



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2026 – 12:08 PM JST

PDB ID : 9XV0 / pdb_00009xv0
Title : Crystal Structure of class C beta-lactamase PDC-16 from *P.aeruginosa*.
Authors : Liji, S.S.; Dhanasingh, I.
Deposited on : 2025-11-25
Resolution : 2.30 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 Phenix2.2
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

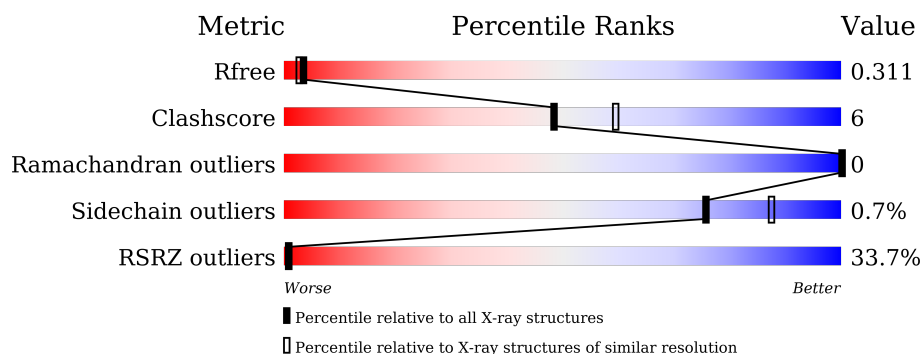
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	358	18% 88% 12%
1	B	358	49% 83% 17%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5908 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 Beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	0	0	0
			2774	1765	491	512	6			
1	B	357	Total	C	N	O	S	0	0	0
			2770	1763	490	511	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP A0A1Z1VQP5
A	-1	HIS	-	expression tag	UNP A0A1Z1VQP5
A	0	MET	-	expression tag	UNP A0A1Z1VQP5
B	-2	SER	-	expression tag	UNP A0A1Z1VQP5
B	-1	HIS	-	expression tag	UNP A0A1Z1VQP5
B	0	MET	-	expression tag	UNP A0A1Z1VQP5

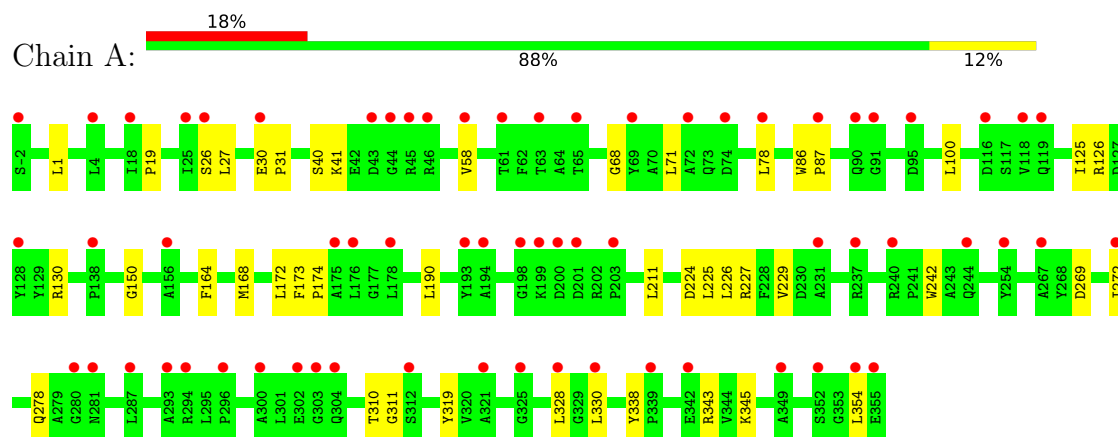
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	214	Total	O	0	0
			214	214		
2	B	150	Total	O	0	0
			150	150		

