



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:00 PM GMT

PDB ID : 3SH7
Title : Crystal structure of fluorophore-labeled beta-lactamase PenP
Authors : Wong, W.-T.; Zhao, Y.-X.; Leung, Y.-C.
Deposited on : 2011-06-16
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

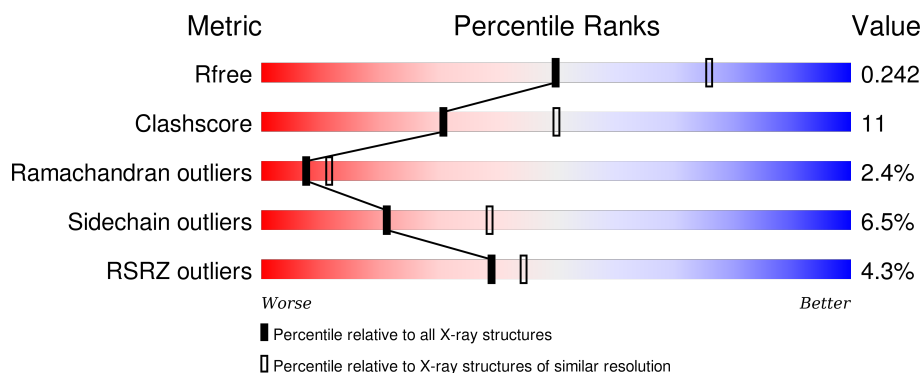
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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

Mol	Chain	Length	Quality of chain
1	A	266	<div> <div>4%</div> <div>77%</div> <div>15%</div> <div>• • •</div> </div>
1	B	266	<div> <div>4%</div> <div>73%</div> <div>18%</div> <div>• • •</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4435 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.

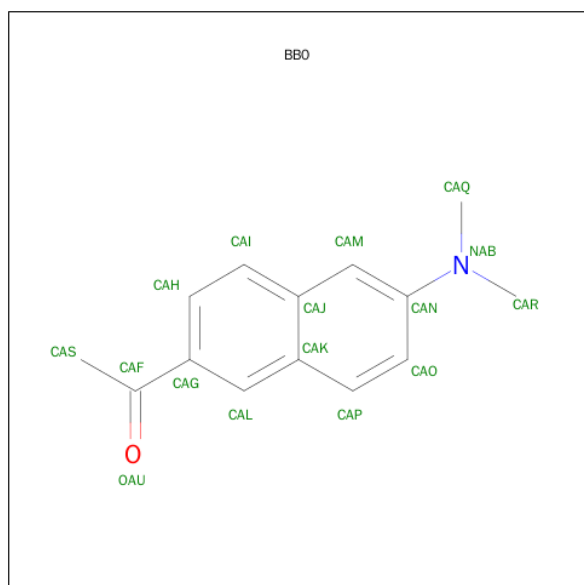
- Molecule 1 is a protein called Beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	0	0
			2009	1260	348	397	4			
1	B	255	Total	C	N	O	S	0	0	0
			1992	1250	345	393	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	MET	-	INITIATING METHIONINE	UNP P00808
A	166	CYS	GLU	ENGINEERED MUTATION	UNP P00808
B	25	MET	-	INITIATING METHIONINE	UNP P00808
B	166	CYS	GLU	ENGINEERED MUTATION	UNP P00808

- Molecule 2 is 1-[6-(DIMETHYLAMINO)NAPHTHALEN-2-YL]ETHANONE (three-letter code: BB0) (formula: C₁₄H₁₅NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			16	14	1	1		
2	B	1	Total	C	N	O	0	0
			16	14	1	1		

