58	LEU	15.8
10	R	19	A	15.8
1	A	20	LYS	15.7
2	L	48	PHE	15.7
10	N	162	C	15.7
2	L	92	HIS	15.7
10	R	20	G	15.7
2	L	55	PRO	15.6
2	L	60	ALA	15.6

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Mol	Chain	Res	Type	RSRZ
6	Y	3	LEU	15.6
10	N	57	G	15.6
6	Y	8	LYS	15.6
7	I	3	LEU	15.5
1	A	49	LEU	15.5
6	V	115	ILE	15.5
9	G	52	GLY	15.5
10	N	79	G	15.5
10	N	65	A	15.5
6	V	76	GLU	15.5
10	N	93	G	15.5
7	F	75	VAL	15.4
4	B	50	LYS	15.4
6	Y	13	PRO	15.4
3	W	51	ARG	15.4
7	I	53	GLY	15.4
2	L	70	LYS	15.4
10	R	17	G	15.4
8	H	28	ARG	15.4
10	N	12	G	15.4
2	S	141	GLY	15.3
4	Q	49	ARG	15.3
8	E	59	ASP	15.3
9	J	58	GLY	15.3
10	N	38	G	15.3
2	S	109	ARG	15.3
5	X	2	LYS	15.3
2	L	51	PRO	15.2
10	R	74	C	15.2
2	S	174	VAL	15.2
3	W	54	ARG	15.2
2	L	67	MET	15.2
6	V	113	PRO	15.1
2	L	87	LYS	15.1
7	I	60	GLY	15.1
10	R	108	G	15.1
11	M	8	DT	15.1
9	J	1	MET	15.1
1	A	50	LYS	15.1
6	V	2	SER	15.1
10	N	37	G	15.1
6	V	29	LEU	15.1

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Mol	Chain	Res	Type	RSRZ
4	Q	44	ASP	15.1
6	V	116	ALA	15.0
5	X	85	PRO	15.0
3	W	3	ILE	15.0
1	A	104	ARG	15.0
5	X	82	ASP	15.0
3	W	37	ASP	15.0
10	N	4	C	15.0
9	G	3	LYS	15.0
10	N	61	A	14.9
6	Y	21	GLU	14.9
10	N	17	G	14.9
7	F	44	LEU	14.9
9	G	75	ARG	14.9
9	G	22	ASN	14.9
10	N	13	C	14.9
4	B	63	GLU	14.9
2	L	86	LEU	14.9
2	L	59	ARG	14.9
6	Y	92	LYS	14.9
2	L	156	ASP	14.9
6	V	114	LEU	14.9
4	B	61	ARG	14.8
9	G	47	GLU	14.8
10	R	109	G	14.8
10	N	77	A	14.8
3	Z	56	ALA	14.8
3	Z	55	VAL	14.8
10	N	121	G	14.8
10	N	46	C	14.8
7	F	3	LEU	14.8
10	N	92	C	14.7
3	Z	80	ALA	14.7
2	L	66	ARG	14.7
6	Y	5	ASN	14.7
10	R	106	G	14.7
2	S	96	ASN	14.6
5	U	2	LYS	14.6
8	H	1	MET	14.6
2	S	139	ARG	14.6
10	N	40	G	14.6
10	R	117	G	14.6

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Mol	Chain	Res	Type	RSRZ
10	N	11	G	14.6
10	R	54	G	14.6
10	R	91	G	14.6
3	Z	54	ARG	14.5
10	R	140	G	14.5
10	R	3	A	14.5
1	A	112	LYS	14.5
10	R	130	G	14.5
10	N	73	C	14.4
11	M	5	DA	14.4
1	P	112	LYS	14.4
10	R	132	G	14.4
10	R	103	A	14.4
10	N	41	G	14.4
11	M	6	DA	14.4
10	R	88	C	14.4
10	R	105	U	14.3
8	E	16	GLN	14.3
5	X	83	VAL	14.3
4	B	51	ILE	14.3
9	G	36	PRO	14.3
10	R	32	A	14.3
10	N	3	A	14.3
10	N	5	U	14.3
9	G	10	LYS	14.3
10	R	52	G	14.3
10	R	53	C	14.3
10	R	4	C	14.2
10	R	28	G	14.2
10	R	133	G	14.2
2	S	169	ILE	14.2
10	N	56	G	14.2
10	N	7	A	14.2
2	S	138	LYS	14.2
10	N	36	A	14.2
10	R	89	C	14.2
5	U	85	PRO	14.2
10	R	125	A	14.1
10	R	110	G	14.1
11	D	9	DA	14.1
10	N	108	G	14.1
10	N	109	G	14.1

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Mol	Chain	Res	Type	RSRZ
1	P	114	LYS	14.1
10	R	41	G	14.1
10	R	142	G	14.1
10	N	2	U	14.1
10	R	139	G	14.1
10	R	157	U	14.1
6	Y	10	GLU	14.0
6	V	90	VAL	14.0
9	G	20	LYS	14.0
10	N	20	G	14.0
10	R	87	C	14.0
4	Q	24	GLY	13.9
10	R	71	C	13.9
10	N	24	C	13.9
2	L	63	ARG	13.9
10	R	70	A	13.9
6	V	49	ASN	13.9
10	R	38	G	13.8
10	R	152	G	13.8
10	N	18	G	13.8
10	N	133	G	13.8
10	N	152	G	13.8
10	N	122	C	13.8
10	R	37	G	13.8
10	N	110	G	13.8
4	B	64	LYS	13.8
6	Y	2	SER	13.8
10	N	15	G	13.8
10	N	100	C	13.8
10	N	16	G	13.7
10	N	31	C	13.7
7	F	38	GLY	13.7
10	R	93	G	13.7
10	N	106	G	13.7
10	N	68	G	13.7
10	R	99	C	13.7
10	R	100	C	13.7
10	N	58	C	13.7
8	E	75	GLY	13.7
10	R	21	A	13.7
11	M	2	DG	13.6
8	H	67	LYS	13.6