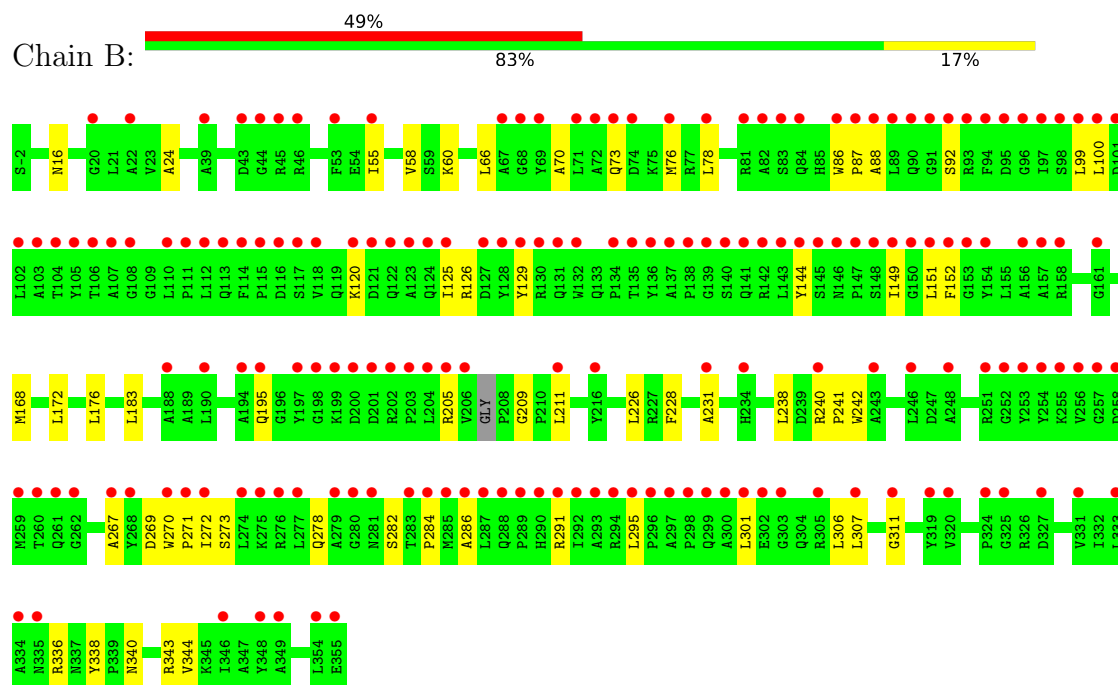
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 ($RSRZ > 2$). 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.

• Molecule 1: Beta-lactamase



• Molecule 1: Beta-lactamase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.86Å 89.70Å 103.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.61 – 2.30 59.61 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (59.61-2.30) 99.8 (59.61-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, R_{free}	0.294 , 0.312 0.294 , 0.311	Depositor DCC
R_{free} test set	1489 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	23.3	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 31.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	5908	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.29% 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	0.13	0/2844	0.38	0/3867
1	B	0.15	0/2839	0.38	0/3858
All	All	0.14	0/5683	0.38	0/7725

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	2774	0	2741	25	0
1	B	2770	0	2738	36	0
2	A	214	0	0	1	0
2	B	150	0	0	0	0
All	All	5908	0	5479	61	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 6.