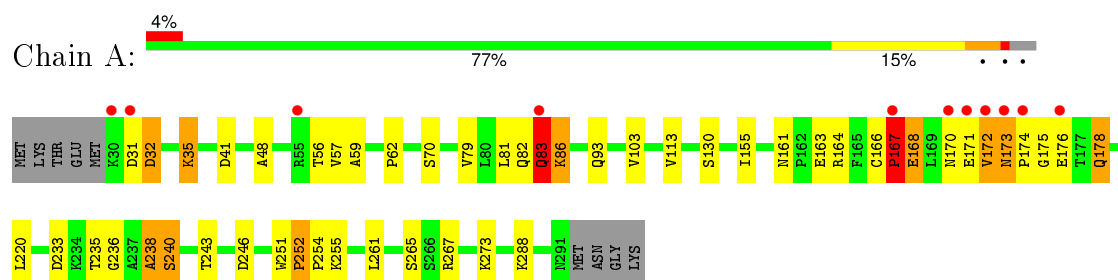
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	224	Total	O	0	0
			224	224		
3	B	178	Total	O	0	0
			178	178		

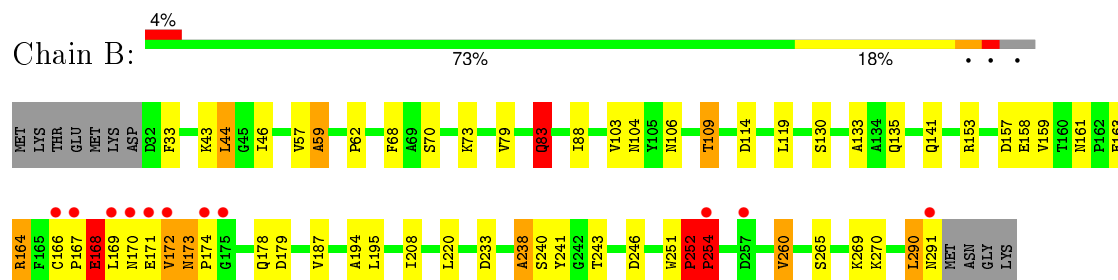
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• 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	43.49Å 91.00Å 66.16Å 90.00° 104.36° 90.00°	Depositor
Resolution (Å)	40.06 – 2.50 40.06 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.06-2.50) 99.8 (40.06-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.86 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.183 , 0.244 0.181 , 0.242	Depositor DCC
R_{free} test set	873 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	16.4	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 40.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 17331 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4435	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.43% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BB0

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	0.74	5/2039 (0.2%)	0.86	11/2760 (0.4%)
1	B	0.68	4/2022 (0.2%)	0.83	8/2738 (0.3%)
All	All	0.71	9/4061 (0.2%)	0.85	19/5498 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	4
All	All	0	7

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	252	PRO	C-N	11.13	1.55	1.34
1	B	238	ALA	C-N	10.98	1.59	1.34
1	A	57	VAL	C-N	10.29	1.57	1.34
1	A	86	LYS	C-N	8.62	1.53	1.34
1	B	83	GLN	C-N	8.52	1.53	1.34
1	A	83	GLN	C-N	7.64	1.51	1.34
1	A	251	TRP	CE3-CZ3	-6.90	1.26	1.38
1	B	238	ALA	CA-CB	-5.59	1.40	1.52
1	A	252	PRO	C-N	-5.54	1.23	1.34

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	83	GLN	O-C-N	-13.69	100.80	122.70
1	B	238	ALA	O-C-N	-13.25	101.50	122.70
1	B	252	PRO	O-C-N	-11.67	98.93	121.10
1	A	83	GLN	CA-C-N	-10.01	95.18	117.20
1	B	238	ALA	CA-C-N	9.45	138.00	117.20
1	A	238	ALA	O-C-N	-8.53	109.05	122.70
1	A	86	LYS	O-C-N	7.73	135.06	122.70
1	A	82	GLN	C-N-CA	-7.63	102.63	121.70
1	A	83	GLN	C-N-CA	-7.29	103.46	121.70
1	A	252	PRO	C-N-CD	-7.10	104.97	120.60
1	B	59	ALA	O-C-N	-6.55	112.22	122.70
1	B	251	TRP	O-C-N	-6.39	108.97	121.10
1	B	57	VAL	O-C-N	-6.38	112.50	122.70
1	B	83	GLN	O-C-N	-6.13	112.89	122.70
1	A	240	SER	O-C-N	5.71	131.84	122.70
1	A	86	LYS	CA-C-N	-5.57	104.94	117.20
1	B	252	PRO	CA-C-N	5.48	132.43	117.10
1	A	240	SER	CA-C-N	-5.32	105.51	117.20
1	A	167	PRO	C-N-CA	5.01	134.23	121.70