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Mol	Chain	Res	Type	RSRZ
6	V	117	GLY	13.6
10	N	8	C	13.6
10	R	102	A	13.6
1	A	27	LYS	13.6
5	X	26	HIS	13.6
4	B	36	LYS	13.6
4	B	55	ASN	13.6
2	L	34	HIS	13.6
4	Q	50	LYS	13.6
10	N	14	A	13.6
10	N	23	A	13.5
10	R	66	U	13.5
6	Y	95	TYR	13.5
6	Y	80	SER	13.5
10	R	101	C	13.5
11	M	7	DG	13.5
10	R	141	G	13.5
10	N	86	C	13.5
10	R	162	C	13.4
10	R	12	G	13.4
10	R	40	G	13.4
2	L	152	GLU	13.4
10	N	25	C	13.4
10	N	81	G	13.4
10	R	94	A	13.4
5	U	34	VAL	13.4
2	S	175	LEU	13.4
10	N	34	G	13.4
6	Y	7	PRO	13.4
1	P	36	GLN	13.4
7	F	46	ASN	13.4
10	R	118	A	13.3
2	L	180	ARG	13.3
7	I	7	PRO	13.3
10	N	47	C	13.3
6	V	59	PHE	13.3
4	B	82	VAL	13.2
10	N	32	A	13.2
10	N	99	C	13.2
7	F	37	ASP	13.2
8	E	52	GLU	13.2
10	N	76	G	13.2

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Mol	Chain	Res	Type	RSRZ
10	R	35	A	13.2
1	P	81	PRO	13.2
10	R	73	C	13.1
10	R	116	C	13.1
10	N	78	U	13.1
7	I	8	LYS	13.1
10	N	120	U	13.1
10	N	9	C	13.0
7	F	84	MET	13.0
10	R	155	C	13.0
2	S	181	GLY	13.0
10	R	143	A	13.0
10	N	132	G	13.0
10	R	56	G	13.0
10	R	61	A	13.0
10	N	114	C	13.0
2	S	54	ALA	13.0
10	R	138	G	12.9
10	N	82	C	12.9
6	V	32	LEU	12.9
1	A	99	GLY	12.9
10	R	24	C	12.9
10	N	60	U	12.9
10	N	28	G	12.9
4	Q	53	PRO	12.9
4	Q	64	LYS	12.9
6	V	40	THR	12.8
10	N	164	G	12.8
10	R	46	C	12.8
10	R	15	G	12.8
10	R	127	U	12.8
10	R	29	A	12.8
10	R	98	C	12.8
10	N	89	C	12.8
11	M	3	DG	12.8
10	R	111	A	12.8
10	N	48	C	12.8
10	R	55	A	12.8
10	R	148	G	12.8
10	R	119	C	12.8
10	R	9	C	12.7
8	E	69	LYS	12.7

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Mol	Chain	Res	Type	RSRZ
10	R	65	A	12.7
10	R	160	C	12.7
10	N	63	C	12.7
9	J	44	GLU	12.7
4	Q	23	ASP	12.6
9	J	59	MET	12.6
3	W	87	LYS	12.6
10	N	49	A	12.6
1	A	5	GLU	12.6
3	Z	44	SER	12.6
4	Q	51	ILE	12.6
5	X	34	VAL	12.6
10	R	62	U	12.6
10	R	144	C	12.6
10	R	158	U	12.6
10	R	161	C	12.6
10	N	97	U	12.6
10	R	159	C	12.5
10	N	151	C	12.5
5	X	41	LYS	12.5
1	A	63	SER	12.5
9	G	1	MET	12.5
10	R	7	A	12.5
10	R	51	G	12.5
10	R	164	G	12.5
10	R	151	C	12.5
10	R	129	U	12.5
10	N	91	G	12.5
10	R	11	G	12.4
10	R	81	G	12.4
10	N	22	U	12.4
5	X	58	LEU	12.4
10	N	62	U	12.4
6	V	74	TRP	12.4
5	U	13	GLU	12.4
6	Y	4	LEU	12.4
10	R	45	U	12.3
10	N	98	C	12.3
10	N	88	C	12.3
6	Y	79	LYS	12.3
10	R	112	A	12.3
10	N	19	A	12.3

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Mol	Chain	Res	Type	RSRZ
10	R	13	C	12.3
10	R	153	C	12.3
10	N	70	A	12.3
10	R	31	C	12.3
10	R	68	G	12.2
10	N	102	A	12.2
10	N	64	C	12.2
10	N	21	A	12.2
10	R	135	A	12.2
10	R	146	G	12.2
10	N	113	A	12.2
10	N	136	G	12.2
10	R	90	U	12.2
4	Q	52	LYS	12.2
10	R	107	U	12.2
10	N	35	A	12.2
2	S	40	GLY	12.1
10	N	71	C	12.1
2	S	45	ILE	12.1
6	Y	38	ASN	12.1
10	N	142	G	12.1
3	W	48	VAL	12.1
10	N	59	U	12.1
10	N	111	A	12.1
10	N	83	U	12.1
10	R	114	C	12.1
10	N	85	A	12.1
10	N	148	G	12.0
10	R	72	U	12.0
10	R	131	U	12.0
10	N	115	U	12.0
6	V	48	ASN	12.0
10	N	33	C	12.0
10	N	26	A	12.0
7	F	67	ASN	12.0
10	N	135	A	12.0
10	N	103	A	12.0
10	N	112	A	12.0
3	Z	60	GLN	12.0
10	N	139	G	12.0
6	Y	104	ASP	12.0
2	L	127	GLY	12.0

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Mol	Chain	Res	Type	RSRZ
10	N	138	G	11.9
10	N	96	U	11.9
10	N	153	C	11.9
10	N	101	C	11.9
6	Y	6	LYS	11.9
10	N	55	A	11.9
10	N	143	A	11.9
10	N	87	C	11.8
10	R	14	A	11.8
7	F	66	CYS	11.8
9	G	11	LYS	11.8
1	A	91	SER	11.8
10	N	146	G	11.8
11	D	8	DT	11.8
3	Z	24	THR	11.8
10	R	6	U	11.8
10	R	147	C	11.8
10	N	130	G	11.8
10	N	29	A	11.7
1	P	45	VAL	11.7
10	N	94	A	11.7
10	N	147	C	11.7
10	R	27	U	11.6
10	R	97	U	11.6
6	Y	63	CYS	11.6
10	N	54	G	11.6
10	N	72	U	11.6
3	W	25	GLY	11.6
10	R	47	C	11.6
2	S	97	ALA	11.6
8	H	66	SER	11.6
10	N	107	U	11.5
10	N	42	U	11.5
3	Z	66	SER	11.5
10	R	23	A	11.5
8	E	82	ASP	11.5
10	N	80	U	11.5
10	R	96	U	11.5
10	R	154	G	11.5
10	R	42	U	11.5
10	N	159	C	11.4
11	D	6	DA	11.4

