



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 01:47 PM UTC

PDB ID : 3UDX / pdb_00003udx
Title : Crystal structure of Acinetobacter baumannii PBP1a in complex with Imipenem
Authors : Han, S.
Deposited on : 2011-10-28
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

<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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

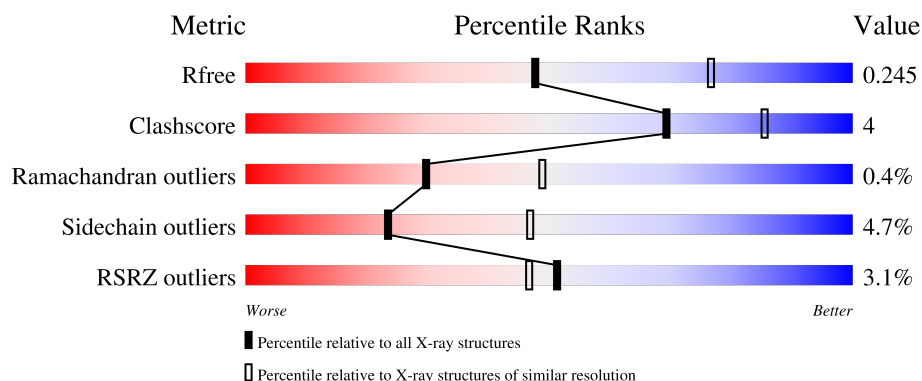
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (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 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	731	
1	B	731	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9771 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	598	Total	C	N	O	S	0	0	0
			4715	3006	832	861	16			
1	B	595	Total	C	N	O	S	0	1	0
			4691	2990	829	856	16			

There are 32 discrepancies between the modelled and reference sequences:

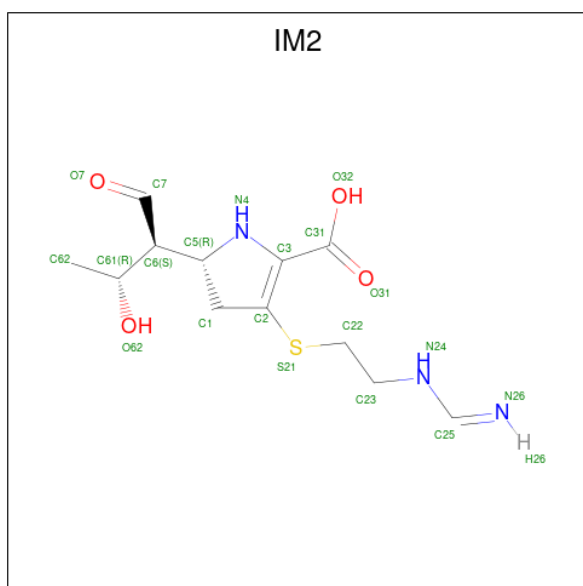
Chain	Residue	Modelled	Actual	Comment	Reference
A	9	MET	-	expression tag	UNP G1C794
A	10	HIS	-	expression tag	UNP G1C794
A	11	HIS	-	expression tag	UNP G1C794
A	12	HIS	-	expression tag	UNP G1C794
A	13	HIS	-	expression tag	UNP G1C794
A	14	HIS	-	expression tag	UNP G1C794
A	15	HIS	-	expression tag	UNP G1C794
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 (5R)-5-[(1S,2R)-1-formyl-2-hydroxypropyl]-3-[(2-{[(E)-iminomethyl]amino}ethyl)sulfanyl]-4,5-dihydro-1H-pyrrole-2-carboxylic acid (CCD ID: IM2) (formula: C₁₂H₁₉N₃O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			20	12	3	4	1		
2	B	1	Total	C	N	O	S	0	0
			20	12	3	4	1		