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	238	ALA	Mainchain
1	A	252	PRO	Mainchain
1	A	83	GLN	Mainchain
1	B	168	GLU	Peptide
1	B	252	PRO	Mainchain
1	B	254	PRO	Mainchain
1	B	83	GLN	Mainchain

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	2009	0	2028	35	0
1	B	1992	0	2010	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	16	0	15	3	0
2	B	16	0	13	3	0
3	A	224	0	0	2	0
3	B	178	0	0	5	0
All	All	4435	0	4066	88	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 11.

All (88) 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:173:ASN:HB3	1:A:174:PRO:HD2	1.28	1.09
1:B:109:THR:HG21	1:B:133:ALA:HB3	1.40	1.01
1:B:290:LEU:HB3	1:B:291:ASN:HA	1.41	0.99
1:B:254:PRO:HD2	3:B:357:HOH:O	1.63	0.97
1:A:173:ASN:HB3	1:A:174:PRO:CD	2.00	0.89
1:B:106:ASN:HB3	1:B:109:THR:HG22	1.56	0.87
1:B:169:LEU:HG	1:B:170:ASN:HB2	1.57	0.84
1:B:290:LEU:CB	1:B:291:ASN:HA	2.06	0.84
1:A:170:ASN:N	1:A:171:GLU:HB3	1.94	0.83
1:A:176:GLU:HB3	1:A:178:GLN:OE1	1.78	0.83
1:B:187:VAL:HG13	1:B:260:VAL:HG22	1.61	0.82
1:B:169:LEU:HB3	1:B:170:ASN:HB2	1.66	0.77
1:B:114:ASP:HB3	3:B:436:HOH:O	1.86	0.76
1:B:169:LEU:CB	1:B:170:ASN:HB2	2.16	0.74
1:B:169:LEU:CG	1:B:170:ASN:HB2	2.18	0.73
1:B:164:ARG:HD3	1:B:179:ASP:OD2	1.88	0.72
1:B:169:LEU:HB3	1:B:170:ASN:CB	2.21	0.70
1:B:106:ASN:HB3	1:B:109:THR:CG2	2.25	0.67
1:B:119:LEU:HD21	1:B:141:GLN:HG3	1.78	0.67
1:B:172:VAL:HG21	1:B:178:GLN:NE2	2.11	0.65
1:B:172:VAL:HG23	1:B:173:ASN:HB2	1.79	0.64
1:B:252:PRO:O	1:B:254:PRO:C	2.32	0.64
1:B:170:ASN:HB3	3:B:438:HOH:O	1.97	0.63
1:B:220:LEU:HD23	1:B:246:ASP:HB2	1.81	0.62
1:A:167:PRO:N	1:A:168:GLU:HB2	2.15	0.62
1:B:173:ASN:H	1:B:174:PRO:HA	1.65	0.60
1:A:166:CYS:SG	2:A:2:BB0:HAS	2.41	0.60
1:A:32:ASP:OD1	1:A:32:ASP:N	2.33	0.60
1:B:290:LEU:CB	1:B:291:ASN:CA	2.80	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:GLU:HB3	1:B:164:ARG:HD2	1.85	0.59
1:B:173:ASN:HB3	1:B:174:PRO:O	2.03	0.59
1:B:33:PHE:CE1	1:B:46:ILE:HD13	2.38	0.58
1:A:48:ALA:HB2	1:A:261:LEU:HD13	1.87	0.57
1:A:79:VAL:O	1:A:83:GLN:HG2	2.04	0.57
1:B:167:PRO:HG2	3:B:445:HOH:O	2.03	0.57
1:A:166:CYS:SG	2:A:2:BB0:CAS	2.93	0.56
1:B:172:VAL:HG21	1:B:178:GLN:HE22	1.70	0.56
