



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 3L10 / pdb_00003L10
Title : Structure of split monoubiquitinated PCNA with ubiquitin in position one
Authors : Freudenthal, B.D.; Gakhar, L.; Ramaswamy, S.; Washington, M.T.
Deposited on : 2009-12-10
Resolution : 2.80 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

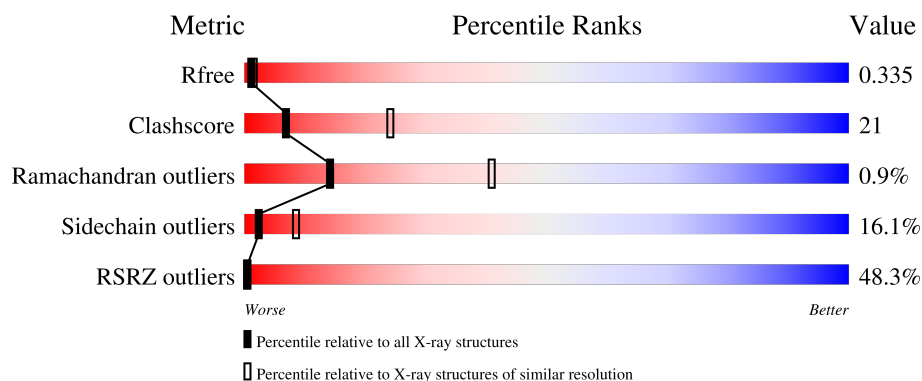
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	169	
2	B	169	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2590 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 Proliferating cell nuclear antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	163	Total	C	N	O	S	0	0	0
			1286	813	204	261	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP P15873
A	-4	HIS	-	expression tag	UNP P15873
A	-3	HIS	-	expression tag	UNP P15873
A	-2	HIS	-	expression tag	UNP P15873
A	-1	HIS	-	expression tag	UNP P15873
A	0	HIS	-	expression tag	UNP P15873

- Molecule 2 is a protein called Monoubiquitinated Proliferating cell nuclear antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	166	Total	C	N	O	S	0	0	0
			1304	835	214	252	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	77	GLY	-	linker	UNP P15873
B	78	GLY	-	linker	UNP P15873

- Molecule 1: Proliferating cell nuclear antigen



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	122.52Å 122.52Å 122.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	86.00 – 2.80 86.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (86.00-2.80) 99.6 (86.00-2.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.277 , 0.314 0.298 , 0.335	Depositor DCC
R_{free} test set	766 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	82.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 83.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	2590	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.90	0/1300	1.02	1/1754 (0.1%)
2	B	0.89	0/1324	1.07	6/1781 (0.3%)
All	All	0.89	0/2624	1.04	7/3535 (0.2%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	38	PRO	CB-CA-C	-6.43	102.29	111.68
2	B	147	ALA	N-CA-C	6.02	113.55	108.13
2	B	62	GLN	CB-CA-C	-5.17	101.73	112.44
2	B	156	LYS	N-CA-C	-5.16	102.27	109.96
1	A	144	PHE	N-CA-C	-5.15	105.67	111.28
2	B	104	HIS	CA-C-N	5.14	126.26	119.84
2	B	104	HIS	C-N-CA	5.14	126.26	119.84

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	1286	0	1298	71	0
2	B	1304	0	1335	48	0
All	All	2590	0	2633	111	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 21.