All (61) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:231:ALA:HB1	1:B:238:LEU:HD11	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:LEU:HD22	1:B:168:MET:HE3	1.74	0.69
1:B:86:TRP:HD1	1:B:87:PRO:HD2	1.64	0.62
1:B:66:LEU:HB2	1:B:168:MET:HE1	1.81	0.61
1:B:70:ALA:HB3	1:B:76:MET:HE2	1.82	0.60
1:B:301:LEU:HB3	1:B:307:LEU:HD11	1.83	0.60
1:B:78:LEU:HD13	1:B:100:LEU:HD13	1.84	0.59
1:A:338:TYR:CZ	1:A:343:ARG:HG2	2.40	0.57
1:B:338:TYR:CZ	1:B:343:ARG:HG2	2.39	0.56
1:A:310:THR:HG22	1:A:319:TYR:HD1	1.72	0.53
1:A:27:LEU:HD12	1:A:354:LEU:HD13	1.89	0.53
1:B:172:LEU:HD13	1:B:242:TRP:CZ3	2.43	0.52
1:A:1:LEU:HD13	1:A:354:LEU:HD21	1.92	0.52
1:B:73:GLN:NE2	1:B:241:PRO:HB3	2.26	0.51
1:B:60:LYS:HB3	1:B:149:ILE:HD13	1.94	0.49
1:A:125:ILE:HG21	1:A:211:LEU:HD11	1.94	0.49
1:A:328:LEU:HD11	1:A:354:LEU:HD12	1.95	0.49
1:B:269:ASP:O	1:B:272:ILE:HB	2.13	0.49
1:B:278:GLN:HG2	1:B:344:VAL:HG11	1.96	0.48
1:B:58:VAL:HG23	1:B:311:GLY:HA3	1.96	0.48
1:B:168:MET:HB2	1:B:183:LEU:HD11	1.96	0.48
1:B:88:ALA:HB1	1:B:126:ARG:HG3	1.95	0.48
1:B:99:LEU:HB3	1:B:152:PHE:HE1	1.79	0.47
1:B:340:ASN:O	1:B:344:VAL:HG12	2.14	0.47
1:A:278:GLN:NE2	1:A:345:LYS:HG3	2.29	0.47
1:A:78:LEU:HD13	1:A:100:LEU:HD13	1.98	0.46
1:B:144:TYR:HB3	1:B:286:ALA:O	2.15	0.46
1:A:40:SER:HB2	2:A:505:HOH:O	2.16	0.46
1:B:291:ARG:CZ	1:B:291:ARG:HB2	2.45	0.46
1:A:269:ASP:O	1:A:272:ILE:HB	2.16	0.46
1:B:195:GLN:HA	1:B:205:ARG:HE	1.81	0.45
1:B:16:ASN:O	1:B:336:ARG:HD3	2.16	0.45
1:A:310:THR:HG22	1:A:319:TYR:CD1	2.51	0.45
1:A:172:LEU:HD23	1:A:242:TRP:CZ3	2.53	0.44
1:B:270:TRP:CG	1:B:271:PRO:HA	2.53	0.44
1:A:26:SER:HB2	1:A:226:LEU:HD21	1.98	0.44
1:B:176:LEU:HD23	1:B:228:PHE:HD1	1.83	0.44
1:B:282:SER:HB2	1:B:284:PRO:HD2	2.00	0.44
1:B:73:GLN:HE21	1:B:241:PRO:HB3	1.82	0.44
1:B:278:GLN:HG2	1:B:344:VAL:CG1	2.47	0.43
1:B:120:LYS:HD2	1:B:209:GLY:O	2.18	0.43
1:B:125:ILE:HG21	1:B:211:LEU:HD21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:SER:N	1:A:226:LEU:HD11	2.33	0.43
1:A:58:VAL:HG23	1:A:311:GLY:HA3	2.00	0.43
1:B:55:ILE:O	1:B:311:GLY:HA3	2.19	0.43
1:A:225:LEU:O	1:A:229:VAL:HG23	2.19	0.42
1:B:168:MET:HA	1:B:168:MET:HE2	2.01	0.42
1:A:19:PRO:HG3	1:A:41:LYS:HD2	2.01	0.42
1:B:129:TYR:CZ	1:B:151:LEU:HB2	2.55	0.42
1:A:164:PHE:O	1:A:168:MET:HG2	2.19	0.42
1:A:173:PHE:HB2	1:A:174:PRO:HD3	2.00	0.42
1:A:224:ASP:OD1	1:A:227:ARG:HD2	2.18	0.42
1:A:68:GLY:HA2	1:A:71:LEU:HD12	2.02	0.42
1:A:30:GLU:HA	1:A:31:PRO:HD3	1.86	0.41
1:A:126:ARG:HD3	1:A:130:ARG:NH1	2.36	0.41
1:A:150:GLY:C	1:A:211:LEU:HD23	2.46	0.41
1:B:24:ALA:HB1	1:B:226:LEU:HD22	2.02	0.41
1:B:240:ARG:HB3	1:B:241:PRO:HD3	2.03	0.40
1:B:267:ALA:HA	1:B:306:LEU:O	2.20	0.40
1:B:272:ILE:HG12	1:B:273:SER:H	1.86	0.40
1:A:86:TRP:HD1	1:A:87:PRO:HD2	1.85	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	356/358 (99%)	348 (98%)	8 (2%)	0	100	100
1	B	353/358 (99%)	345 (98%)	8 (2%)	0	100	100
All	All	709/716 (99%)	693 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	281/282 (100%)	279 (99%)	2 (1%)	76	87
1	B	281/282 (100%)	279 (99%)	2 (1%)	76	87
All	All	562/564 (100%)	558 (99%)	4 (1%)	76	87

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	190	LEU
1	A	330	LEU
1	B	92	SER
1	B	295	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	GLN
1	A	182	HIS
1	A	192	GLN
1	A	195	GLN
1	A	244	GLN
1	A	304	GLN