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Mol	Chain	Res	Type	RSRZ
10	R	39	U	11.4
10	N	104	A	11.4
9	G	35	ASP	11.4
10	R	121	G	11.4
7	I	61	GLU	11.4
10	N	10	U	11.4
2	L	115	THR	11.4
10	R	8	C	11.4
10	R	79	G	11.4
2	S	170	ASP	11.4
10	N	44	U	11.4
4	B	75	GLU	11.3
10	R	128	U	11.3
10	R	113	A	11.3
10	R	69	C	11.3
10	N	144	C	11.3
10	N	45	U	11.3
2	L	114	THR	11.3
5	U	63	ASN	11.2
10	R	22	U	11.2
10	N	90	U	11.2
10	R	86	C	11.2
10	R	163	U	11.2
1	A	16	ASN	11.2
6	Y	23	GLU	11.2
10	R	2	U	11.2
10	N	134	U	11.2
10	R	76	G	11.2
7	F	68	ASN	11.1
10	R	92	C	11.1
10	R	57	G	11.1
10	N	52	G	11.1
6	Y	62	HIS	11.1
4	B	16	ARG	11.1
10	R	134	U	11.1
10	N	127	U	11.1
4	Q	47	GLU	11.1
7	I	55	LEU	11.1
10	N	140	G	11.1
10	R	26	A	11.0
10	R	95	U	11.0
10	N	39	U	11.0

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Mol	Chain	Res	Type	RSRZ
10	N	125	A	11.0
9	G	6	PRO	11.0
2	S	75	ILE	11.0
6	V	46	CYS	11.0
10	R	60	U	11.0
10	N	150	U	11.0
10	R	16	G	11.0
1	A	100	THR	11.0
11	D	7	DG	10.9
4	B	76	ASN	10.9
10	R	25	C	10.9
10	R	44	U	10.9
8	H	82	ASP	10.9
1	P	91	SER	10.9
2	L	170	ASP	10.9
10	R	137	U	10.9
10	N	126	A	10.9
10	N	69	C	10.9
10	N	95	U	10.8
6	Y	64	ASN	10.8
10	N	30	U	10.8
10	R	36	A	10.8
6	V	66	VAL	10.8
3	Z	74	PRO	10.7
6	Y	34	GLN	10.7
2	L	113	ASP	10.7
6	Y	46	CYS	10.7
10	N	43	U	10.7
8	H	83	ASN	10.6
10	R	43	U	10.6
10	R	82	C	10.6
10	N	149	U	10.6
3	Z	5	VAL	10.6
10	N	128	U	10.6
8	H	88	GLN	10.6
10	R	59	U	10.6
6	Y	81	GLY	10.6
1	A	90	ASP	10.6
10	R	150	U	10.6
1	P	9	ASN	10.5
1	P	103	GLU	10.5
3	W	66	SER	10.5

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Mol	Chain	Res	Type	RSRZ
6	Y	105	SER	10.5
2	L	179	GLU	10.5
8	H	40	ASN	10.5
10	R	5	U	10.5
8	H	38	GLN	10.5
9	J	57	ILE	10.5
7	I	9	PRO	10.5
10	N	123	A	10.5
10	R	30	U	10.4
4	B	23	ASP	10.4
10	R	58	C	10.4
9	J	33	GLY	10.4
10	R	64	C	10.4
1	A	92	ASP	10.4
6	V	45	ASN	10.4
10	N	145	U	10.4
6	V	34	GLN	10.4
3	Z	34	GLU	10.4
2	L	39	CYS	10.3
3	Z	40	ASN	10.3
6	Y	49	ASN	10.3
8	H	89	SER	10.3
2	L	111	ASN	10.3
10	R	63	C	10.3
6	V	93	ASP	10.3
11	M	4	DT	10.3
10	R	67	U	10.3
9	J	56	ASN	10.3
6	V	9	SER	10.3
1	P	8	PRO	10.2
2	S	165	ASP	10.2
7	I	68	ASN	10.2
8	E	83	ASN	10.2
8	H	85	THR	10.2
10	N	158	U	10.2
3	Z	41	CYS	10.1
10	N	51	G	10.1
4	B	11	GLN	10.1
1	A	89	THR	10.1
5	U	64	ASN	10.1
4	B	7	SER	10.1
10	N	105	U	10.1

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Mol	Chain	Res	Type	RSRZ
1	P	90	ASP	10.1
3	Z	17	ILE	10.1
10	R	50	G	10.1
7	F	39	TYR	10.1
3	Z	37	ASP	10.0
2	L	116	GLU	10.0
9	G	56	ASN	10.0
3	Z	12	GLU	10.0
2	S	100	ASP	10.0
10	R	120	U	10.0
10	N	27	U	10.0
3	W	24	THR	10.0
10	R	10	U	10.0
1	P	6	THR	10.0
9	G	65	ASN	10.0
10	R	149	U	10.0
10	N	129	U	10.0
3	Z	14	GLU	9.9
2	L	137	SER	9.9
2	S	133	HIS	9.9
5	X	63	ASN	9.9
8	H	70	SER	9.9
10	R	145	U	9.9
2	L	104	THR	9.9
6	Y	103	GLY	9.9
3	W	41	CYS	9.8
1	P	27	LYS	9.8
6	Y	82	LYS	9.8
5	U	59	SER	9.8
4	Q	35	ASP	9.8
4	B	24	GLY	9.8
10	R	80	U	9.8
10	N	163	U	9.8
8	H	34	TRP	9.8
2	L	125	VAL	9.7
6	V	6	LYS	9.7
2	L	177	ASP	9.7
2	L	117	SER	9.7
10	R	124	U	9.7
10	R	156	U	9.7
4	B	6	SER	9.7
8	H	37	GLU	9.7

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Mol	Chain	Res	Type	RSRZ
8	H	36	TYR	9.6
6	Y	20	GLU	9.6
1	A	11	THR	9.6
3	Z	65	GLY	9.6
10	N	157	U	9.6
10	N	160	C	9.6
10	N	124	U	9.6
1	P	10	HIS	9.6
4	B	79	SER	9.6
10	N	53	C	9.6
3	Z	11	HIS	9.5
1	A	101	PHE	9.5
5	X	35	SER	9.5
3	Z	38	ASN	9.5
6	V	69	ASN	9.5
10	N	131	U	9.5
2	S	91	PRO	9.5
6	Y	45	ASN	9.5
7	I	35	SER	9.5
2	S	101	ALA	9.4
2	L	165	ASP	9.4
9	G	28	GLN	9.4
9	J	65	ASN	9.4
4	Q	83	GLU	9.4
8	H	63	GLU	9.4
10	R	136	G	9.4
2	S	163	HIS	9.4
9	J	24	GLY	9.3
2	L	122	GLU	9.3
1	P	11	THR	9.3
8	E	53	TYR	9.3
8	E	85	THR	9.3
4	B	54	LYS	9.3
1	A	102	VAL	9.3
2	S	126	TYR	9.3
5	U	37	ASN	9.3
2	S	102	PHE	9.3
10	R	78	U	9.3
5	U	67	TYR	9.2
4	B	35	ASP	9.2
8	E	23	ARG	9.2
3	Z	15	GLY	9.2

