



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 08:52 AM UTC

PDB ID : 1NSA / pdb_00001nsa
Title : THREE-DIMENSIONAL STRUCTURE OF PORCINE PROCAR-
BOXYPEPTIDASE B: A STRUCTURAL BASIS OF ITS INACTIVITY
Authors : Huber, R.
Deposited on : 1997-07-25
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 Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

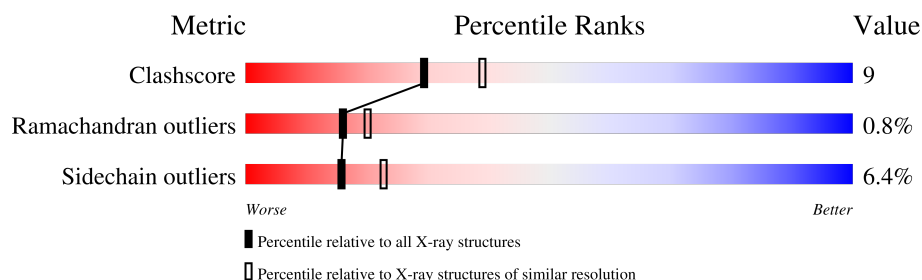
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	395	 61% 34% 5%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3406 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 PROCARBOXYPEPTIDASE B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	395	3174	2012	524	626	12	64	0	0

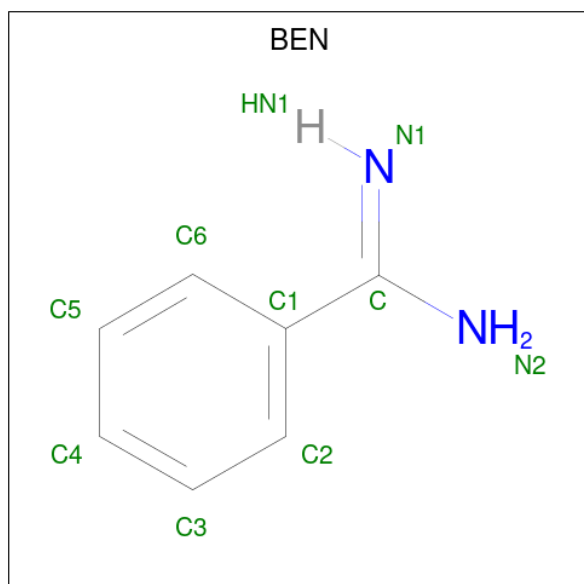
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	93A	VAL	ARG	conflict	UNP P09955
A	94A	SER	CYS	conflict	UNP P09955

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is BENZAMIDINE (CCD ID: BEN) (formula: C₇H₈N₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 9 7 2	0	0
3	A	1	Total C N 9 7 2	0	0
3	A	1	Total C N 9 7 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	204	Total O 204 204	0	0

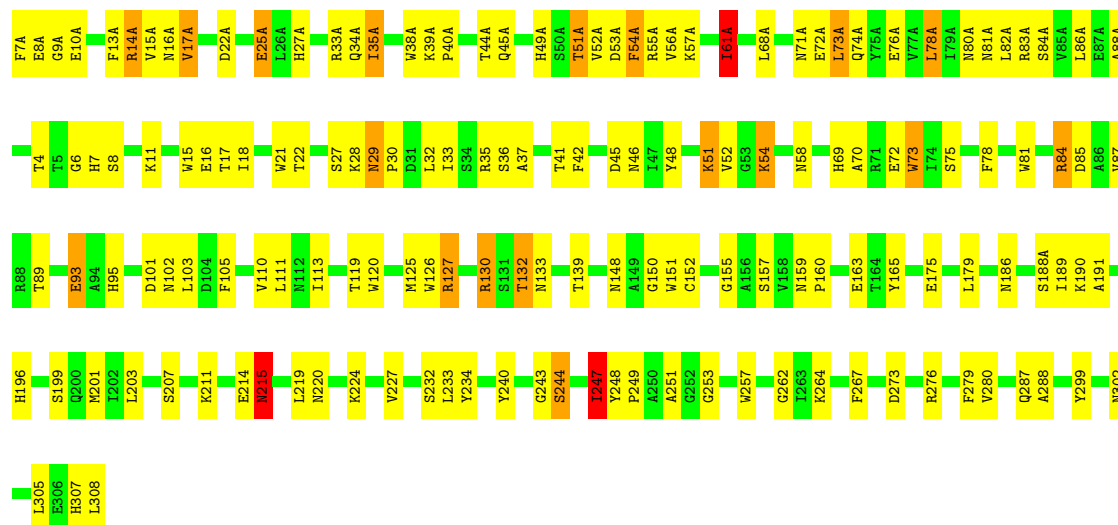
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