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 [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	358/358 (100%)	1.38	66 (18%) 3 4	13, 21, 38, 48	0
1	B	357/358 (99%)	2.09	175 (49%) 0 0	16, 34, 53, 61	0
All	All	715/716 (99%)	1.73	241 (33%) 1 1	13, 25, 51, 61	0

All (241) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	204	LEU	5.8
1	B	107	ALA	5.8
1	B	253	TYR	5.5
1	B	105	TYR	5.4
1	B	136	TYR	5.2
1	B	300	ALA	5.1
1	B	289	PRO	4.9
1	B	92	SER	4.7
1	B	201	ASP	4.7
1	B	129	TYR	4.7
1	B	99	LEU	4.6
1	B	354	LEU	4.6
1	B	94	PHE	4.5
1	B	104	THR	4.4
1	B	78	LEU	4.3
1	B	256	VAL	4.2
1	B	288	GLN	4.2
1	B	89	LEU	4.2
1	B	108	GLY	4.1
1	B	270	TRP	4.0
1	B	303	GLY	4.0
1	B	280	GLY	4.0
1	B	95	ASP	4.0
1	B	246	LEU	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	200	ASP	3.9
1	B	257	GLY	3.9
1	B	271	PRO	3.8
1	B	284	PRO	3.8
1	B	132	TRP	3.8
1	B	206	VAL	3.8
1	B	103	ALA	3.8
1	B	297	ALA	3.8
1	B	138	PRO	3.8
1	B	116	ASP	3.8
1	B	254	TYR	3.7
1	B	140	SER	3.7
1	B	305	ARG	3.7
1	B	290	HIS	3.7
1	B	106	THR	3.7
1	B	110	LEU	3.7
1	B	295	LEU	3.7
1	B	154	TYR	3.6
1	B	111	PRO	3.6
1	B	45	ARG	3.5
1	B	287	LEU	3.5
1	B	114	PHE	3.5
1	B	149	ILE	3.4
1	A	91	GLY	3.4
1	B	130	ARG	3.4
1	B	243	ALA	3.4
1	B	151	LEU	3.3
1	B	144	TYR	3.3
1	B	93	ARG	3.3
1	B	205	ARG	3.3
1	A	138	PRO	3.3
1	B	325	GLY	3.3
1	B	97	ILE	3.3
1	B	286	ALA	3.2
1	B	67	ALA	3.2
1	B	291	ARG	3.2
1	B	123	ALA	3.2
1	B	100	LEU	3.2
1	B	211	LEU	3.2
1	B	55	ILE	3.2
1	B	146	ASN	3.1
1	A	69	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	128	TYR	3.1
1	A	90	GLN	3.1
1	B	102	LEU	3.1
1	B	240	ARG	3.1
1	B	145	SER	3.1
1	A	280	GLY	3.1
1	B	150	GLY	3.1
1	B	301	LEU	3.1
1	B	260	THR	3.1
1	B	281	ASN	3.1
1	B	76	MET	3.1
1	B	72	ALA	3.0
1	B	88	ALA	3.0
1	B	156	ALA	3.0
1	A	87	PRO	3.0
1	B	296	PRO	3.0
1	B	91	GLY	3.0
1	B	274	LEU	3.0
1	B	285	MET	3.0
1	B	147	PRO	3.0
1	B	158	ARG	2.9
1	B	161	GLY	2.9
1	A	178	LEU	2.9
1	B	71	LEU	2.9
1	B	307	LEU	2.9
1	B	43	ASP	2.9
1	A	-2	SER	2.8
1	A	352	SER	2.8
1	B	200	ASP	2.9
1	B	261	GLN	2.8
1	B	302	GLU	2.8
1	A	116	ASP	2.8
1	A	355	GLU	2.8
1	A	118	VAL	2.8
1	B	272	ILE	2.7
1	B	148	SER	2.7
1	B	311	GLY	2.7
1	B	143	LEU	2.7
1	B	277	LEU	2.7
1	B	113	GLN	2.7
1	A	272	ILE	2.7
1	B	101	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	325	GLY	2.7
1	B	153	GLY	2.7
1	B	294	ARG	2.7
