



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:37 PM GMT

PDB ID : 3UDI
Title : Crystal structure of Acinetobacter baumannii PBP1a in complex with penicillin G
Authors : Han, S.
Deposited on : 2011-10-28
Resolution : 2.60 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

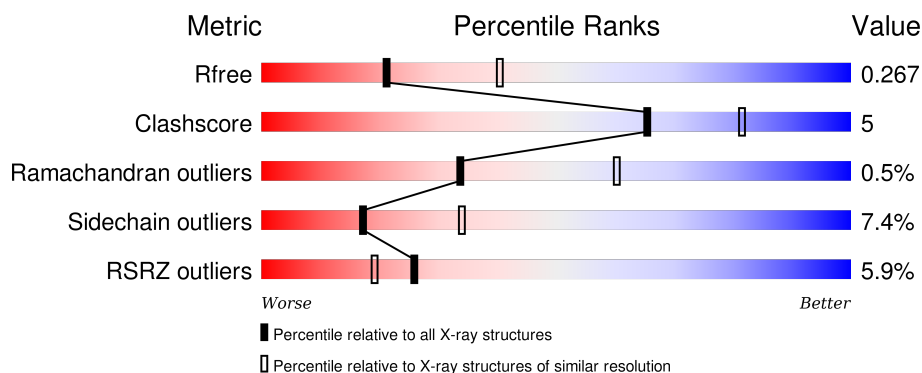
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


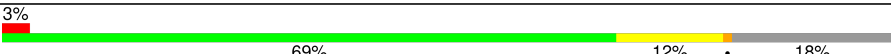
The reported resolution of this entry is 2.60 Å.

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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	731	
1	B	731	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9726 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 Penicillin-binding protein 1a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	600	Total	C	N	O	S	0	0	0
			4723	3010	834	863	16			
1	B	601	Total	C	N	O	S	0	0	0
			4734	3014	837	867	16			

There are 32 discrepancies between the modelled and reference sequences:

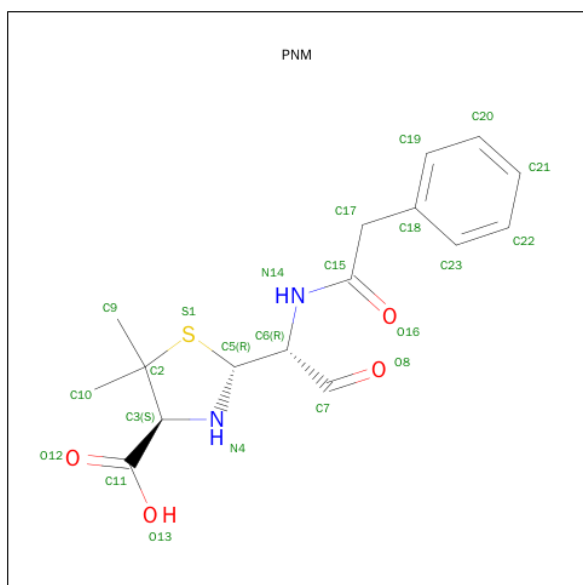
Chain	Residue	Modelled	Actual	Comment	Reference
A	9	MET	-	EXPRESSION TAG	UNP G1C794
A	10	HIS	-	EXPRESSION TAG	UNP G1C794
A	11	HIS	-	EXPRESSION TAG	UNP G1C794
A	12	HIS	-	EXPRESSION TAG	UNP G1C794
A	13	HIS	-	EXPRESSION TAG	UNP G1C794
A	14	HIS	-	EXPRESSION TAG	UNP G1C794
A	15	HIS	-	EXPRESSION TAG	UNP G1C794
A	16	GLU	-	EXPRESSION TAG	UNP G1C794
A	17	ASN	-	EXPRESSION TAG	UNP G1C794
A	18	LEU	-	EXPRESSION TAG	UNP G1C794
A	19	TYR	-	EXPRESSION TAG	UNP G1C794
A	20	PHE	-	EXPRESSION TAG	UNP G1C794
A	21	GLN	-	EXPRESSION TAG	UNP G1C794
A	22	SER	-	EXPRESSION TAG	UNP G1C794
A	23	HIS	-	EXPRESSION TAG	UNP G1C794
A	24	MET	-	EXPRESSION TAG	UNP G1C794
B	9	MET	-	EXPRESSION TAG	UNP G1C794
B	10	HIS	-	EXPRESSION TAG	UNP G1C794
B	11	HIS	-	EXPRESSION TAG	UNP G1C794
B	12	HIS	-	EXPRESSION TAG	UNP G1C794
B	13	HIS	-	EXPRESSION TAG	UNP G1C794
B	14	HIS	-	EXPRESSION TAG	UNP G1C794
B	15	HIS	-	EXPRESSION TAG	UNP G1C794
B	16	GLU	-	EXPRESSION TAG	UNP G1C794
B	17	ASN	-	EXPRESSION TAG	UNP G1C794