All (111) 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)
2:B:9:THR:HG23	2:B:110:LYS:NZ	1.78	0.98
2:B:9:THR:CG2	2:B:110:LYS:NZ	2.28	0.96
1:A:38:GLN:HB2	1:A:125:PHE:CE2	2.04	0.92
1:A:88:LEU:HD12	1:A:89:THR:H	1.34	0.92
2:B:9:THR:CG2	2:B:110:LYS:HZ1	1.84	0.89
2:B:10:GLY:CA	2:B:138:ARG:HB2	2.12	0.79
1:A:24:GLN:HA	1:A:24:GLN:HE21	1.49	0.77
1:A:19:PHE:HB3	1:A:72:LEU:HD11	1.67	0.76
2:B:101:ASP:O	2:B:105:PRO:HG3	1.85	0.76
1:A:38:GLN:HB2	1:A:125:PHE:CZ	2.20	0.76
2:B:9:THR:CG2	2:B:110:LYS:HZ3	2.00	0.74
2:B:104:HIS:CE1	2:B:106:GLU:HB2	2.21	0.74
1:A:14:ARG:HG3	1:A:14:ARG:HH11	1.50	0.74
2:B:10:GLY:N	2:B:138:ARG:HB2	2.03	0.74
1:A:104:GLU:HG2	1:A:105:ASP:H	1.54	0.73
1:A:88:LEU:HD12	1:A:89:THR:N	2.04	0.72
1:A:104:GLU:HG2	1:A:105:ASP:N	2.06	0.70
1:A:14:ARG:HH11	1:A:14:ARG:CG	2.04	0.70
1:A:32:GLU:HG3	1:A:62:CYS:O	1.93	0.69
1:A:19:PHE:CB	1:A:72:LEU:HD11	2.25	0.67
1:A:80:ARG:C	1:A:82:GLY:H	2.05	0.65
2:B:8:LEU:HB2	2:B:110:LYS:HD3	1.79	0.63
2:B:9:THR:HG22	2:B:110:LYS:NZ	2.12	0.63
1:A:90:LEU:HB3	1:A:99:ILE:HD11	1.81	0.62
2:B:9:THR:HG23	2:B:110:LYS:HZ3	1.57	0.62
2:B:10:GLY:H	2:B:138:ARG:HD3	1.65	0.62
1:A:22:CYS:HB3	2:B:128:ASP:OD2	2.00	0.62
1:A:162:ILE:HB	2:B:117:VAL:HG22	1.83	0.61
1:A:83:ASN:HB2	1:A:86:ASP:OD1	2.01	0.60
2:B:9:THR:C	2:B:138:ARG:HB2	2.26	0.59
1:A:155:SER:HB3	2:B:85:ALA:HB1	1.83	0.59
2:B:68:HIS:CE1	2:B:104:HIS:HA	2.38	0.59
2:B:10:GLY:HA3	2:B:138:ARG:HB2	1.85	0.58
2:B:6:LYS:HB3	2:B:106:GLU:CD	2.30	0.56
1:A:154:LEU:H	1:A:154:LEU:HD12	1.70	0.56
1:A:26:VAL:CG1	1:A:72:LEU:HD21	2.36	0.56
1:A:87:THR:HG22	1:A:87:THR:O	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:GLY:O	1:A:83:ASN:ND2	2.38	0.56
1:A:82:GLY:C	1:A:83:ASN:ND2	2.63	0.56
2:B:118:ASP:OD1	2:B:118:ASP:C	2.48	0.56
1:A:35:ILE:HD12	1:A:57:PHE:HZ	1.71	0.55
2:B:6:LYS:HD3	2:B:106:GLU:HG3	1.87	0.55
2:B:9:THR:HG22	2:B:110:LYS:HZ3	1.71	0.55
1:A:24:GLN:HA	1:A:24:GLN:NE2	2.21	0.55
2:B:150:LEU:HD21	2:B:152:GLN:HB2	1.89	0.55
1:A:26:VAL:HG11	1:A:72:LEU:HD21	1.88	0.54
1:A:136:THR:HG23	2:B:142:ARG:HG2	1.91	0.53
1:A:142:SER:HA	1:A:145:SER:HB2	1.90	0.53
1:A:151:LEU:HA	1:A:154:LEU:HD13	1.92	0.52
1:A:87:THR:O	1:A:87:THR:CG2	2.58	0.52
2:B:124:LYS:HE3	2:B:125:TYR:CE1	2.45	0.52
1:A:5:LYS:HE3	1:A:87:THR:HG21	1.92	0.52
2:B:104:HIS:HE1	2:B:106:GLU:HB2	1.72	0.51
1:A:76:SER:O	1:A:77:LYS:C	2.53	0.51
1:A:110:ARG:C	1:A:111:ILE:HG13	2.34	0.51
2:B:10:GLY:N	2:B:138:ARG:HD3	2.25	0.50
1:A:30:CYS:O	1:A:65:PRO:HA	2.11	0.50
1:A:76:SER:O	1:A:79:LEU:N	2.41	0.50