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Mol	Chain	Res	Type	RSRZ
7	F	56	SER	9.2
2	S	92	HIS	9.2
3	Z	23	ASN	9.2
4	B	74	GLY	9.1
5	U	72	ASP	9.1
7	I	67	ASN	9.1
2	S	104	THR	9.1
7	I	14	LEU	9.1
6	Y	102	ARG	9.1
2	S	65	GLU	9.1
10	R	85	A	9.1
1	P	85	GLN	9.1
1	P	89	THR	9.1
3	W	40	ASN	9.1
6	Y	60	ASP	9.0
8	H	39	VAL	9.0
1	P	66	THR	9.0
1	A	9	ASN	9.0
2	S	98	GLN	9.0
10	R	122	C	9.0
3	W	23	ASN	9.0
8	E	88	GLN	9.0
5	X	37	ASN	9.0
2	L	106	PHE	8.9
3	W	26	GLU	8.9
7	I	56	SER	8.9
2	L	108	ALA	8.9
5	X	33	ASP	8.9
10	R	84	G	8.9
2	L	98	GLN	8.9
3	W	65	GLY	8.9
1	A	94	ILE	8.8
5	U	62	GLY	8.8
1	P	92	ASP	8.8
2	L	146	TYR	8.8
8	E	26	GLN	8.8
3	W	62	TYR	8.8
5	U	12	HIS	8.8
1	A	67	ASN	8.8
2	S	64	GLU	8.8
8	H	62	GLU	8.8
7	F	25	TRP	8.8

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Mol	Chain	Res	Type	RSRZ
9	G	43	ASP	8.8
2	L	169	ILE	8.7
2	L	133	HIS	8.7
1	P	42	ASP	8.7
10	N	141	G	8.7
10	N	156	U	8.7
2	L	150	GLU	8.7
2	L	99	GLY	8.7
6	V	54	GLY	8.7
1	A	10	HIS	8.7
1	A	7	ARG	8.7
1	A	93	ILE	8.7
8	H	86	LEU	8.7
5	U	57	THR	8.7
2	L	147	ALA	8.7
4	B	19	CYS	8.7
7	F	19	VAL	8.7
2	L	107	VAL	8.6
1	A	58	ILE	8.6
2	L	102	PHE	8.6
1	A	29	SER	8.6
10	R	77	A	8.6
2	L	100	ASP	8.6
6	V	44	ILE	8.6
5	U	66	ARG	8.6
6	Y	106	VAL	8.6
3	W	20	CYS	8.5
7	F	28	GLU	8.5
4	Q	46	ASP	8.5
1	P	7	ARG	8.5
6	Y	68	GLU	8.5
3	Z	25	GLY	8.5
2	L	118	LYS	8.5
7	F	24	LYS	8.5
8	E	38	GLN	8.5
2	L	164	ALA	8.5
5	X	62	GLY	8.5
1	P	2	ALA	8.5
1	P	5	GLU	8.5
2	L	159	SER	8.5
4	B	37	HIS	8.5
7	I	13	GLY	8.4

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Mol	Chain	Res	Type	RSRZ
3	W	64	ARG	8.4
3	Z	64	ARG	8.4
5	U	61	ARG	8.4
9	G	17	LEU	8.4
6	V	105	SER	8.4
9	J	5	HIS	8.4
4	B	25	ARG	8.4
8	H	81	GLY	8.4
10	N	137	U	8.4
1	A	36	GLN	8.4
4	B	22	GLN	8.4
5	U	38	THR	8.4
6	Y	61	ARG	8.4
10	N	67	U	8.4
3	W	63	ILE	8.4
8	H	71	ARG	8.4
7	I	26	GLY	8.4
7	F	71	TYR	8.4
5	U	30	THR	8.3
7	F	69	VAL	8.3
1	A	87	ALA	8.3
1	P	87	ALA	8.3
9	J	66	SER	8.3
3	Z	69	ARG	8.3
6	Y	69	ASN	8.3
4	B	78	VAL	8.3
1	P	86	TYR	8.3
2	S	115	THR	8.3
3	Z	35	ALA	8.3
6	Y	65	MET	8.3
5	U	18	GLU	8.3
4	Q	76	ASN	8.3
3	W	22	THR	8.3
2	L	110	VAL	8.2
7	F	49	GLU	8.2
1	P	73	GLN	8.2
2	S	177	ASP	8.2
6	Y	100	PHE	8.2
2	L	145	GLY	8.2
8	E	81	GLY	8.2
8	E	46	CYS	8.2
5	X	5	ARG	8.2

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Mol	Chain	Res	Type	RSRZ
2	S	111	ASN	8.2
9	J	69	MET	8.2
2	L	148	PHE	8.2
8	E	37	GLU	8.2
3	W	78	LYS	8.2
3	W	42	GLN	8.2
6	Y	101	LEU	8.2
7	F	65	ARG	8.2
2	S	154	GLU	8.2
8	H	20	LEU	8.2
4	B	39	ASN	8.2
1	P	29	SER	8.1
3	Z	42	GLN	8.1
1	P	58	ILE	8.1
2	L	168	LYS	8.1
9	G	7	PRO	8.1
1	A	57	VAL	8.1
6	Y	107	ILE	8.1
4	Q	37	HIS	8.1
5	X	12	HIS	8.1
10	R	83	U	8.1
8	H	87	LEU	8.1
2	L	166	GLY	8.1
6	V	94	ARG	8.1
5	X	38	THR	8.1
2	L	176	VAL	8.1
6	V	52	LEU	8.1
7	F	70	LEU	8.1
5	U	68	PHE	8.1
9	G	64	GLY	8.0
5	X	11	SER	8.0
5	U	39	HIS	8.0
6	V	107	ILE	8.0
1	P	77	PHE	8.0
6	Y	48	ASN	8.0
9	G	39	ASN	8.0
8	H	84	ILE	8.0
2	L	38	TYR	8.0
8	H	42	ARG	8.0
9	G	63	ARG	8.0
3	Z	13	ALA	8.0
2	L	119	LEU	8.0