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Chain	Residue	Modelled	Actual	Comment	Reference
B	18	LEU	-	EXPRESSION TAG	UNP G1C794
B	19	TYR	-	EXPRESSION TAG	UNP G1C794
B	20	PHE	-	EXPRESSION TAG	UNP G1C794
B	21	GLN	-	EXPRESSION TAG	UNP G1C794
B	22	SER	-	EXPRESSION TAG	UNP G1C794
B	23	HIS	-	EXPRESSION TAG	UNP G1C794
B	24	MET	-	EXPRESSION TAG	UNP G1C794

- Molecule 2 is OPEN FORM - PENICILLIN G (three-letter code: PNM) (formula: $C_{16}H_{20}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			23	16	2	4	1		
2	B	1	Total	C	N	O	S	0	0
			23	16	2	4	1		

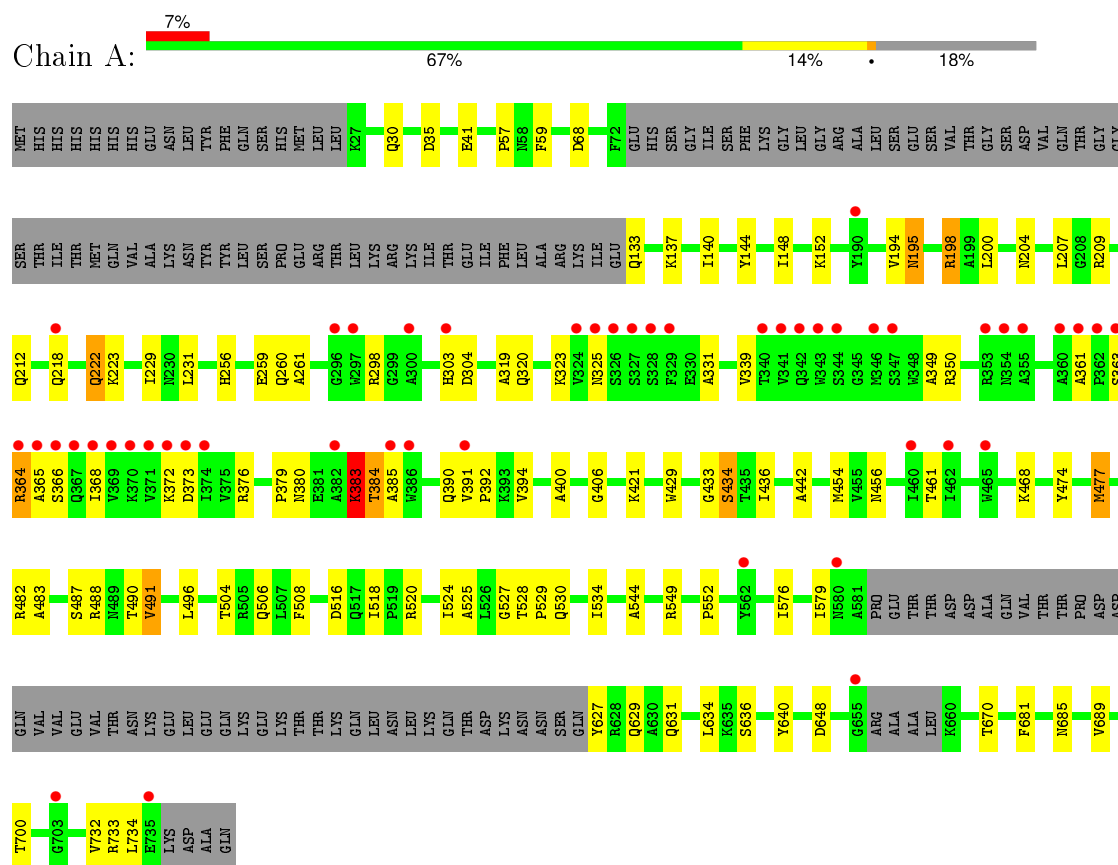
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	77	Total	O	0	0
			77	77		
3	B	146	Total	O	0	0
			146	146		