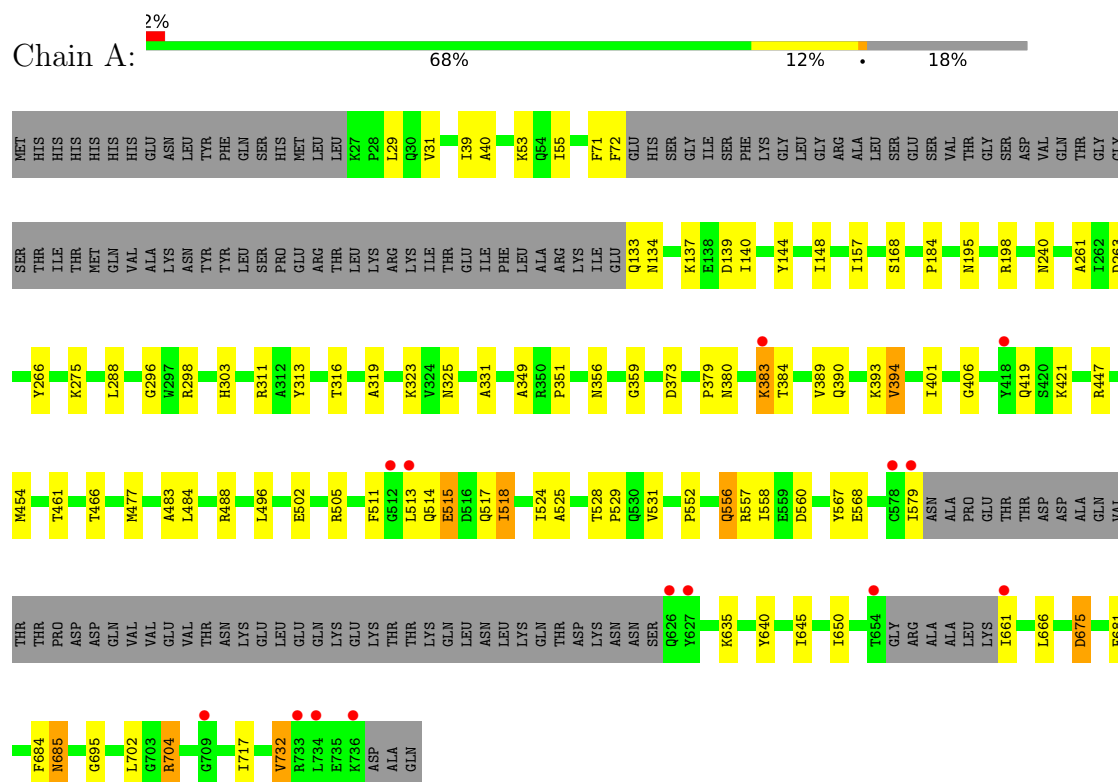
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	133	Total	O	0	0
			133	133		
3	B	192	Total	O	0	0
			192	192		

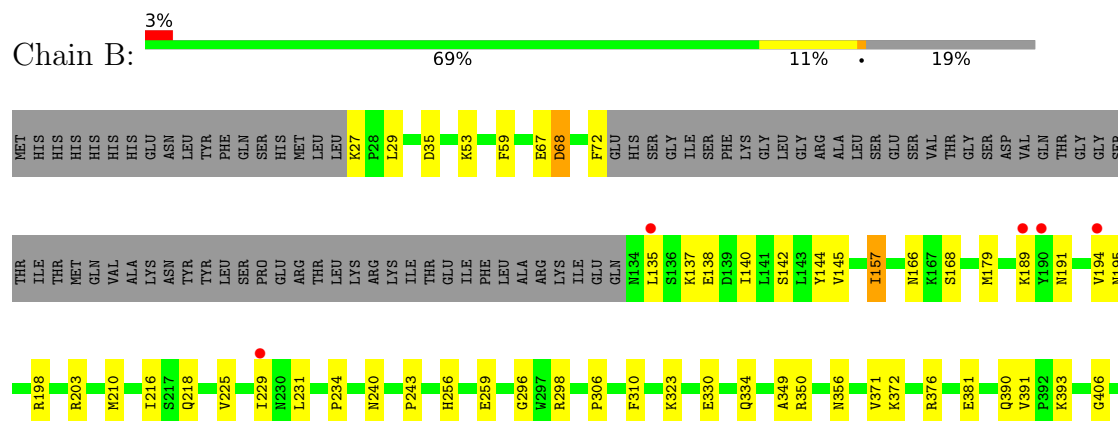
3 Residue-property plots [i](#)