2:B:101:ASP:HB3	2:B:105:PRO:HA	1.93	0.50
1:A:38:GLN:CB	1:A:125:PHE:CE2	2.89	0.50
1:A:154:LEU:HD12	1:A:154:LEU:N	2.26	0.50
1:A:5:LYS:HE3	1:A:87:THR:CG2	2.42	0.49
1:A:1:MET:HG3	1:A:61:ARG:HH21	1.77	0.49
1:A:105:ASP:CG	1:A:106:THR:H	2.21	0.49
1:A:14:ARG:CG	1:A:14:ARG:NH1	2.69	0.49
1:A:82:GLY:C	1:A:84:ASN:H	2.20	0.49
1:A:147:ILE:O	1:A:148:VAL:C	2.54	0.49
2:B:8:LEU:HD13	2:B:108:SER:HB2	1.95	0.49
1:A:37:ALA:HB3	1:A:50:LEU:HD23	1.95	0.48
2:B:150:LEU:C	2:B:150:LEU:HD23	2.37	0.48
1:A:20:LYS:O	1:A:21:ASP:HB2	2.13	0.48
2:B:6:LYS:HB3	2:B:106:GLU:OE2	2.13	0.48
2:B:158:GLY:O	2:B:159:PHE:HB3	2.13	0.48
1:A:136:THR:O	2:B:111:LEU:HD12	2.14	0.47
1:A:107:LYS:C	1:A:109:ASP:H	2.22	0.47
2:B:125:TYR:O	2:B:129:ILE:HG13	2.14	0.47
1:A:68:LEU:HB2	1:A:70:MET:HE3	1.96	0.47
1:A:105:ASP:OD1	1:A:109:ASP:HB3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:SER:HA	1:A:145:SER:CB	2.44	0.47
1:A:121:ILE:HD13	1:A:121:ILE:HA	1.80	0.46
2:B:8:LEU:HB2	2:B:110:LYS:CD	2.44	0.46
2:B:9:THR:HA	2:B:138:ARG:HE	1.80	0.45
1:A:11:LEU:O	1:A:14:ARG:HB2	2.16	0.45
2:B:86:ASP:C	2:B:86:ASP:OD2	2.59	0.45
1:A:159:ASN:HB2	2:B:120:THR:OG1	2.16	0.45
1:A:7:GLU:HG3	1:A:8:GLU:N	2.32	0.43
1:A:30:CYS:HB2	1:A:66:VAL:HG23	1.99	0.43
1:A:104:GLU:HB2	1:A:110:ARG:O	2.18	0.43
2:B:104:HIS:O	2:B:107:THR:HG22	2.18	0.43
1:A:14:ARG:O	1:A:17:ASP:HB2	2.19	0.43
1:A:86:ASP:OD1	1:A:86:ASP:N	2.52	0.43
2:B:99:PHE:CD1	2:B:99:PHE:C	2.97	0.42
2:B:68:HIS:CE1	2:B:105:PRO:HD2	2.54	0.42
2:B:98:PRO:HA	2:B:109:ILE:HG22	2.01	0.42
1:A:119:MET:HE2	1:A:119:MET:HB3	1.97	0.42
2:B:9:THR:HG23	2:B:110:LYS:HZ1	1.57	0.42
2:B:79:GLU:O	2:B:97:LYS:HD2	2.19	0.42
1:A:26:VAL:O	1:A:69:GLY:HA2	2.19	0.42
1:A:82:GLY:O	1:A:86:ASP:OD1	2.37	0.41
1:A:2:LEU:O	1:A:91:ILE:HA	2.20	0.41
1:A:134:ASP:O	2:B:114:ASP:HB2	2.21	0.41
1:A:80:ARG:C	1:A:82:GLY:N	2.69	0.41
2:B:150:LEU:HD23	2:B:151:PHE:N	2.36	0.41
1:A:34:GLY:HA2	1:A:60:TYR:CZ	2.56	0.41
1:A:20:LYS:O	1:A:21:ASP:CB	2.69	0.40
1:A:10:SER:HB3	1:A:84:ASN:O	2.21	0.40
1:A:88:LEU:CD1	1:A:89:THR:N	2.79	0.40
1:A:75:LEU:HG	1:A:79:LEU:HD22	2.02	0.40
1:A:110:ARG:O	1:A:111:ILE:HG13	2.22	0.40
2:B:157:SER:O	2:B:157:SER:OG	2.28	0.40
1:A:151:LEU:HB3	2:B:85:ALA:CB	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	161/169 (95%)	140 (87%)	20 (12%)	1 (1%)	21	51
2	B	162/169 (96%)	147 (91%)	13 (8%)	2 (1%)	10	34
All	All	323/338 (96%)	287 (89%)	33 (10%)	3 (1%)	14	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	17	VAL
1	A	21	ASP
2	B	47	GLY