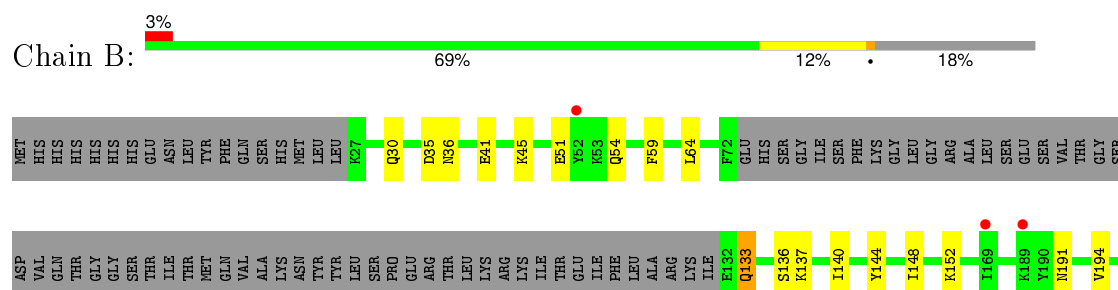
3 Residue-property plots

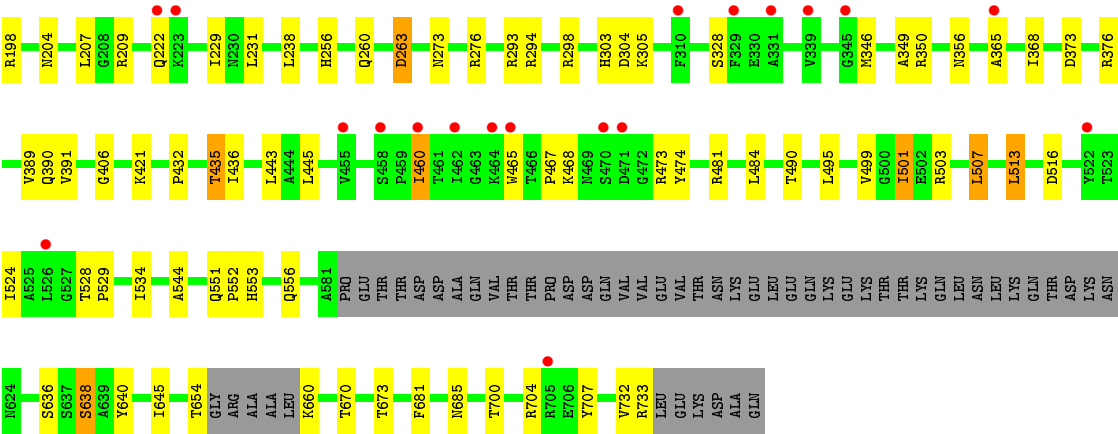
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($RSRZ > 2$). 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: Penicillin-binding protein 1a