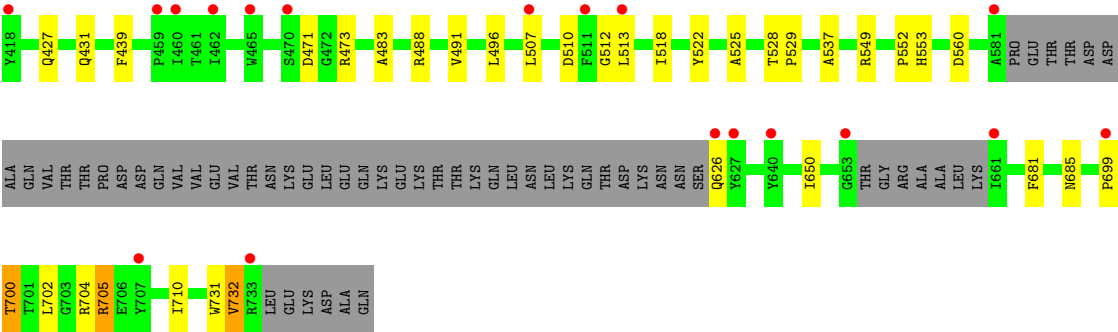
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Penicillin-binding protein 1a



• Molecule 1: Penicillin-binding protein 1a





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	119.27Å 242.93Å 49.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.02 – 2.50 48.02 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.1 (48.02-2.50) 93.5 (48.02-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.9.6	Depositor
R, R_{free}	0.187 , 0.238 0.188 , 0.245	Depositor DCC
R_{free} test set	2376 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	43.8	Xtriage
Anisotropy	0.343	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 66.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9771	wwPDB-VP
Average B, all atoms (Å ²)	54.0	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, 0.333 respectively for untwinned datasets, and 0.375, 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: IM2

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	0.82	0/4824	1.31	22/6541 (0.3%)
1	B	0.87	0/4803	1.33	28/6514 (0.4%)
All	All	0.85	0/9627	1.32	50/13055 (0.4%)

There are no bond length outliers.

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	685	ASN	CA-CB-CG	7.43	120.03	112.60
1	A	666	LEU	CA-C-N	7.36	127.28	121.61
1	A	666	LEU	C-N-CA	7.36	127.28	121.61
1	B	525	ALA	N-CA-C	-6.81	105.01	113.38
1	A	685	ASN	N-CA-C	-6.70	99.41	108.86
1	A	157	ILE	N-CA-C	6.54	117.23	110.36
1	B	702	LEU	N-CA-C	-6.52	105.15	113.23
1	B	296	GLY	N-CA-C	6.24	119.88	112.33
1	B	700	THR	N-CA-C	-6.20	99.89	109.24
1	A	560	ASP	CA-CB-CG	6.02	118.62	112.60
1	A	524	ILE	CA-C-N	5.99	128.90	120.28
1	A	524	ILE	C-N-CA	5.99	128.90	120.28
1	B	157	ILE	N-CA-C	5.90	116.09	110.42
1	B	699	PRO	CA-C-N	5.82	131.64	122.21
1	B	699	PRO	C-N-CA	5.82	131.64	122.21
1	A	685	ASN	CA-CB-CG	5.78	118.38	112.60
1	A	675	ASP	CA-CB-CG	5.77	118.37	112.60
1	B	393	LYS	N-CA-C	-5.75	106.42	113.50
1	A	502	GLU	N-CA-C	5.75	117.55	111.28
1	B	512	GLY	CA-C-N	5.74	128.99	120.90
1	B	512	GLY	C-N-CA	5.74	128.99	120.90
1	A	55	ILE	N-CA-C	5.72	113.55	108.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	137	LYS	CA-C-N	5.70	128.23	120.54
1	B	137	LYS	C-N-CA	5.70	128.23	120.54
1	A	393	LYS	N-CA-C	-5.65	105.11	112.23
1	A	296	GLY	N-CA-C	5.63	119.78	112.68
1	B	439	PHE	CA-CB-CG	5.55	119.35	113.80
1	B	67	GLU	CA-C-N	5.54	128.01	120.54
1	B	67	GLU	C-N-CA	5.54	128.01	120.54
1	B	537	ALA	CA-C-N	5.40	127.47	120.44
1	B	537	ALA	C-N-CA	5.40	127.47	120.44
1	B	259	GLU	N-CA-C	5.38	117.90	111.71
1	A	515	GLU	CA-C-N	5.38	128.02	120.28
1	A	515	GLU	C-N-CA	5.38	128.02	120.28
1	B	306	PRO	CA-C-N	5.36	128.21	120.38
1	B	306	PRO	C-N-CA	5.36	128.21	120.38
1	A	684	PHE	CA-C-N	5.36	131.16	122.53
1	A	684	PHE	C-N-CA	5.36	131.16	122.53
1	B	681	PHE	CA-CB-CG	-5.34	108.46	113.80
1	A	134	ASN	CA-C-N	5.27	129.57	121.19
1	A	134	ASN	C-N-CA	5.27	129.57	121.19
1	B	68	ASP	CA-CB-CG	5.27	117.87	112.60
1	B	243	PRO	N-CA-C	5.26	121.59	113.75
1	A	168	SER	N-CA-C	-5.24	102.30	110.42
1	A	511	PHE	CA-CB-CG	5.21	119.01	113.80
1	A	681	PHE	CA-CB-CG	-5.20	108.60	113.80
1	B	513	LEU	N-CA-C	5.12	117.45	110.24
1	B	168	SER	N-CA-C	-5.08	103.00	110.52
1	B	560	ASP	CA-CB-CG	5.02	117.62	112.60
1	B	350	ARG	N-CA-C	-5.00	103.29	109.64