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	150/156 (96%)	118 (79%)	32 (21%)	1	4
2	B	148/148 (100%)	132 (89%)	16 (11%)	6	21
All	All	298/304 (98%)	250 (84%)	48 (16%)	2	8

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	GLU
1	A	14	ARG
1	A	20	LYS

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Mol	Chain	Res	Type
1	A	23	VAL
1	A	24	GLN
1	A	26	VAL
1	A	38	GLN
1	A	41	ASP
1	A	63	ASP
1	A	64	HIS
1	A	66	VAL
1	A	68	LEU
1	A	72	LEU
1	A	73	THR
1	A	76	SER
1	A	79	LEU
1	A	83	ASN
1	A	85	THR
1	A	86	ASP
1	A	87	THR
1	A	97	ASP
1	A	99	ILE
1	A	100	ILE
1	A	104	GLU
1	A	107	LYS
1	A	111	ILE
1	A	117	LYS
1	A	121	ILE
1	A	125	PHE
1	A	157	SER
1	A	159	ASN
1	A	163	THR
2	B	17	VAL
2	B	20	SER
2	B	21	ASP
2	B	22	THR
2	B	23	ILE
2	B	32	ASP
2	B	54	ARG
2	B	61	ILE
2	B	67	LEU
2	B	69	LEU
2	B	74	ARG
2	B	103	GLU
2	B	112	GLU

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Mol	Chain	Res	Type
2	B	124	LYS
2	B	133	SER
2	B	168	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	58	GLN
1	A	83	ASN
1	A	159	ASN
2	B	2	GLN
2	B	31	GLN
2	B	40	GLN
2	B	49	GLN
2	B	60	ASN
2	B	104	HIS
2	B	169	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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	A	163/169 (96%)	1.48	46 (28%) 1 1	58, 81, 106, 117	0
2	B	166/169 (98%)	4.68	113 (68%) 0 0	24, 59, 101, 121	72 (43%)
All	All	329/338 (97%)	3.10	159 (48%) 0 0	24, 74, 106, 121	72 (21%)

All (159) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	75	GLY	16.4
2	B	73	LEU	16.1
2	B	71	LEU	15.7
2	B	11	LYS	15.1
2	B	9	THR	14.4
2	B	22	THR	14.0
2	B	35	GLY	13.0
2	B	13	ILE	12.6
2	B	12	THR	12.4
2	B	7	THR	12.1
2	B	5	VAL	12.0
2	B	67	LEU	11.9
2	B	24	ASP	11.3
2	B	53	GLY	11.0
2	B	15	LEU	10.7
2	B	69	LEU	10.4
2	B	6	LYS	10.3
2	B	19	SER	9.8
2	B	33	LYS	9.8
2	B	34	GLU	9.6
2	B	10	GLY	9.6
2	B	3	ILE	9.4
2	B	8	LEU	9.3
2	B	46	ALA	9.3