• Molecule 1: Penicillin-binding protein 1a





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	119.00 Å 242.68 Å 49.05 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.08 – 2.60 48.08 – 2.60	Depositor EDS
% Data completeness (in resolution range)	91.7 (48.08-2.60) 91.5 (48.08-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.61 Å)	Xtriage
Refinement program	BUSTER 2.9.6	Depositor
R, R_{free}	0.187 , 0.250 0.201 , 0.267	Depositor DCC
R_{free} test set	2060 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	52.2	Xtriage
Anisotropy	0.544	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 75.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	2 of 41143 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9726	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% 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, 0.375 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: PNM

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	0.50	0/4832	0.72	0/6552
1	B	0.52	0/4843	0.73	0/6567
All	All	0.51	0/9675	0.72	0/13119

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

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	4723	0	4707	53	0
1	B	4734	0	4712	47	0
2	A	23	0	18	1	0
2	B	23	0	18	3	0
3	A	77	0	0	1	0
3	B	146	0	0	1	0
All	All	9726	0	9455	95	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 5.

All (95) 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:298:ARG:H	1:A:390:GLN:HE22	1.19	0.90
1:B:298:ARG:H	1:B:390:GLN:HE22	1.17	0.89
1:A:323:LYS:HE3	1:A:325:ASN:HD21	1.53	0.73
1:A:350:ARG:HG2	1:A:361:ALA:HA	1.79	0.64
1:B:707:TYR:HE1	2:B:999:PNM:H21	1.62	0.64
1:A:436:ILE:HG12	1:A:508:PHE:HZ	1.63	0.63
1:A:137:LYS:NZ	1:B:256:HIS:HD2	1.96	0.63
1:A:488:ARG:HB2	1:A:491:VAL:HG12	1.81	0.62
1:A:488:ARG:HB2	1:A:491:VAL:CG1	2.30	0.62
1:A:303:HIS:HD2	1:A:373:ASP:OD1	1.83	0.61
1:B:528:THR:N	1:B:529:PRO:HD2	2.15	0.61
1:B:303:HIS:HD2	1:B:373:ASP:OD1	1.83	0.60
1:A:229:ILE:HG22	1:A:231:LEU:HG	1.84	0.59
1:A:436:ILE:HG12	1:A:508:PHE:CZ	2.37	0.59
1:B:707:TYR:CE1	2:B:999:PNM:H21	2.38	0.58
1:B:229:ILE:HG22	1:B:231:LEU:HG	1.84	0.57
1:A:57:PRO:HD2	3:A:759:HOH:O	2.04	0.57
1:B:406:GLY:O	1:B:552:PRO:HA	2.05	0.57
1:A:524:ILE:HG22	1:A:529:PRO:HG3	1.87	0.56
1:A:218:GLN:O	1:A:222:GLN:HG2	2.06	0.56
1:B:551:GLN:O	1:B:553:HIS:HD2	1.89	0.56
1:A:406:GLY:O	1:A:552:PRO:HA	2.08	0.54
1:A:209:ARG:NH2	1:A:212:GLN:HE22	2.06	0.54
1:A:483:ALA:HB1	1:A:491:VAL:HG11	1.89	0.53
1:B:524:ILE:HG22	1:B:529:PRO:HD3	1.92	0.52
1:A:496:LEU:HD22	1:A:525:ALA:HB2	1.93	0.51
1:B:294:ARG:HA	1:B:350:ARG:HH22	1.75	0.51
1:B:654:THR:HG21	1:B:660:LYS:N	2.27	0.50
1:A:376:ARG:HD2	1:A:391:VAL:HG23	1.94	0.50
1:A:195:ASN:HD21	1:A:198:ARG:HD2	1.77	0.49
1:B:229:ILE:HG21	1:B:231:LEU:CD1	2.42	0.49
1:A:229:ILE:HG21	1:A:231:LEU:HD11	1.94	0.48
1:A:487:SER:HB2	2:A:998:PNM:HC5	1.93	0.48
1:A:670:THR:HG22	1:A:681:PHE:HD1	1.79	0.48
