



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 08:48 PM UTC

PDB ID : 6J25 / pdb_00006j25
Title : CTX-M-64 beta-lactamase mutant-S130T
Authors : Cheng, Q.; Chen, S.
Deposited on : 2018-12-30
Resolution : 1.20 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

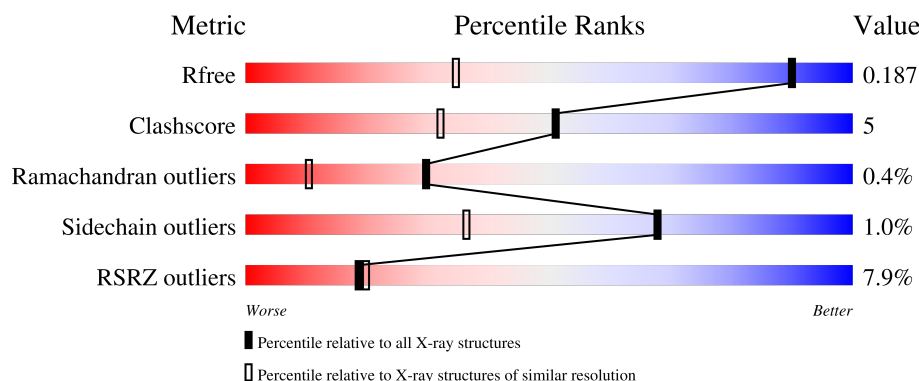
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.20 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	1216 (1.20-1.20)
Clashscore	190562	1265 (1.20-1.20)
Ramachandran outliers	187476	1226 (1.20-1.20)
Sidechain outliers	187428	1226 (1.20-1.20)
RSRZ outliers	180081	1214 (1.20-1.20)

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	274	6% 84% 11% 5%
1	B	274	9% 80% 12% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4520 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	260	Total	C	N	O	S	0	1	0
			1953	1216	351	380	6			
1	B	260	Total	C	N	O	S	0	1	0
			1953	1216	351	380	6			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	GLY	-	expression tag	UNP C8CP57
A	15	SER	-	expression tag	UNP C8CP57
A	16	HIS	-	expression tag	UNP C8CP57
A	17	MET	-	expression tag	UNP C8CP57
A	18	ALA	-	expression tag	UNP C8CP57
A	19	SER	-	expression tag	UNP C8CP57
A	20	GLY	-	expression tag	UNP C8CP57
A	21	GLY	-	expression tag	UNP C8CP57
A	22	THR	-	expression tag	UNP C8CP57
A	23	GLU	-	expression tag	UNP C8CP57
A	24	LEU	-	expression tag	UNP C8CP57
A	130	THR	SER	engineered mutation	UNP C8CP57
B	14	GLY	-	expression tag	UNP C8CP57
B	15	SER	-	expression tag	UNP C8CP57
B	16	HIS	-	expression tag	UNP C8CP57
B	17	MET	-	expression tag	UNP C8CP57
B	18	ALA	-	expression tag	UNP C8CP57
B	19	SER	-	expression tag	UNP C8CP57
B	20	GLY	-	expression tag	UNP C8CP57
B	21	GLY	-	expression tag	UNP C8CP57
B	22	THR	-	expression tag	UNP C8CP57
B	23	GLU	-	expression tag	UNP C8CP57
B	24	LEU	-	expression tag	UNP C8CP57
B	130	THR	SER	engineered mutation	UNP C8CP57