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Mol	Chain	Res	Type	RSRZ
6	V	108	VAL	8.0
1	P	94	ILE	8.0
10	R	115	U	8.0
6	V	53	LEU	8.0
7	F	26	GLY	8.0
7	I	58	HIS	8.0
1	P	63	SER	8.0
2	S	155	ARG	8.0
5	U	16	THR	8.0
6	V	10	GLU	8.0
4	B	73	ARG	8.0
2	S	128	PRO	7.9
6	Y	44	ILE	7.9
4	B	77	LEU	7.9
7	F	52	ASP	7.9
9	J	9	LEU	7.9
6	V	51	LYS	7.9
10	N	155	C	7.9
8	E	87	LEU	7.9
3	Z	61	VAL	7.9
2	L	40	GLY	7.9
3	W	69	ARG	7.9
8	H	73	GLN	7.9
1	P	93	ILE	7.9
5	U	69	ILE	7.9
6	Y	66	VAL	7.9
6	Y	97	SER	7.9
6	V	43	LEU	7.9
2	L	167	LYS	7.9
2	L	131	ARG	7.9
3	Z	36	GLU	7.9
2	S	99	GLY	7.9
2	L	161	TYR	7.9
9	G	58	GLY	7.9
2	L	96	ASN	7.8
2	L	149	ILE	7.8
2	L	105	LEU	7.8
2	L	112	TYR	7.8
3	W	67	LYS	7.8
8	H	72	LYS	7.8
3	W	68	ILE	7.8
5	X	81	VAL	7.8

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Mol	Chain	Res	Type	RSRZ
5	U	65	ILE	7.8
5	U	60	ILE	7.8
3	Z	39	MET	7.8
4	B	8	LYS	7.8
9	G	61	VAL	7.8
2	S	150	GLU	7.8
4	B	21	LEU	7.8
5	U	8	MET	7.8
8	H	44	GLU	7.8
3	Z	33	ILE	7.8
3	W	60	GLN	7.8
4	B	30	THR	7.7
6	V	39	ASN	7.7
2	L	45	ILE	7.7
8	E	86	LEU	7.7
2	L	44	TYR	7.7
9	J	64	GLY	7.7
2	L	178	VAL	7.7
8	E	84	ILE	7.7
1	A	42	ASP	7.7
8	H	55	ASN	7.7
9	G	60	VAL	7.7
9	G	62	ILE	7.7
2	S	103	LYS	7.7
2	S	67	MET	7.7
2	L	134	MET	7.7
7	F	48	GLU	7.6
2	L	132	ILE	7.6
7	I	25	TRP	7.6
2	S	158	HIS	7.6
2	S	66	ARG	7.6
8	H	64	ILE	7.6
1	A	85	GLN	7.6
6	V	106	VAL	7.6
6	V	109	VAL	7.6
2	L	109	ARG	7.6
7	F	23	LEU	7.6
3	Z	67	LYS	7.6
9	J	43	ASP	7.6
9	J	68	ILE	7.6
2	L	174	VAL	7.6
2	L	171	GLY	7.6

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Mol	Chain	Res	Type	RSRZ
9	J	71	GLU	7.6
4	B	53	PRO	7.6
7	F	57	GLY	7.5
8	H	35	LEU	7.5
5	X	61	ARG	7.5
7	F	58	HIS	7.5
6	V	42	VAL	7.5
9	G	46	VAL	7.5
2	L	43	PRO	7.5
2	L	173	ARG	7.5
3	W	61	VAL	7.5
7	I	57	GLY	7.5
8	H	53	TYR	7.5
6	V	72	GLU	7.5
7	F	27	MET	7.5
6	V	47	ARG	7.5
3	Z	68	ILE	7.5
4	B	20	ILE	7.5
9	J	67	ILE	7.5
7	F	50	TYR	7.5
7	F	22	LYS	7.5
2	L	97	ALA	7.5
6	V	70	VAL	7.5
4	B	38	MET	7.5
2	L	172	ARG	7.5
6	Y	54	GLY	7.5
9	G	59	MET	7.4
2	L	143	PRO	7.4
2	S	68	GLU	7.4
7	F	41	ASN	7.4
2	S	63	ARG	7.4
3	W	12	GLU	7.4
1	P	62	VAL	7.4
1	A	56	PHE	7.4
1	A	8	PRO	7.4
1	P	61	GLU	7.4
5	U	42	ALA	7.4
8	H	80	LYS	7.4
8	E	36	TYR	7.4
8	H	60	ASP	7.3
1	A	12	ILE	7.3
2	L	163	HIS	7.3

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Mol	Chain	Res	Type	RSRZ
5	U	20	LYS	7.3
3	W	74	PRO	7.3
3	W	70	PHE	7.3
5	U	35	SER	7.3
1	A	70	ARG	7.3
1	P	84	ILE	7.3
7	I	49	GLU	7.2
5	U	33	ASP	7.2
7	I	28	GLU	7.2
1	A	13	TYR	7.2
9	J	70	LEU	7.2
2	S	94	ASP	7.2
6	V	95	TYR	7.2
6	Y	99	MET	7.2
9	J	34	PHE	7.2
1	P	57	VAL	7.2
4	B	45	CYS	7.2
9	J	18	SER	7.2
2	S	37	PRO	7.2
5	X	13	GLU	7.2
1	P	70	ARG	7.2
1	P	88	LYS	7.2
9	J	4	ALA	7.2
3	W	27	VAL	7.1
2	L	95	PRO	7.1
2	S	161	TYR	7.1
2	S	95	PRO	7.1
1	P	59	PHE	7.1
6	V	71	LYS	7.1
9	G	45	CYS	7.1
6	Y	58	ALA	7.1
5	X	9	LYS	7.1
9	J	72	ALA	7.1
7	I	66	CYS	7.1
1	A	43	ILE	7.1
2	S	178	VAL	7.1
6	Y	108	VAL	7.1
4	Q	75	GLU	7.1
7	F	29	TYR	7.1
8	H	41	MET	7.0
1	A	84	ILE	7.0
2	S	105	LEU	7.0

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Mol	Chain	Res	Type	RSRZ
6	Y	67	LEU	7.0
2	S	106	PHE	7.0
5	X	36	MET	7.0
8	H	54	MET	7.0
2	S	117	SER	7.0
7	F	83	GLU	7.0
7	F	40	MET	7.0
6	Y	56	VAL	7.0
9	J	22	ASN	7.0
6	Y	52	LEU	7.0
8	H	69	LYS	7.0
6	V	104	ASP	7.0
7	F	53	GLY	7.0
8	E	80	LYS	7.0
8	E	34	TRP	7.0
2	L	94	ASP	6.9
1	P	60	LYS	6.9
5	X	64	ASN	6.9
1	A	73	GLN	6.9
4	Q	14	ASP	6.9
6	V	97	SER	6.9
1	A	95	ALA	6.9
2	S	61	GLU	6.9
3	W	5	VAL	6.9
7	F	51	ILE	6.9
1	A	86	TYR	6.9
8	H	43	ILE	6.9
6	V	68	GLU	6.9
2	S	153	HIS	6.9
2	S	157	MET	6.9
4	B	9	MET	6.9
6	Y	51	LYS	6.9
7	F	78	GLU	6.9
6	Y	59	PHE	6.9
3	W	39	MET	6.9
3	W	71	LEU	6.9
3	Z	63	ILE	6.8
6	V	111	ARG	6.8
2	L	123	PHE	6.8
3	W	38	ASN	6.8
2	L	101	ALA	6.8
9	G	66	SER	6.8