1:A:229:ILE:HG21	1:A:231:LEU:CD1	2.44	0.48
1:A:504:THR:O	1:A:508:PHE:HD1	1.97	0.48
1:B:376:ARG:HD2	1:B:391:VAL:HG23	1.97	0.47
1:A:433:GLY:O	1:A:527:GLY:HA3	2.15	0.47
1:B:229:ILE:HG21	1:B:231:LEU:HD12	1.97	0.46
1:B:673:THR:O	2:B:999:PNM:H19	2.15	0.46
1:B:356:ASN:HD21	1:B:704:ARG:H	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:670:THR:HG22	1:B:681:PHE:HD1	1.80	0.45
1:B:191:ASN:HB3	1:B:194:VAL:HB	1.96	0.45
1:A:454:MET:HB3	1:A:477:MET:HG3	1.98	0.45
1:B:551:GLN:O	1:B:553:HIS:CD2	2.69	0.45
1:B:293:ARG:HH12	1:B:389:VAL:HG12	1.82	0.45
1:A:365:ALA:HA	1:A:368:ILE:HD12	1.99	0.45
1:B:484:LEU:HD23	1:B:645:ILE:HG21	1.98	0.45
1:B:495:LEU:O	1:B:499:VAL:HG22	2.17	0.44
1:B:365:ALA:HA	1:B:368:ILE:HD12	1.99	0.44
1:A:528:THR:N	1:A:529:PRO:HD2	2.32	0.44
1:A:195:ASN:ND2	1:A:198:ARG:HD2	2.33	0.44
1:A:30:GLN:HG2	1:A:41:GLU:HG2	2.00	0.44
1:A:204:ASN:HA	1:A:207:LEU:HD12	2.00	0.44
1:B:474:TYR:HE1	1:B:490:THR:HG21	1.83	0.44
1:B:432:PRO:O	1:B:435:THR:HB	2.18	0.44
1:B:443:LEU:HB2	1:B:507:LEU:HD22	2.00	0.43
1:A:474:TYR:HE1	1:A:490:THR:HG21	1.83	0.43
1:A:640:TYR:CD1	1:A:732:VAL:HG23	2.53	0.43
1:A:544:ALA:HA	1:A:732:VAL:HG12	1.99	0.43
1:A:261:ALA:HA	1:B:144:TYR:CE1	2.54	0.43
1:B:465:TRP:CZ2	1:B:467:PRO:HB3	2.54	0.42
1:A:640:TYR:CD1	1:A:734:LEU:HB2	2.54	0.42
1:A:380:ASN:HD21	1:A:385:ALA:HB3	1.84	0.42
1:B:501:ILE:HG13	1:B:501:ILE:H	1.57	0.42
1:B:273:ASN:HB3	1:B:276:ARG:HB2	2.01	0.42
1:B:544:ALA:HA	1:B:732:VAL:HG12	2.01	0.42
1:B:640:TYR:CD1	1:B:732:VAL:HG23	2.54	0.42
1:A:392:PRO:HB3	1:A:394:VAL:HG12	2.00	0.42
1:A:137:LYS:HZ1	1:B:256:HIS:HD2	1.66	0.42
1:A:442:ALA:HB1	1:A:634:LEU:HD21	2.01	0.42
1:B:51:GLU:HB2	1:B:54:GLN:HG3	2.02	0.42
1:A:319:ALA:HB1	1:A:331:ALA:HB1	2.01	0.42
1:B:707:TYR:HB3	3:B:881:HOH:O	2.18	0.42
1:B:460:ILE:HG22	1:B:490:THR:HG22	2.02	0.42
1:A:364:ARG:HE	1:A:366:SER:HG	1.68	0.42
1:A:144:TYR:O	1:A:148:ILE:HG13	2.20	0.41
1:A:576:ILE:HD11	1:A:629:GLN:HB2	2.02	0.41
1:B:445:LEU:HB3	1:B:638:SER:HB3	2.01	0.41
1:B:204:ASN:HA	1:B:207:LEU:HD12	2.01	0.41
1:A:229:ILE:CG2	1:A:231:LEU:CD1	2.98	0.41
1:A:434:SER:OG	1:A:487:SER:HB3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:ASN:ND2	1:B:704:ARG:H	2.18	0.41
1:A:256:HIS:HD2	1:B:137:LYS:NZ	2.18	0.41
1:B:144:TYR:O	1:B:148:ILE:HG13	2.20	0.41
1:A:429:TRP:HB3	1:A:530:GLN:HB3	2.02	0.41
1:B:30:GLN:HG2	1:B:41:GLU:HG2	2.03	0.41
1:A:400:ALA:HA	1:A:689:VAL:O	2.20	0.41
1:A:320:GLN:HE21	1:A:372:LYS:HG2	1.86	0.41
1:B:328:SER:HA	1:B:346:MET:HE1	2.03	0.41
1:A:383:LYS:HB3	1:A:384:THR:H	1.66	0.41
1:B:45:LYS:H	1:B:263:ASP:HB3	1.86	0.41
1:B:436:ILE:HD11	1:B:513:LEU:HD21	2.02	0.41
1:A:549:ARG:HH22	1:B:133:GLN:HE22	1.68	0.40
1:A:488:ARG:O	1:A:491:VAL:HG13	2.22	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	592/731 (81%)	557 (94%)	30 (5%)	5 (1%)	24	46
1	B	593/731 (81%)	560 (94%)	32 (5%)	1 (0%)	52	77
All	All	1185/1462 (81%)	1117 (94%)	62 (5%)	6 (0%)	34	60