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	4715	0	4701	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	4691	0	4673	33	0
2	A	20	0	16	0	0
2	B	20	0	16	0	0
3	A	133	0	0	0	0
3	B	192	0	0	0	0
All	All	9771	0	9406	66	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 4.

All (66) 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:298:ARG:H	1:B:390:GLN:HE22	1.17	0.88
1:A:298:ARG:H	1:A:390:GLN:HE22	1.23	0.83
1:B:356:ASN:HD21	1:B:704:ARG:H	1.38	0.71
1:A:323:LYS:HE3	1:A:325:ASN:HD21	1.58	0.68
1:A:505:ARG:HH22	1:A:515:GLU:HG3	1.58	0.68
1:A:513:LEU:HB3	1:A:518:ILE:HD11	1.79	0.65
1:B:406:GLY:O	1:B:552:PRO:HA	1.97	0.64
1:B:704:ARG:O	1:B:705:ARG:HB2	1.96	0.64
1:B:528:THR:N	1:B:529:PRO:HD2	2.13	0.63
1:B:356:ASN:ND2	1:B:704:ARG:HG2	2.18	0.59
1:A:288:LEU:HD22	1:A:394:VAL:HG13	1.85	0.59
1:B:179:MET:HE2	1:B:203:ARG:HD3	1.83	0.58
1:A:556:GLN:HE21	1:A:557:ARG:HH11	1.50	0.58
1:B:376:ARG:HD2	1:B:391:VAL:HG23	1.86	0.57
1:B:471:ASP:HB2	1:B:473:ARG:HH11	1.71	0.56
1:A:496:LEU:HD22	1:A:525:ALA:HB2	1.87	0.56
1:A:71:PHE:O	1:B:553:HIS:HA	2.08	0.54
1:A:695:GLY:HA2	1:A:702:LEU:HD21	1.90	0.53
1:A:661:ILE:HD11	1:A:717:ILE:HA	1.92	0.52
1:A:351:PRO:HG2	1:A:359:GLY:HA3	1.92	0.52
1:B:431:GLN:HG2	1:B:528:THR:O	2.10	0.51
1:A:31:VAL:HB	1:A:40:ALA:HB3	1.93	0.51
1:A:261:ALA:HA	1:B:144:TYR:CE1	2.45	0.50
1:A:528:THR:N	1:A:529:PRO:HD2	2.26	0.50
1:B:528:THR:H	1:B:529:PRO:HD2	1.75	0.49
1:A:513:LEU:HD21	1:A:531:VAL:HG12	1.93	0.49
1:A:461:THR:HG22	1:A:466:THR:OG1	2.12	0.49
1:A:313:TYR:CE1	1:A:419:GLN:HB2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:510:ASP:O	1:B:549:ARG:HD3	2.13	0.48
1:B:473:ARG:O	1:B:488:ARG:NH2	2.46	0.48
1:A:148:ILE:HG21	1:A:184:PRO:HB3	1.94	0.47