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Mol	Chain	Res	Type	RSRZ
2	L	41	ILE	6.8
5	U	17	ILE	6.8
6	Y	40	THR	6.8
10	N	154	G	6.8
2	S	159	SER	6.8
2	L	175	LEU	6.8
4	B	56	SER	6.8
1	P	43	ILE	6.8
2	L	37	PRO	6.8
2	L	42	ALA	6.8
3	Z	16	HIS	6.8
4	Q	7	SER	6.8
8	H	21	ILE	6.8
2	L	135	VAL	6.8
2	S	151	TYR	6.7
2	S	179	GLU	6.7
9	G	44	GLU	6.7
1	P	13	TYR	6.7
9	J	19	LEU	6.7
7	I	27	MET	6.7
9	J	37	PHE	6.7
5	U	36	MET	6.7
5	X	65	ILE	6.7
2	S	35	ASN	6.7
6	Y	55	ARG	6.7
3	W	21	GLU	6.7
2	S	77	ARG	6.7
8	E	89	SER	6.7
7	I	6	ASN	6.7
3	Z	22	THR	6.7
2	S	152	GLU	6.7
1	A	59	PHE	6.7
1	P	12	ILE	6.6
6	V	41	GLN	6.6
5	U	21	ASN	6.6
3	W	45	ASN	6.6
7	F	55	LEU	6.6
3	Z	10	LEU	6.6
1	A	88	LYS	6.6
6	Y	98	LYS	6.6
3	Z	9	VAL	6.6
1	A	69	LEU	6.6

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Mol	Chain	Res	Type	RSRZ
3	Z	62	TYR	6.6
4	B	52	LYS	6.6
2	L	160	ALA	6.6
2	L	93	ASN	6.5
1	P	69	LEU	6.5
8	E	35	LEU	6.5
3	W	72	ILE	6.5
7	F	64	ILE	6.5
7	I	23	LEU	6.5
2	L	120	ARG	6.5
6	Y	47	ARG	6.5
2	S	180	ARG	6.5
1	A	60	LYS	6.5
7	I	65	ARG	6.5
5	X	14	THR	6.5
2	L	103	LYS	6.5
7	F	54	ALA	6.5
2	S	39	CYS	6.4
1	P	4	PRO	6.4
5	U	58	LEU	6.4
2	L	158	HIS	6.4
7	I	24	LYS	6.4
2	S	76	GLU	6.4
9	J	20	LYS	6.4
1	P	98	LYS	6.4
3	W	43	MET	6.4
5	X	67	TYR	6.4
1	P	65	ALA	6.4
1	A	44	LEU	6.4
1	P	40	ILE	6.4
5	U	47	LEU	6.4
1	A	41	LEU	6.4
9	G	37	PHE	6.3
8	H	32	GLN	6.3
5	U	19	LEU	6.3
2	S	48	PHE	6.3
1	A	72	MET	6.3
5	X	7	LEU	6.3
3	W	59	GLU	6.3
1	P	41	LEU	6.3
1	A	97	MET	6.3
7	I	69	VAL	6.3

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Mol	Chain	Res	Type	RSRZ
2	S	164	ALA	6.3
4	B	80	MET	6.3
8	H	51	ASP	6.3
6	V	50	LYS	6.2
4	Q	67	LEU	6.2
2	S	131	ARG	6.2
2	L	130	LYS	6.2
1	A	40	ILE	6.2
5	X	10	LEU	6.2
7	I	22	LYS	6.2
5	X	68	PHE	6.2
9	G	14	ASP	6.2
1	A	98	LYS	6.2
2	S	149	ILE	6.2
5	X	30	THR	6.2
6	Y	57	LYS	6.2
8	E	71	ARG	6.1
9	G	41	VAL	6.1
6	V	73	MET	6.1
3	W	11	HIS	6.1
8	H	65	HIS	6.1
2	S	41	ILE	6.1
5	U	31	GLY	6.1
2	S	114	THR	6.1
7	I	64	ILE	6.1
2	S	148	PHE	6.1
5	X	72	ASP	6.1
1	P	56	PHE	6.1
3	W	14	GLU	6.0
9	J	45	CYS	6.0
6	V	55	ARG	6.0
3	W	36	GLU	6.0
2	S	69	ARG	6.0
7	I	33	LEU	6.0
3	Z	21	GLU	6.0
3	W	10	LEU	6.0
4	B	72	LEU	6.0
3	Z	70	PHE	6.0
6	Y	109	VAL	6.0
5	X	60	ILE	6.0
4	B	40	LEU	6.0
5	U	11	SER	6.0

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Mol	Chain	Res	Type	RSRZ
2	S	49	GLU	5.9
1	A	71	SER	5.9
3	W	44	SER	5.9
2	L	121	ARG	5.9
7	F	21	VAL	5.9
1	P	83	ARG	5.9
2	L	144	ARG	5.9
5	X	27	GLY	5.9
2	S	56	PRO	5.9
1	P	72	MET	5.9
2	S	36	GLN	5.9
2	S	62	THR	5.9
4	B	10	LEU	5.9
9	J	21	LEU	5.9
7	I	29	TYR	5.9
5	X	20	LYS	5.9
4	Q	22	GLN	5.9
3	Z	32	LEU	5.9
8	H	74	LEU	5.9
1	P	74	GLY	5.9
5	X	15	VAL	5.9
3	W	34	GLU	5.8
1	A	83	ARG	5.8
2	S	118	LYS	5.8
9	G	42	ILE	5.8
8	E	54	MET	5.8
8	H	61	ALA	5.8
9	J	62	ILE	5.8
5	X	16	THR	5.8
6	V	63	CYS	5.8
6	V	103	GLY	5.8
2	L	151	TYR	5.8
3	W	6	PRO	5.8
3	W	35	ALA	5.8
2	S	156	ASP	5.8
6	Y	43	LEU	5.8
7	F	42	MET	5.7
7	I	48	GLU	5.7
8	E	39	VAL	5.7
1	A	14	ILE	5.7
8	E	44	GLU	5.7
8	H	79	LEU	5.7