1:B:44:LEU:HG	1:B:46:ILE:HD11	1.88	0.56
1:B:172:VAL:CG2	1:B:173:ASN:HB2	2.35	0.56
1:A:172:VAL:H	1:A:173:ASN:CG	2.09	0.55
1:B:254:PRO:CD	3:B:357:HOH:O	2.38	0.55
1:B:168:GLU:H	1:B:169:LEU:CB	2.22	0.53
1:A:172:VAL:H	1:A:173:ASN:HA	1.73	0.53
1:B:171:GLU:OE2	1:B:270:LYS:HD2	2.07	0.53
1:B:169:LEU:HD13	2:B:2:BB0:CAG	2.41	0.51
1:A:79:VAL:O	1:A:83:GLN:CG	2.59	0.50
1:A:167:PRO:CA	1:A:168:GLU:HB2	2.41	0.50
1:B:73:LYS:HE3	1:B:135:GLN:HB2	1.94	0.50
1:A:173:ASN:CB	1:A:174:PRO:CD	2.84	0.50
1:A:81:LEU:O	1:A:86:LYS:O	2.30	0.49
1:A:167:PRO:CB	1:A:168:GLU:HB2	2.43	0.49
1:B:194:ALA:O	1:B:208:ILE:HD11	2.12	0.49
1:B:166:CYS:O	1:B:169:LEU:HD23	2.13	0.48
1:A:59:ALA:HB1	1:A:62:PRO:HG3	1.96	0.48
1:A:167:PRO:HB2	1:A:168:GLU:HB2	1.96	0.48
1:B:168:GLU:H	1:B:169:LEU:HB3	1.78	0.47
1:B:169:LEU:HD22	2:B:2:BB0:HASA	1.96	0.47
1:B:104:ASN:HB3	2:B:2:BB0:CAH	2.44	0.47
1:A:220:LEU:HD22	1:A:235:THR:HG22	1.97	0.47
1:B:79:VAL:O	1:B:83:GLN:HG3	2.15	0.47
1:B:173:ASN:N	1:B:174:PRO:HA	2.30	0.46
1:B:171:GLU:CD	1:B:270:LYS:HD2	2.36	0.46
1:A:41:ASP:HB3	1:A:267:ARG:HH21	1.81	0.45
1:A:178:GLN:H	1:A:178:GLN:CD	2.20	0.45
1:A:171:GLU:HA	1:A:172:VAL:HB	1.99	0.45
1:B:70:SER:OG	1:B:73:LYS:NZ	2.47	0.45
1:B:243:THR:HA	1:B:265:SER:O	2.17	0.45
1:A:86:LYS:NZ	1:A:93:GLN:HE22	2.14	0.45
1:A:220:LEU:HD23	1:A:246:ASP:HB2	1.98	0.44
1:A:70:SER:HB2	1:A:236:GLY:HA2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:153:ARG:HH22	1:B:161:ASN:HD22	1.65	0.44
1:A:172:VAL:H	1:A:173:ASN:CA	2.31	0.44
1:A:79:VAL:HG13	1:A:83:GLN:NE2	2.33	0.44
1:B:241:TYR:HA	1:B:269:LYS:O	2.18	0.43
1:B:172:VAL:HA	1:B:173:ASN:CB	2.48	0.43
1:A:79:VAL:HG13	1:A:83:GLN:HE21	1.83	0.43
1:A:81:LEU:C	1:A:83:GLN:N	2.68	0.43
1:A:163:GLU:HG3	1:A:178:GLN:HB3	2.00	0.42
1:B:59:ALA:HB1	1:B:62:PRO:HG3	2.01	0.42
1:B:43:LYS:O	1:B:265:SER:HA	2.19	0.42
1:A:86:LYS:HZ1	1:A:93:GLN:HE22	1.68	0.42
1:A:35:LYS:HD3	3:A:335:HOH:O	2.19	0.41
1:A:174:PRO:HA	1:A:175:GLY:HA2	1.66	0.41
1:B:153:ARG:HH22	1:B:161:ASN:ND2	2.17	0.41
1:A:243:THR:HA	1:A:265:SER:O	2.21	0.41
1:B:168:GLU:O	1:B:238:ALA:HB1	2.20	0.41
2:A:2:BB0:HAP	3:A:460:HOH:O	2.20	0.41
1:B:153:ARG:HD3	1:B:157:ASP:O	2.21	0.40

There are no symmetry-related clashes.