1:A:514:GLN:HB2	1:A:517:GLN:HG2	1.96	0.47
1:A:640:TYR:HD1	1:A:732:VAL:HG23	1.81	0.46
1:B:72:PHE:HB3	1:B:140:ILE:HD12	1.96	0.46
1:B:298:ARG:H	1:B:390:GLN:NE2	1.99	0.46
1:A:298:ARG:H	1:A:390:GLN:NE2	2.03	0.46
1:A:137:LYS:NZ	1:B:256:HIS:HD2	2.14	0.46
1:A:558:ILE:HB	1:A:567:TYR:HB3	1.98	0.46
1:B:229:ILE:HD12	1:B:231:LEU:H	1.80	0.45
1:A:144:TYR:O	1:A:148:ILE:HG13	2.18	0.44
1:A:29:LEU:HD22	1:A:266:TYR:O	2.18	0.44
1:A:406:GLY:O	1:A:552:PRO:HA	2.18	0.44
1:B:528:THR:N	1:B:529:PRO:CD	2.81	0.43
1:B:371:VAL:O	1:B:372:LYS:HB2	2.17	0.43
1:B:731:TRP:CG	1:B:732:VAL:H	2.36	0.43
1:A:454:MET:HB3	1:A:477:MET:HE3	2.00	0.43
1:B:310:PHE:O	1:B:334:GLN:NE2	2.52	0.42
1:A:303:HIS:HD2	1:A:373:ASP:OD1	2.02	0.42
1:B:483:ALA:HB1	1:B:491:VAL:HG11	2.01	0.42
1:B:191:ASN:HB3	1:B:194:VAL:HG12	2.02	0.42
1:B:145:VAL:HG22	1:B:157:ILE:HG12	2.01	0.42
1:A:483:ALA:HA	1:A:488:ARG:HG2	2.01	0.42
1:B:356:ASN:HD21	1:B:704:ARG:N	2.12	0.42
1:B:704:ARG:O	1:B:705:ARG:CB	2.65	0.42
1:B:323:LYS:HB3	1:B:330:GLU:HB2	2.02	0.41
1:A:72:PHE:HB3	1:A:140:ILE:HD12	2.02	0.41
1:A:316:THR:HG22	1:A:389:VAL:HG21	2.02	0.41
1:A:484:LEU:HD23	1:A:645:ILE:HG21	2.01	0.41
1:A:383:LYS:HB3	1:A:384:THR:H	1.66	0.41
1:B:496:LEU:HD23	1:B:522:TYR:HD1	1.86	0.41
1:A:356:ASN:OD1	1:A:704:ARG:HB2	2.21	0.40
1:A:380:ASN:HB2	1:A:383:LYS:O	2.21	0.40
1:A:319:ALA:HB1	1:A:331:ALA:HB1	2.03	0.40
1:B:166:ASN:HB2	1:B:234:PRO:HD3	2.03	0.40
1:B:195:ASN:HB3	1:B:198:ARG:HB3	2.03	0.40
1:B:210:MET:HB3	1:B:216:ILE:HG12	2.03	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	590/731 (81%)	564 (96%)	23 (4%)	3 (0%)	24	43
1	B	588/731 (80%)	562 (96%)	24 (4%)	2 (0%)	36	55
All	All	1178/1462 (81%)	1126 (96%)	47 (4%)	5 (0%)	30	49