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Mol	Chain	Res	Type	RSRZ
2	B	25	ASN	9.2
2	B	37	PRO	9.0
2	B	40	GLN	8.8
2	B	4	PHE	8.6
2	B	52	ASP	8.5
2	B	23	ILE	8.2
2	B	36	ILE	8.2
2	B	66	THR	8.1
2	B	74	ARG	8.0
2	B	43	LEU	7.9
2	B	70	VAL	7.8
2	B	2	GLN	7.7
2	B	45	PHE	7.7
2	B	38	PRO	7.4
2	B	31	GLN	7.3
2	B	39	ASP	7.3
2	B	68	HIS	7.2
2	B	47	GLY	7.1
2	B	44	ILE	7.0
2	B	17	VAL	6.9
2	B	14	THR	6.8
2	B	59	TYR	6.7
2	B	20	SER	6.5
2	B	27	LYS	6.5
2	B	30	ILE	6.4
2	B	61	ILE	6.4
2	B	42	ARG	6.4
2	B	72	ARG	6.4
2	B	32	ASP	6.3
2	B	48	LYS	6.3
2	B	57	SER	6.3
2	B	54	ARG	6.0
2	B	63	LYS	5.9
2	B	28	SER	5.9
2	B	21	ASP	5.9
2	B	51	GLU	5.8
2	B	56	LEU	5.8
2	B	106	GLU	5.7
2	B	50	LEU	5.6
2	B	55	THR	5.5
2	B	49	GLN	5.4
2	B	65	SER	5.3

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Mol	Chain	Res	Type	RSRZ
2	B	58	ASP	5.3
2	B	114	ASP	5.2
2	B	16	GLU	5.2
2	B	29	LYS	5.2
2	B	26	VAL	4.9
2	B	1	MET	4.8
2	B	41	GLN	4.8
2	B	168	PHE	4.6
1	A	144	PHE	4.3
2	B	62	GLN	4.2
2	B	82	LYS	4.2
2	B	64	GLU	4.2
2	B	102	MET	4.1
1	A	28	PHE	3.9
1	A	83	ASN	3.8
1	A	2	LEU	3.8
1	A	149	ARG	3.6
2	B	81	ILE	3.6
2	B	132	GLY	3.6
2	B	135	LEU	3.6
2	B	125	TYR	3.5
2	B	83	PHE	3.4
1	A	90	LEU	3.4
2	B	18	GLU	3.3
1	A	116	LEU	3.3
1	A	66	VAL	3.3
2	B	103	GLU	3.3
1	A	64	HIS	3.2
2	B	111	LEU	3.2
1	A	55	GLU	3.2
1	A	114	TYR	3.2
1	A	78	ILE	3.2
2	B	88	ASP	3.2
1	A	82	GLY	3.2
1	A	88	LEU	3.1
1	A	110	ARG	3.1
2	B	79	GLU	3.1
1	A	35	ILE	3.1
1	A	95	THR	3.0
2	B	107	THR	3.0
2	B	131	LYS	3.0
2	B	87	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	151	LEU	2.9
1	A	3	GLU	2.9
1	A	30	CYS	2.9
2	B	97	LYS	2.8
2	B	93	SER	2.8
2	B	89	ILE	2.8
2	B	92	GLY	2.8
1	A	143	GLU	2.8
1	A	19	PHE	2.8
2	B	115	GLN	2.8
1	A	137	LEU	2.8
1	A	32	GLU	2.7
1	A	62	CYS	2.7
1	A	61	ARG	2.7
1	A	12	PHE	2.7
2	B	141	ILE	2.7
1	A	111	ILE	2.7
1	A	160	ILE	2.6
1	A	70	MET	2.6
1	A	99	ILE	2.6
2	B	112	GLU	2.6
1	A	103	PHE	2.6
2	B	100	VAL	2.5
1	A	117	LYS	2.5
2	B	109	ILE	2.5
2	B	137	ASP	2.4
1	A	101	LEU	2.4
2	B	98	PRO	2.4
1	A	94	ASN	2.3
2	B	85	ALA	2.3
1	A	68	LEU	2.3
1	A	113	GLU	2.3
1	A	121	ILE	2.3
1	A	52	ILE	2.2
1	A	93	ASP	2.2
2	B	155	LEU	2.2
2	B	164	LEU	2.2
1	A	57	PHE	2.2
2	B	169	ASN	2.2
2	B	134	SER	2.2
1	A	26	VAL	2.1
1	A	91	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	122	ASP	2.1
2	B	101	ASP	2.1
2	B	151	PHE	2.1
2	B	96	ILE	2.1
2	B	160	LEU	2.1
1	A	108	LYS	2.1
2	B	86	ASP	2.1
2	B	60	ASN	2.0
1	A	107	LYS	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 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.