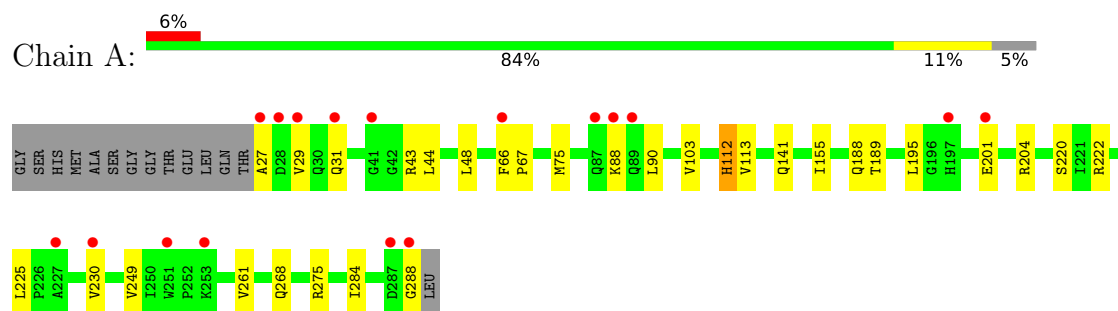
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	295	Total 295	O 295	0	0
2	B	319	Total 319	O 319	0	0

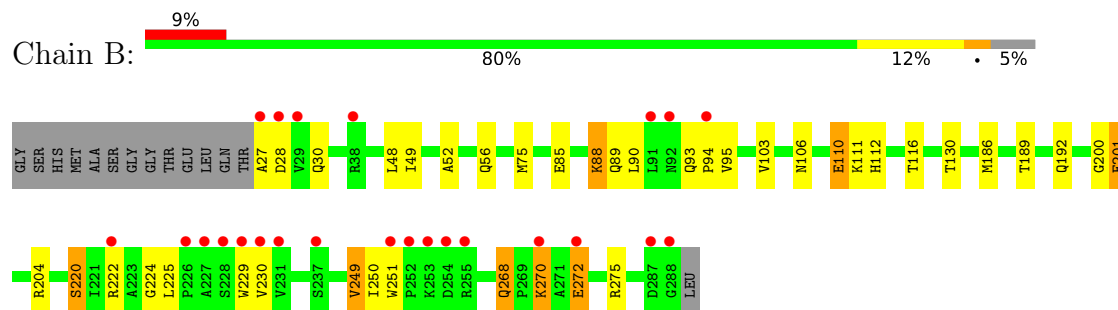
3 Residue-property plots [i](#)

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 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	45.25Å 105.99Å 47.97Å 90.00° 100.73° 90.00°	Depositor
Resolution (Å)	52.99 – 1.20 52.99 – 1.20	Depositor EDS
% Data completeness (in resolution range)	98.2 (52.99-1.20) 98.2 (52.99-1.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.55 (at 1.20Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.182 , 0.194 0.173 , 0.187	Depositor DCC
R_{free} test set	6736 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	10.0	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4520	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% 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

5.1 Standard geometry

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	1.61	15/1986 (0.8%)	1.23	3/2703 (0.1%)
1	B	1.72	19/1986 (1.0%)	1.33	7/2703 (0.3%)
All	All	1.67	34/3972 (0.9%)	1.28	10/5406 (0.2%)

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	220	SER	CA-C	-13.03	1.46	1.53
1	A	113[A]	VAL	CA-C	8.02	1.63	1.52
1	A	113[B]	VAL	CA-C	8.02	1.63	1.52
1	B	229	TRP	CA-C	7.74	1.62	1.52
1	A	220	SER	CA-C	-6.86	1.49	1.53
1	A	225	LEU	C-O	-6.83	1.17	1.24
1	B	90	LEU	C-N	-6.81	1.24	1.33
1	B	230	VAL	CA-C	6.70	1.60	1.52
1	B	268	GLN	CA-C	-6.60	1.43	1.52
1	B	225	LEU	C-O	-6.55	1.17	1.24
1	A	48	LEU	C-O	6.44	1.31	1.24
1	A	230	VAL	CA-CB	-6.13	1.46	1.54
1	B	95	VAL	N-CA	-6.08	1.39	1.46
1	B	249	VAL	C-N	5.98	1.41	1.33
1	B	200	GLY	CA-C	-5.96	1.45	1.52
1	B	93	GLN	N-CA	-5.72	1.36	1.46
1	A	261	VAL	C-O	5.64	1.30	1.24
1	A	284	ILE	CA-C	-5.57	1.46	1.52
1	B	224	GLY	C-O	5.45	1.30	1.23
1	B	94	PRO	CA-C	-5.43	1.45	1.52
1	A	141	GLN	C-O	5.35	1.30	1.24
1	A	44	LEU	CA-C	-5.34	1.46	1.52
1	A	195	LEU	C-O	5.33	1.31	1.24
1	B	89	GLN	C-O	5.24	1.30	1.24
1	B	106	ASN	CA-CB	5.23	1.61	1.53
1	B	88	LYS	N-CA	-5.19	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	275	ARG	C-O	-5.18	1.17	1.24
1	B	250	ILE	C-O	-5.14	1.18	1.24
1	A	90	LEU	C-O	-5.12	1.18	1.24
1	A	268	GLN	CD-OE1	5.07	1.33	1.23
1	B	56	GLN	CA-C	-5.06	1.46	1.52
1	B	110	GLU	CA-C	-5.06	1.45	1.52
1	B	52	ALA	C-O	5.05	1.30	1.24
1	A	155	ILE	CA-C	-5.02	1.47	1.53