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	349	ALA
1	A	383	LYS
1	B	349	ALA
1	B	705	ARG
1	A	379	PRO

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%)	466 (95%)	24 (5%)	22	45
1	B	487/608 (80%)	465 (96%)	22 (4%)	24	49
All	All	977/1216 (80%)	931 (95%)	46 (5%)	23	47

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ILE

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Mol	Chain	Res	Type
1	A	53	LYS
1	A	133	GLN
1	A	139	ASP
1	A	195	ASN
1	A	198	ARG
1	A	240	ASN
1	A	263	ASP
1	A	275	LYS
1	A	311	ARG
1	A	394	VAL
1	A	401	ILE
1	A	421	LYS
1	A	447	ARG
1	A	518	ILE
1	A	556	GLN
1	A	568	GLU
1	A	579	ILE
1	A	635	LYS
1	A	650	ILE
1	A	675	ASP
1	A	685	ASN
1	A	704	ARG
1	A	732	VAL
1	B	27	LYS
1	B	29	LEU
1	B	35	ASP
1	B	53	LYS
1	B	59	PHE
1	B	68	ASP
1	B	135	LEU
1	B	138	GLU
1	B	142	SER
1	B	189	LYS
1	B	218	GLN
1	B	225	VAL
1	B	240	ASN
1	B	381	GLU
1	B	427	GLN
1	B	507	LEU
1	B	518	ILE
1	B	626	GLN
1	B	650	ILE

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Mol	Chain	Res	Type
1	B	700	THR
1	B	710	ILE
1	B	732	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	HIS
1	A	134	ASN
1	A	212	GLN
1	A	240	ASN
1	A	285	GLN
1	A	295	HIS
1	A	303	HIS
1	A	325	ASN
1	A	390	GLN
1	A	427	GLN
1	A	506	GLN
1	A	530	GLN
1	A	551	GLN
1	A	556	GLN
1	A	629	GLN
1	A	652	HIS
1	A	718	ASN
1	A	722	GLN
1	B	37	GLN
1	B	212	GLN
1	B	230	ASN
1	B	235	ASN
1	B	256	HIS
1	B	356	ASN
1	B	390	GLN
1	B	469	ASN
1	B	506	GLN
1	B	514	GLN
1	B	551	GLN
1	B	556	GLN
1	B	629	GLN
1	B	674	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 ⓘ

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	IM2	B	999	1	15,20,20	0.85	0	8,26,26	1.14	0
2	IM2	A	998	1	15,20,20	0.90	0	8,26,26	1.92	2 (25%)

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	IM2	B	999	1	-	7/18/32/32	0/1/1/1
2	IM2	A	998	1	-	5/18/32/32	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	998	IM2	O32-C31-C3	3.40	122.13	116.73
2	A	998	IM2	C3-C2-S21	2.71	128.19	124.37

There are no chirality outliers.