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	255/266 (96%)	240 (94%)	9 (4%)	6 (2%)	7	11
1	B	253/266 (95%)	238 (94%)	9 (4%)	6 (2%)	7	11
All	All	508/532 (96%)	478 (94%)	18 (4%)	12 (2%)	7	11

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	173	ASN
1	A	240	SER
1	A	254	PRO
1	B	240	SER
1	B	254	PRO
1	A	168	GLU
1	B	172	VAL
1	B	173	ASN
1	B	290	LEU
1	A	167	PRO
1	A	103	VAL
1	B	103	VAL

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	217/225 (96%)	201 (93%)	16 (7%)	17	31
1	B	215/225 (96%)	203 (94%)	12 (6%)	26	47
All	All	432/450 (96%)	404 (94%)	28 (6%)	21	39

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	ASP
1	A	32	ASP
1	A	35	LYS
1	A	56	THR
1	A	83	GLN
1	A	113	VAL
1	A	130	SER
1	A	155	ILE
1	A	161	ASN
1	A	164	ARG
1	A	172	VAL
1	A	178	GLN

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Mol	Chain	Res	Type
1	A	233	ASP
1	A	255	LYS
1	A	273	LYS
1	A	288	LYS
1	B	44	LEU
1	B	68	PHE
1	B	88	ILE
1	B	109	THR
1	B	130	SER
1	B	158	GLU
1	B	159	VAL
1	B	164	ARG
1	B	168	GLU
1	B	195	LEU
1	B	233	ASP
1	B	260	VAL

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

Mol	Chain	Res	Type
1	A	54	ASN
1	A	83	GLN
1	A	93	GLN
1	A	141	GLN
1	B	54	ASN
1	B	82	GLN
1	B	112	HIS
1	B	141	GLN
1	B	161	ASN
1	B	173	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	BB0	A	2	-	17,17,17	0.90	0	23,24,24	0.73	0
2	BB0	B	2	-	17,17,17	1.29	3 (17%)	23,24,24	1.49	4 (17%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BB0	A	2	-	-	0/8/8/8	0/2/2/2
2	BB0	B	2	-	-	0/8/8/8	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	BB0	CAP-CAK	-2.39	1.36	1.41
2	B	2	BB0	CAI-CAJ	-2.17	1.36	1.41
2	B	2	BB0	CAL-CAK	-2.09	1.37	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	BB0	CAO-CAN-NAB	-4.04	115.87	121.64
2	B	2	BB0	CAP-CAK-CAL	-2.69	117.45	122.08
2	B	2	BB0	OAU-CAF-CAS	2.04	125.02	120.13
2	B	2	BB0	CAL-CAK-CAJ	2.76	122.69	118.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2	BB0	3	0
2	B	2	BB0	3	0

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	257/266 (96%)	-0.24	11 (4%) 39 44	5, 14, 35, 51	0
1	B	255/266 (95%)	-0.22	11 (4%) 39 44	5, 15, 38, 58	0
All	All	512/532 (96%)	-0.23	22 (4%) 39 44	5, 15, 35, 58	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	291	ASN	5.1
1	B	172	VAL	5.0
1	A	172	VAL	5.0
1	B	169	LEU	4.8
1	A	173	ASN	4.5
1	B	174	PRO	4.2
1	B	170	ASN	3.9
1	A	171	GLU	3.9
1	A	170	ASN	3.7
1	A	31	ASP	3.4
1	B	175	GLY	2.9
1	B	254	PRO	2.9
1	A	55	ARG	2.9
1	B	171	GLU	2.8
1	A	30	LYS	2.4
1	A	176	GLU	2.4
1	B	166	CYS	2.3
1	B	167	PRO	2.1
1	A	174	PRO	2.1
1	A	83	GLN	2.0
1	A	167	PRO	2.0
1	B	257	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 carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	BB0	A	2	16/16	0.83	0.25	1.85	40,42,44,45	0
2	BB0	B	2	16/16	0.71	0.33	1.26	84,84,84,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.