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Mol	Chain	Res	Type	RSRZ
9	G	70	LEU	5.7
2	L	162	LYS	5.7
5	U	70	LEU	5.7
4	Q	71	LEU	5.7
1	P	67	ASN	5.6
8	H	75	GLY	5.6
8	H	33	VAL	5.6
9	J	8	GLU	5.6
2	S	38	TYR	5.6
9	G	4	ALA	5.6
6	Y	53	LEU	5.6
2	S	130	LYS	5.6
7	I	51	ILE	5.6
7	F	82	GLY	5.6
1	A	31	TYR	5.6
8	E	55	ASN	5.6
2	S	160	ALA	5.6
9	G	38	MET	5.6
1	A	66	THR	5.6
8	H	46	CYS	5.6
4	Q	12	HIS	5.6
2	S	127	GLY	5.6
2	L	157	MET	5.6
1	A	38	GLY	5.5
6	Y	70	VAL	5.5
8	E	19	ASN	5.5
3	W	15	GLY	5.5
1	P	39	GLN	5.5
7	F	81	ASP	5.5
3	W	8	LYS	5.5
6	Y	35	SER	5.5
5	U	15	VAL	5.5
8	E	33	VAL	5.5
1	A	96	LYS	5.5
2	S	70	LYS	5.5
2	S	107	VAL	5.5
9	J	17	LEU	5.5
2	S	116	GLU	5.5
2	L	142	LYS	5.4
1	P	95	ALA	5.4
5	U	22	GLY	5.4
8	E	63	GLU	5.4

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Mol	Chain	Res	Type	RSRZ
6	Y	42	VAL	5.4
2	S	44	TYR	5.4
5	X	29	ILE	5.4
2	S	59	ARG	5.4
9	J	74	GLU	5.4
3	Z	8	LYS	5.4
6	Y	72	GLU	5.4
4	Q	41	ILE	5.4
3	W	58	LEU	5.4
4	Q	73	ARG	5.3
9	J	63	ARG	5.3
9	J	38	MET	5.3
8	H	52	GLU	5.3
4	Q	11	GLN	5.3
6	V	99	MET	5.3
9	J	28	GLN	5.3
9	G	32	ARG	5.3
1	P	64	SER	5.3
8	H	19	ASN	5.3
3	W	19	THR	5.3
7	I	50	TYR	5.3
8	E	90	VAL	5.3
6	V	67	LEU	5.3
7	F	72	ILE	5.3
5	X	31	GLY	5.3
5	U	71	PRO	5.3
6	V	101	LEU	5.3
7	I	70	LEU	5.3
8	E	57	VAL	5.2
4	B	71	LEU	5.2
7	F	47	THR	5.2
5	X	32	VAL	5.2
6	V	110	LEU	5.2
1	A	68	ALA	5.2
2	L	126	TYR	5.2
5	X	66	ARG	5.2
8	E	20	LEU	5.2
1	A	74	GLY	5.2
1	A	39	GLN	5.1
2	S	119	LEU	5.1
8	E	79	LEU	5.1
4	B	81	THR	5.1

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Mol	Chain	Res	Type	RSRZ
8	E	43	ILE	5.1
5	U	40	LEU	5.1
3	W	32	LEU	5.1
5	X	8	MET	5.1
9	J	26	HIS	5.1
9	G	40	LEU	5.0
8	E	32	GLN	5.0
1	P	97	MET	5.0
9	J	23	GLY	5.0
4	Q	39	ASN	5.0
6	Y	50	LYS	5.0
2	S	162	LYS	5.0
3	W	73	LEU	5.0
9	J	30	ILE	5.0
1	A	37	PHE	5.0
1	A	61	GLU	5.0
4	Q	25	ARG	5.0
1	P	3	VAL	4.9
3	W	9	VAL	4.9
4	Q	68	GLY	4.9
7	I	39	TYR	4.9
4	B	26	ILE	4.9
8	E	22	PHE	4.9
2	S	124	GLU	4.9
3	W	13	ALA	4.9
1	P	44	LEU	4.9
9	J	73	LEU	4.9
6	V	26	THR	4.9
4	B	43	CYS	4.9
1	P	76	PRO	4.9
2	L	129	ILE	4.8
9	J	75	ARG	4.8
5	X	28	THR	4.8
9	G	57	ILE	4.8
4	Q	40	LEU	4.8
9	J	27	VAL	4.8
1	A	82	MET	4.8
1	P	14	ILE	4.8
4	B	41	ILE	4.8
8	H	77	ILE	4.8
5	X	17	ILE	4.8
2	S	122	GLU	4.8

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Mol	Chain	Res	Type	RSRZ
4	Q	70	VAL	4.8
1	A	65	ALA	4.8
6	V	100	PHE	4.8
4	Q	19	CYS	4.8
3	Z	78	LYS	4.8
9	J	47	GLU	4.8
6	Y	41	GLN	4.8
4	Q	74	GLY	4.8
5	X	76	LEU	4.8
9	J	25	ARG	4.8
6	V	96	ILE	4.7
3	Z	6	PRO	4.7
8	H	22	PHE	4.7
1	A	45	VAL	4.7
2	S	129	ILE	4.7
3	Z	7	ILE	4.7
2	S	60	ALA	4.7
5	U	56	GLU	4.6
5	U	14	THR	4.6
8	E	78	MET	4.6
9	G	69	MET	4.6
1	A	32	ALA	4.6
7	I	63	LEU	4.6
7	I	41	ASN	4.6
2	S	55	PRO	4.6
7	F	20	MET	4.6
9	G	67	ILE	4.6
4	Q	72	LEU	4.6
4	Q	77	LEU	4.6
3	W	33	ILE	4.6
1	A	75	PHE	4.6
4	B	34	PHE	4.6
6	Y	39	ASN	4.5
4	Q	31	PHE	4.5
1	P	71	SER	4.5
9	J	60	VAL	4.5
5	U	26	HIS	4.5
1	P	96	LYS	4.5
2	L	136	TYR	4.5
2	S	73	GLU	4.5
9	G	30	ILE	4.5
1	P	32	ALA	4.5