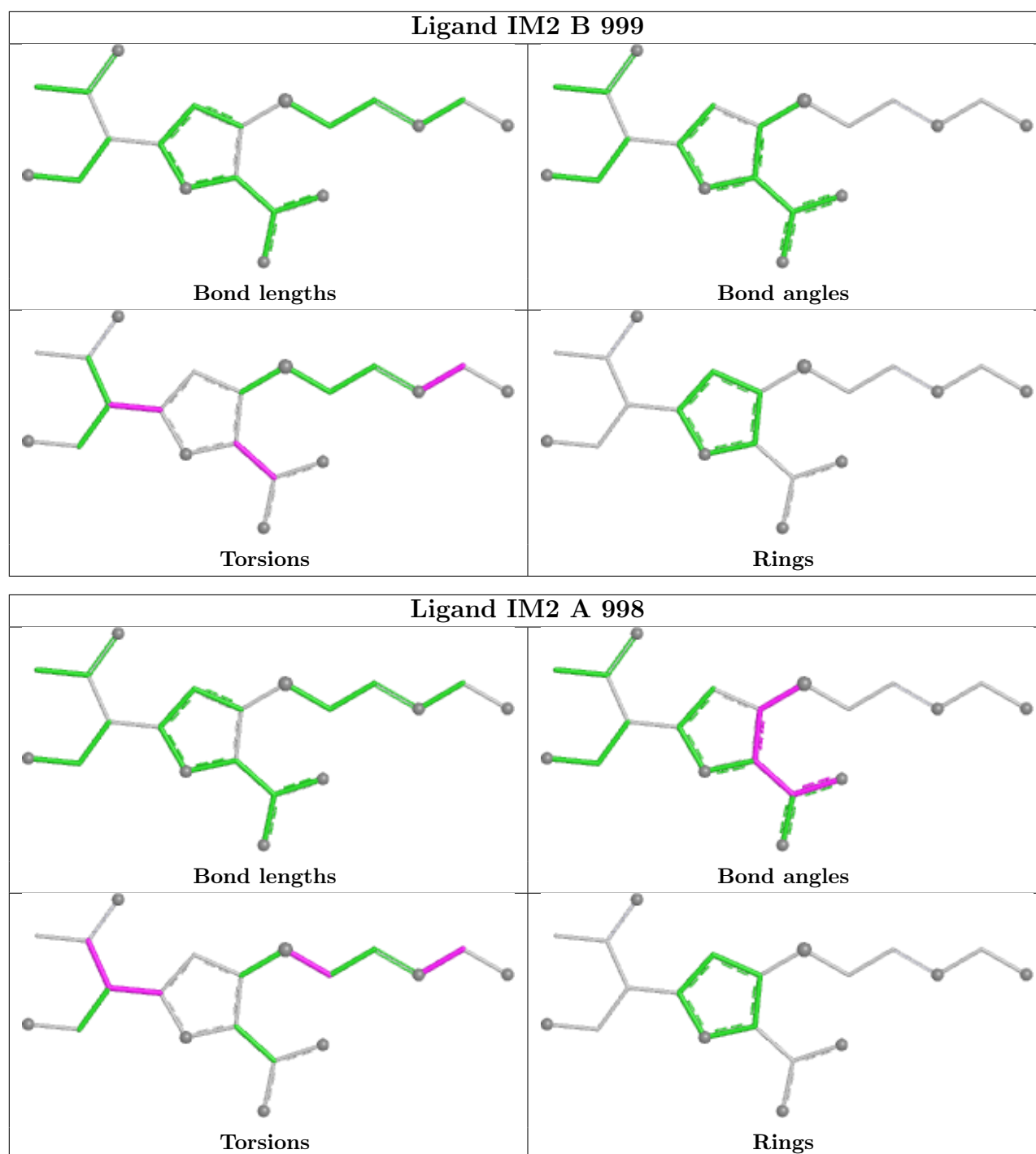
All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	998	IM2	C1-C5-C6-C7
2	A	998	IM2	C1-C5-C6-C61
2	A	998	IM2	C7-C6-C61-C62
2	A	998	IM2	C23-C22-S21-C2
2	A	998	IM2	N26-C25-N24-C23
2	B	999	IM2	C1-C5-C6-C7
2	B	999	IM2	C1-C5-C6-C61
2	B	999	IM2	N4-C3-C31-O31
2	B	999	IM2	N4-C3-C31-O32
2	B	999	IM2	N26-C25-N24-C23
2	B	999	IM2	C2-C3-C31-O31
2	B	999	IM2	C2-C3-C31-O32