1	A	194	ALA	2.7
1	B	283	THR	2.7
1	B	190	LEU	2.7
1	A	349	ALA	2.7
1	B	115	PRO	2.7
1	B	203	PRO	2.7
1	B	349	ALA	2.6
1	B	258	ASP	2.6
1	B	125	ILE	2.6
1	B	141	GLN	2.6
1	A	294	ARG	2.6
1	B	142	ARG	2.6
1	B	84	GLN	2.6
1	A	176	LEU	2.6
1	B	112	LEU	2.6
1	A	300	ALA	2.6
1	B	267	ALA	2.6
1	A	74	ASP	2.6
1	B	96	GLY	2.6
1	B	118	VAL	2.6
1	A	26	SER	2.6
1	B	117	SER	2.6
1	A	58	VAL	2.5
1	B	259	MET	2.5
1	B	120	LYS	2.5
1	B	252	GLY	2.5
1	B	131	GLN	2.5
1	A	45	ARG	2.5
1	A	293	ALA	2.5
1	B	74	ASP	2.5
1	B	279	ALA	2.5
1	B	324	PRO	2.5
1	B	216	TYR	2.5
1	A	4	LEU	2.5
1	B	202	ARG	2.4
1	A	354	LEU	2.4
1	B	331	VAL	2.4
1	A	201	ASP	2.4
1	B	90	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	30	GLU	2.4
1	B	188	ALA	2.4
1	B	298	PRO	2.4
1	B	319	TYR	2.4
1	B	39	ALA	2.4
1	B	44	GLY	2.4
1	B	293	ALA	2.4
1	B	135	THR	2.4
1	B	292	ILE	2.4
1	A	237	ARG	2.4
1	A	302	GLU	2.4
1	B	69	TYR	2.3
1	A	18	ILE	2.3
1	B	320	VAL	2.3
1	B	248	ALA	2.3
1	A	328	LEU	2.3
1	B	127	ASP	2.3
1	A	296	PRO	2.3
1	B	139	GLY	2.3
1	B	348	TYR	2.3
1	A	175	ALA	2.3
1	A	240	ARG	2.3
1	B	195	GLN	2.3
1	A	199	LYS	2.3
1	A	43	ASP	2.3
1	B	82	ALA	2.3
1	A	65	THR	2.3
1	B	73	GLN	2.3
1	B	122	GLN	2.3
1	A	95	ASP	2.2
1	B	134	PRO	2.2
1	A	321	ALA	2.2
1	A	119	GLN	2.2
1	B	86	TRP	2.2
1	B	299	GLN	2.2
1	B	199	LYS	2.2
1	B	346	ILE	2.2
1	A	78	LEU	2.2
1	B	124	GLN	2.2
1	B	255	LYS	2.2
1	A	193	TYR	2.2
1	A	312	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	46	ARG	2.2
1	B	234	HIS	2.2
1	B	355	GLU	2.2
1	A	304	GLN	2.2
1	B	231	ALA	2.2
1	A	46	ARG	2.2
1	B	251	ARG	2.2
1	B	276	ARG	2.2
1	B	327	ASP	2.2
1	A	342	GLU	2.2
1	B	275	LYS	2.2
1	A	44	GLY	2.2
1	A	244	GLN	2.2
1	B	198	GLY	2.2
1	A	267	ALA	2.2
1	A	128	TYR	2.1
1	B	197	TYR	2.1
1	A	25	ILE	2.1
1	A	281	ASN	2.1
1	B	53	PHE	2.1
1	A	61	THR	2.1
1	A	72	ALA	2.1
1	B	98	SER	2.1
1	B	137	ALA	2.1
1	B	333	LEU	2.1
1	A	254	TYR	2.1
1	B	121	ASP	2.1
1	B	268	TYR	2.1
1	B	68	GLY	2.1
1	B	262	GLY	2.1
1	B	81	ARG	2.1
1	A	287	LEU	2.1
1	A	330	LEU	2.1
1	A	203	PRO	2.1
1	B	87	PRO	2.1
1	A	198	GLY	2.1
1	A	303	GLY	2.1
1	B	83	SER	2.0
1	A	156	ALA	2.0
1	B	22	ALA	2.0
1	B	194	ALA	2.0
1	B	20	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	152	PHE	2.0
1	A	63	THR	2.0
1	A	231	ALA	2.0
1	B	157	ALA	2.0
1	B	334	ALA	2.0
1	B	335	ASN	2.0
1	A	339	PRO	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.