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Mol	Chain	Res	Type	RSRZ
7	F	30	LYS	4.5
2	S	71	ARG	4.5
9	J	39	ASN	4.5
2	S	72	ARG	4.4
9	J	29	GLY	4.4
9	G	27	VAL	4.4
5	X	75	PRO	4.4
2	L	124	GLU	4.4
6	Y	96	ILE	4.4
5	U	41	LYS	4.4
9	G	16	LYS	4.4
1	P	15	ASN	4.4
5	X	78	THR	4.4
8	E	47	ILE	4.4
7	I	21	VAL	4.4
8	E	11	GLN	4.4
1	P	75	PHE	4.4
4	Q	21	LEU	4.4
3	Z	18	VAL	4.3
4	Q	17	MET	4.3
9	J	12	PHE	4.3
8	E	45	GLY	4.3
6	V	56	VAL	4.3
3	Z	73	LEU	4.3
3	Z	82	MET	4.3
1	A	30	LEU	4.2
1	A	15	ASN	4.2
5	X	39	HIS	4.2
5	X	59	SER	4.2
2	S	132	ILE	4.2
9	G	8	GLU	4.2
2	S	53	ASP	4.2
1	A	62	VAL	4.2
1	P	68	ALA	4.2
8	E	42	ARG	4.2
8	E	73	GLN	4.2
2	S	58	THR	4.2
6	Y	71	LYS	4.2
3	W	16	HIS	4.1
6	V	64	ASN	4.1
7	I	71	TYR	4.1
4	B	12	HIS	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	81	PRO	4.1
3	W	7	ILE	4.1
6	V	102	ARG	4.1
7	F	73	ARG	4.1
5	X	70	LEU	4.1
3	Z	43	MET	4.1
3	W	28	TYR	4.0
8	E	61	ALA	4.0
1	A	35	SER	4.0
6	V	62	HIS	4.0
4	Q	33	ALA	4.0
5	X	18	GLU	4.0
8	H	47	ILE	4.0
5	X	73	SER	4.0
6	V	98	LYS	4.0
2	S	108	ALA	4.0
5	U	24	GLN	4.0
2	S	147	ALA	4.0
4	Q	80	MET	4.0
8	H	50	PHE	4.0
4	B	33	ALA	4.0
8	E	62	GLU	3.9
8	H	59	ASP	3.9
4	B	42	LEU	3.9
7	F	63	LEU	3.9
9	G	76	VAL	3.9
9	G	31	LEU	3.9
5	X	4	VAL	3.9
4	Q	42	LEU	3.9
5	U	25	VAL	3.9
1	A	76	PRO	3.9
5	X	71	PRO	3.9
8	H	45	GLY	3.9
4	Q	79	SER	3.9
4	Q	32	LYS	3.9
3	W	18	VAL	3.9
5	U	32	VAL	3.9
3	Z	72	ILE	3.8
9	J	15	LYS	3.8
4	B	70	VAL	3.8
6	Y	36	VAL	3.8
4	Q	78	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
1	P	82	MET	3.7
8	E	70	SER	3.7
5	U	23	THR	3.7
4	Q	81	THR	3.7
4	Q	82	VAL	3.7
1	P	31	TYR	3.7
4	Q	43	CYS	3.7
2	S	176	VAL	3.7
6	Y	37	LYS	3.7
2	S	74	LYS	3.7
6	V	22	GLU	3.7
4	B	13	ILE	3.6
1	A	55	ALA	3.6
9	J	42	ILE	3.6
2	S	146	TYR	3.6
5	X	79	LEU	3.6
3	Z	31	LYS	3.6
4	B	28	ILE	3.6
1	P	35	SER	3.6
3	W	31	LYS	3.6
7	I	30	LYS	3.6
1	A	64	SER	3.5
4	Q	8	LYS	3.5
5	U	7	LEU	3.5
9	J	16	LYS	3.5
1	A	103	GLU	3.5
5	X	74	LEU	3.5
7	F	59	LEU	3.5
2	S	123	PHE	3.5
8	E	74	LEU	3.5
1	P	38	GLY	3.5
5	U	29	ILE	3.5
2	S	121	ARG	3.4
5	X	77	ASP	3.4
5	X	69	ILE	3.4
3	W	29	ARG	3.4
8	E	14	MET	3.4
1	A	33	ILE	3.4
8	H	56	LEU	3.4
9	G	21	LEU	3.4
9	G	29	GLY	3.4
4	B	27	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
3	W	30	GLY	3.4
8	E	21	ILE	3.4
8	E	77	ILE	3.4
8	E	72	LYS	3.4
4	B	18	ARG	3.3
6	V	65	MET	3.3
8	E	18	ILE	3.3
5	U	4	VAL	3.2
9	J	40	LEU	3.2
9	G	5	HIS	3.2
9	J	61	VAL	3.2
9	G	13	MET	3.2
7	I	62	VAL	3.2
8	H	76	ARG	3.1
8	H	78	MET	3.1
7	I	20	MET	3.1
9	G	33	GLY	3.1
1	P	55	ALA	3.1
8	H	18	ILE	3.1
4	B	69	LEU	3.0
2	S	120	ARG	3.0
8	E	41	MET	3.0
7	F	31	GLY	3.0
4	B	29	GLY	3.0
5	X	6	PHE	3.0
9	G	68	ILE	3.0
4	Q	10	LEU	3.0
3	W	17	ILE	2.9
4	Q	15	TYR	2.9
4	Q	34	PHE	2.9
6	Y	31	VAL	2.9
5	U	27	GLY	2.9
4	Q	20	ILE	2.9
6	V	5	ASN	2.9
8	E	15	VAL	2.8
7	I	47	THR	2.8
1	A	34	PHE	2.8
5	X	19	LEU	2.8
3	W	46	ILE	2.8
4	Q	18	ARG	2.8
7	I	31	GLY	2.8
2	S	52	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
4	Q	26	ILE	2.8
9	J	46	VAL	2.8
4	Q	30	THR	2.7
6	V	35	SER	2.7
8	E	56	LEU	2.7
6	Y	28	PRO	2.7
4	Q	69	LEU	2.6
8	H	49	GLY	2.6
3	Z	71	LEU	2.6
1	A	77	PHE	2.6
8	E	64	ILE	2.5
5	U	28	THR	2.5
2	S	57	PRO	2.5
7	I	59	LEU	2.5
8	E	58	LEU	2.5
2	S	145	GLY	2.5
4	Q	16	ARG	2.5
7	I	5	LEU	2.5
7	I	72	ILE	2.5
9	G	15	LYS	2.4
6	V	28	PRO	2.4
6	Y	110	LEU	2.4
7	F	62	VAL	2.4
4	Q	13	ILE	2.4
4	B	32	LYS	2.3
7	I	44	LEU	2.3
6	V	19	ARG	2.2
9	J	41	VAL	2.2
5	U	44	LYS	2.2
9	J	31	LEU	2.2
8	H	23	ARG	2.2
4	B	31	PHE	2.2
1	P	37	PHE	2.1
4	Q	9	MET	2.1
8	H	48	ILE	2.0
4	B	17	MET	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.