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	598/731 (81%)	0.11	14 (2%) 61 57	31, 53, 88, 122	0
1	B	595/731 (81%)	-0.01	23 (3%) 43 38	21, 46, 93, 120	1 (0%)
All	All	1193/1462 (81%)	0.05	37 (3%) 51 47	21, 50, 93, 122	1 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	511	PHE	4.7
1	A	579	ILE	4.2
1	A	654	THR	4.0
1	B	627	TYR	3.8
1	B	194	VAL	3.5
1	B	653	GLY	3.5
1	B	707	TYR	3.4
1	B	581	ALA	3.3
1	B	470	SER	3.2
1	A	709	GLY	3.2
1	A	513	LEU	3.1
1	B	462	ILE	2.9
1	B	661	ILE	2.9
1	B	465	TRP	2.9
1	A	512	GLY	2.9
1	B	507	LEU	2.8
1	B	626	GLN	2.8
1	B	135	LEU	2.8
1	A	736	LYS	2.7
1	B	460	ILE	2.7
1	B	229	ILE	2.6
1	A	627	TYR	2.6
1	B	733	ARG	2.5
1	B	640	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	190	TYR	2.4
1	A	626	GLN	2.4
1	A	383	LYS	2.3
1	A	578	CYS	2.3
1	B	513	LEU	2.2
1	A	733	ARG	2.2
1	B	189	LYS	2.2
1	A	734	LEU	2.1
1	A	418	TYR	2.1
1	B	459	PRO	2.1
1	B	418	TYR	2.0
1	B	699	PRO	2.0
1	A	661	ILE	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](#)

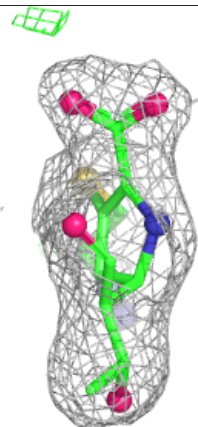
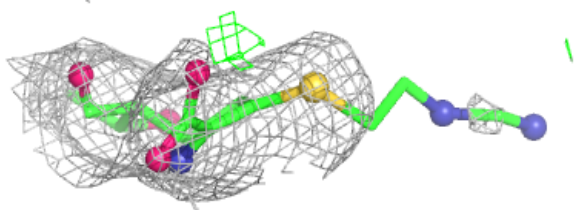
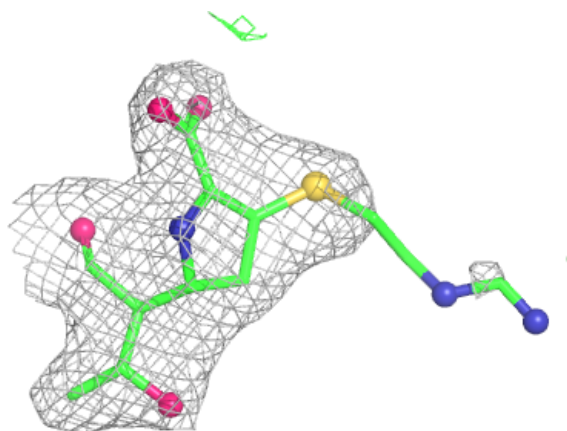
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	IM2	B	999	20/20	0.88	0.13	46,70,98,99	0
2	IM2	A	998	20/20	0.90	0.13	52,76,95,95	0

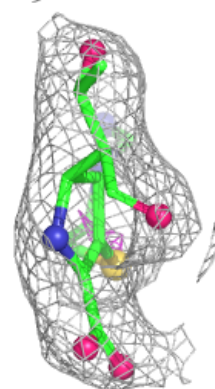
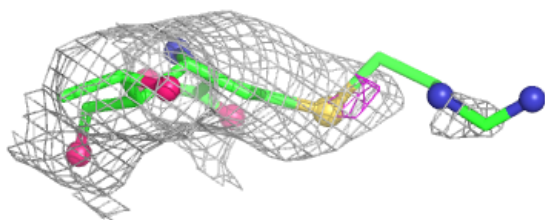
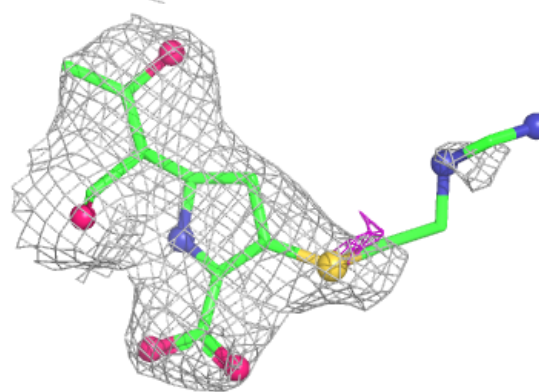
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around IM2 B 999:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around IM2 A 998:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers

There are no such residues in this entry.