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	383	LYS
1	A	349	ALA
1	B	349	ALA
1	A	384	THR
1	A	379	PRO

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Mol	Chain	Res	Type
1	A	579	ILE

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	490/608 (81%)	451 (92%)	39 (8%)	15	29
1	B	492/608 (81%)	458 (93%)	34 (7%)	19	38
All	All	982/1216 (81%)	909 (93%)	73 (7%)	17	34

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	ASP
1	A	59	PHE
1	A	68	ASP
1	A	133	GLN
1	A	140	ILE
1	A	152	LYS
1	A	194	VAL
1	A	195	ASN
1	A	198	ARG
1	A	200	LEU
1	A	222	GLN
1	A	223	LYS
1	A	259	GLU
1	A	260	GLN
1	A	304	ASP
1	A	339	VAL
1	A	363	SER
1	A	364	ARG
1	A	383	LYS
1	A	421	LYS
1	A	434	SER
1	A	456	ASN

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Mol	Chain	Res	Type
1	A	461	THR
1	A	468	LYS
1	A	477	MET
1	A	482	ARG
1	A	491	VAL
1	A	506	GLN
1	A	516	ASP
1	A	518	ILE
1	A	520	ARG
1	A	534	ILE
1	A	627	TYR
1	A	631	GLN
1	A	636	SER
1	A	648	ASP
1	A	685	ASN
1	A	700	THR
1	A	733	ARG
1	B	35	ASP
1	B	36	ASN
1	B	59	PHE
1	B	64	LEU
1	B	133	GLN
1	B	136	SER
1	B	140	ILE
1	B	152	LYS
1	B	198	ARG
1	B	209	ARG
1	B	222	GLN
1	B	238	LEU
1	B	260	GLN
1	B	263	ASP
1	B	304	ASP
1	B	305	LYS
1	B	421	LYS
1	B	435	THR
1	B	460	ILE
1	B	468	LYS
1	B	473	ARG
1	B	481	ARG
1	B	501	ILE
1	B	503	ARG
1	B	507	LEU

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Mol	Chain	Res	Type
1	B	513	LEU
1	B	516	ASP
1	B	534	ILE
1	B	556	GLN
1	B	636	SER
1	B	638	SER
1	B	685	ASN
1	B	700	THR
1	B	733	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	A	170	ASN
1	A	195	ASN
1	A	212	GLN
1	A	222	GLN
1	A	256	HIS
1	A	303	HIS
1	A	325	ASN
1	A	390	GLN
1	A	456	ASN
1	A	551	GLN
1	A	629	GLN
1	A	725	GLN
1	B	170	ASN
1	B	195	ASN
1	B	222	GLN
1	B	256	HIS
1	B	303	HIS
1	B	325	ASN
1	B	356	ASN
1	B	390	GLN
1	B	456	ASN
1	B	553	HIS
1	B	629	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 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	PNM	A	998	1	17,24,24	0.77	1 (5%)	21,34,34	1.16	1 (4%)
2	PNM	B	999	1	17,24,24	0.76	1 (5%)	21,34,34	1.27	4 (19%)