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	28	ASP	CA-C-O	-7.33	112.66	120.42
1	B	201	GLU	CB-CG-CD	6.28	123.28	112.60
1	B	90	LEU	CA-C-O	-6.08	113.98	120.42
1	B	116	THR	CA-C-O	5.97	128.43	121.44
1	B	249	VAL	O-C-N	5.75	129.22	123.18
1	B	85	GLU	CA-C-O	-5.38	113.78	119.97
1	A	112	HIS	CB-CG-CD2	-5.37	124.22	131.20
1	B	220	SER	O-C-N	-5.33	117.22	121.65
1	A	112	HIS	CB-CG-ND1	5.21	130.51	122.70
1	A	249	VAL	N-CA-C	-5.03	101.13	108.17

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	1953	0	1983	13	0
1	B	1953	0	1983	28	0
2	A	295	0	0	5	1
2	B	319	0	0	11	1
All	All	4520	0	3966	41	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 5.

All (41) 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:A:201:GLU:OE1	1:A:204:ARG:NH2	1.91	1.01
1:B:222:ARG:HG3	2:B:400:HOH:O	1.67	0.92
1:B:270:LYS:HE3	1:B:270:LYS:H	1.38	0.88
1:A:288:GLY:O	2:A:301:HOH:O	2.00	0.79
1:B:222:ARG:NH2	2:B:302:HOH:O	2.16	0.77
1:B:270:LYS:HE3	1:B:270:LYS:N	2.05	0.70
1:B:201:GLU:OE2	1:B:204:ARG:NH1	2.24	0.70
1:B:110:GLU:HG3	1:B:111:LYS:HE3	1.78	0.66
1:B:270:LYS:H	1:B:270:LYS:CE	2.09	0.63
1:A:222:ARG:O	1:A:222:ARG:HD3	2.01	0.60
1:A:29:VAL:HG12	2:A:498:HOH:O	2.02	0.59
1:B:110:GLU:HG3	1:B:111:LYS:CE	2.32	0.59
1:B:272:GLU:H	1:B:272:GLU:CD	2.11	0.58
1:B:222:ARG:CZ	2:B:302:HOH:O	2.49	0.58
1:A:43:ARG:NH2	1:A:66:PHE:CZ	2.73	0.56
1:B:192:GLN:HE21	1:B:192:GLN:HA	1.71	0.55
1:A:67:PRO:HD3	2:A:530:HOH:O	2.09	0.52
1:B:27:ALA:HB1	1:B:30:GLN:HB2	1.90	0.52
1:A:222:ARG:HD3	1:A:222:ARG:C	2.36	0.50
1:B:75:MET:HE1	1:B:189:THR:HG21	1.94	0.50
1:B:88:LYS:HD2	2:B:361:HOH:O	2.12	0.49
1:A:75:MET:HE1	1:A:189:THR:HG21	1.95	0.49
1:B:48:LEU:HD13	1:B:48:LEU:C	2.38	0.48
1:A:112:HIS:HE1	2:A:517:HOH:O	1.96	0.48
1:B:112:HIS:HE1	2:B:561:HOH:O	1.96	0.48
1:B:222:ARG:NH1	2:B:302:HOH:O	2.45	0.47
1:B:220:SER:OG	1:B:275:ARG:HG2	2.13	0.47
1:B:186:MET:HE1	2:B:342:HOH:O	2.14	0.47
1:A:27:ALA:N	1:A:31:GLN:OE1	2.48	0.46
1:A:188:GLN:HG3	2:A:437:HOH:O	2.15	0.45
1:A:201:GLU:OE1	1:A:204:ARG:CZ	2.62	0.45
1:B:48:LEU:HD13	1:B:49:ILE:N	2.31	0.45
1:B:88:LYS:HE3	2:B:325:HOH:O	2.15	0.45
1:B:48:LEU:HD13	1:B:49:ILE:C	2.42	0.44
1:B:268:GLN:HB3	1:B:270:LYS:HZ2	1.82	0.43
1:B:110:GLU:CG	1:B:111:LYS:HE3	2.46	0.43
1:B:27:ALA:CA	2:B:530:HOH:O	2.66	0.42
1:A:27:ALA:HB3	1:A:31:GLN:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:VAL:HG13	1:B:251:TRP:CZ3	2.55	0.42
1:B:27:ALA:HA	2:B:530:HOH:O	2.19	0.42
1:B:27:ALA:HB1	2:B:530:HOH:O	2.19	0.40