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	PNM	A	998	1	-	0/8/33/33	0/2/2/2
2	PNM	B	999	1	-	0/8/33/33	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	998	PNM	C6-N14	2.15	1.48	1.46
2	B	999	PNM	C6-N14	2.22	1.48	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	999	PNM	C3-C2-S1	-2.62	99.41	103.96
2	B	999	PNM	O8-C7-C6	-2.07	119.38	125.74
2	B	999	PNM	C2-S1-C5	2.33	99.00	93.98
2	B	999	PNM	C17-C15-N14	2.70	120.30	115.96
2	A	998	PNM	C17-C15-N14	2.90	120.61	115.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	998	PNM	1	0
2	B	999	PNM	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	600/731 (82%)	0.39	49 (8%)	14 10	43, 77, 129, 165	0
1	B	601/731 (82%)	0.18	22 (3%)	45 37	26, 66, 113, 141	0
All	All	1201/1462 (82%)	0.29	71 (5%)	26 19	26, 73, 122, 165	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	327	SER	8.3
1	A	369	VAL	6.8
1	A	328	SER	6.4
1	A	362	PRO	6.1
1	A	326	SER	6.0
1	A	324	VAL	5.9
1	A	382	ALA	5.9
1	A	329	PHE	5.3
1	A	343	TRP	5.1
1	A	370	LYS	5.0
1	A	363	SER	4.9
1	A	368	ILE	4.8
1	A	361	ALA	4.8
1	A	325	ASN	4.5
1	A	371	VAL	4.4
1	A	347	SER	4.4
1	A	364	ARG	4.3
1	A	703	GLY	4.3
1	A	355	ALA	4.2
1	A	341	VAL	4.0
1	A	367	GLN	3.8
1	A	386	TRP	3.7
1	A	297	TRP	3.7
1	A	296	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	52	TYR	3.6
1	A	340	THR	3.6
1	A	300	ALA	3.6
1	A	462	ILE	3.5
1	A	353	ARG	3.2
1	A	360	ALA	3.2
1	A	562	TYR	3.1
1	B	310	PHE	3.1
1	B	331	ALA	3.1
1	A	190	TYR	3.1
1	A	460	ILE	3.0
1	B	470	SER	3.0
1	A	372	LYS	2.9
1	A	366	SER	2.9
1	B	455	VAL	2.8
1	A	385	ALA	2.8
1	B	329	PHE	2.8
1	A	354	ASN	2.8
1	A	303	HIS	2.8
1	A	374	ILE	2.7
1	B	462	ILE	2.7
1	A	346	MET	2.6
1	A	342	GLN	2.6
1	A	365	ALA	2.4
1	B	458	SER	2.4
1	A	465	TRP	2.4
1	B	471	ASP	2.4
1	B	464	LYS	2.4
1	A	373	ASP	2.4
1	A	391	VAL	2.4
1	B	189	LYS	2.4
1	A	580	ASN	2.3
1	A	735	GLU	2.3
1	B	223	LYS	2.3
1	B	522	TYR	2.3
1	B	365	ALA	2.3
1	B	465	TRP	2.3
1	B	345	GLY	2.2
1	B	526	LEU	2.1
1	B	339	VAL	2.1
1	B	169	ILE	2.1
1	B	705	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	218	GLN	2.1
1	B	460	ILE	2.0
1	A	655	GLY	2.0
1	B	222	GLN	2.0
1	A	344	SER	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(Å ²)	Q<0.9
2	PNM	A	998	23/23	0.84	0.25	1.78	97,100,101,101	0
2	PNM	B	999	23/23	0.89	0.20	0.31	55,74,78,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.