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)
2:A:571:HOH:O	2:B:428:HOH:O[1_556]	2.09	0.11

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	259/274 (94%)	254 (98%)	4 (2%)	1 (0%)	30	10
1	B	259/274 (94%)	253 (98%)	5 (2%)	1 (0%)	30	10
All	All	518/548 (94%)	507 (98%)	9 (2%)	2 (0%)	30	10

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	103	VAL
1	B	103	VAL

5.3.2 Protein sidechains [i](#)

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	205/214 (96%)	204 (100%)	1 (0%)	81	59
1	B	205/214 (96%)	202 (98%)	3 (2%)	57	21
All	All	410/428 (96%)	406 (99%)	4 (1%)	68	36

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

Mol	Chain	Res	Type
1	A	88	LYS
1	B	130	THR
1	B	270	LYS
1	B	272	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
1	A	112	HIS
1	A	197	HIS
1	A	206	GLN
1	B	83	GLN
1	B	92	ASN
1	B	112	HIS
1	B	141	GLN
1	B	192	GLN
1	B	206	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 ⓘ

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	260/274 (94%)	0.48	17 (6%) 25 26	6, 9, 18, 30	1 (0%)
1	B	260/274 (94%)	0.46	24 (9%) 14 15	6, 9, 19, 42	1 (0%)
All	All	520/548 (94%)	0.47	41 (7%) 18 20	6, 9, 19, 42	2 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	66	PHE	8.3
1	A	288	GLY	8.1
1	B	27	ALA	7.9
1	A	27	ALA	7.4
1	B	288	GLY	5.3
1	A	41	GLY	4.6
1	B	229	TRP	4.5
1	A	88	LYS	4.4
1	B	227	ALA	4.2
1	B	251	TRP	4.2
1	A	28	ASP	3.6
1	A	87	GLN	3.6
1	B	254	ASP	3.2
1	B	287	ASP	3.1
1	B	226	PRO	3.0
1	B	230	VAL	3.0
1	B	270	LYS	3.0
1	B	94	PRO	2.9
1	A	29	VAL	2.6
1	B	253	LYS	2.5
1	B	255	ARG	2.5
1	B	38	ARG	2.4
1	A	230	VAL	2.4
1	A	89	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	287	ASP	2.3
1	B	272	GLU	2.2
1	B	91	LEU	2.2
1	B	252	PRO	2.2
1	A	253	LYS	2.2
1	B	92	ASN	2.2
1	B	228	SER	2.2
1	A	251	TRP	2.1
1	A	31	GLN	2.1
1	A	227	ALA	2.1
1	B	231	VAL	2.1
1	A	197	HIS	2.1
1	B	29	VAL	2.1
1	B	222	ARG	2.0
1	B	237	SER	2.0
1	A	201	GLU	2.0
1	B	28	ASP	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.