• Molecule 1: PROCARBOXYPEPTIDASE B

Chain A: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	103.10 Å 103.10 Å 46.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.30)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	EREF	Depositor
R, R_{free}	0.169 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3406	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	1.37	24/3254 (0.7%)	1.89	74/4421 (1.7%)

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	16

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	307	HIS	CE1-NE2	12.09	1.44	1.32
1	A	49(A)	HIS	CE1-NE2	11.44	1.44	1.32
1	A	95	HIS	ND1-CE1	10.47	1.43	1.32
1	A	7	HIS	ND1-CE1	10.33	1.42	1.32
1	A	307	HIS	ND1-CE1	10.17	1.42	1.32
1	A	151	TRP	NE1-CE2	-10.05	1.26	1.37
1	A	7	HIS	CE1-NE2	9.78	1.42	1.32
1	A	95	HIS	CE1-NE2	9.57	1.42	1.32
1	A	120	TRP	NE1-CE2	-9.43	1.27	1.37
1	A	27(A)	HIS	ND1-CE1	9.20	1.41	1.32
1	A	15	TRP	NE1-CE2	-8.81	1.27	1.37
1	A	38(A)	TRP	NE1-CE2	-8.76	1.27	1.37
1	A	21	TRP	NE1-CE2	-8.41	1.28	1.37
1	A	49(A)	HIS	ND1-CE1	7.47	1.40	1.32
1	A	73	TRP	NE1-CE2	-7.13	1.29	1.37
1	A	257	TRP	NE1-CE2	-6.99	1.29	1.37
1	A	196	HIS	ND1-CE1	6.85	1.39	1.32
1	A	126	TRP	NE1-CE2	-6.83	1.29	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	81	TRP	NE1-CE2	-6.43	1.30	1.37
1	A	27(A)	HIS	CE1-NE2	6.32	1.38	1.32
1	A	69	HIS	ND1-CE1	6.03	1.38	1.32
1	A	196	HIS	CE1-NE2	5.96	1.38	1.32
1	A	76(A)	GLU	C-N	-5.71	1.28	1.33
1	A	54(A)	PHE	N-CA	5.26	1.52	1.46

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	186	ASN	CA-CB-CG	-14.42	98.18	112.60
1	A	215	ASN	CA-CB-CG	-13.90	98.70	112.60
1	A	220	ASN	CA-CB-CG	-12.33	100.27	112.60
1	A	125	MET	N-CA-CB	-10.40	95.37	110.56
1	A	25(A)	GLU	CB-CG-CD	-10.26	95.16	112.60
1	A	29	ASN	O-C-N	9.69	129.34	121.20
1	A	133	ASN	CA-CB-CG	-8.90	103.70	112.60
1	A	46	ASN	CA-CB-CG	-8.68	103.92	112.60
1	A	211	LYS	N-CA-CB	-8.30	97.77	109.97
1	A	302	ASN	CA-CB-CG	-7.92	104.68	112.60
1	A	25(A)	GLU	N-CA-CB	-7.59	98.51	110.28
1	A	55(A)	ARG	CG-CD-NE	-7.30	95.94	112.00
1	A	15(A)	VAL	CA-C-N	-7.25	111.84	122.65
1	A	15(A)	VAL	C-N-CA	-7.25	111.84	122.65
1	A	14(A)	ARG	NE-CZ-NH2	-7.20	112.72	119.20
1	A	215	ASN	CB-CG-ND2	-7.15	105.68	116.40
1	A	132	THR	N-CA-CB	-7.03	99.44	110.06
1	A	127	ARG	NE-CZ-NH1	6.96	128.46	121.50
1	A	101	ASP	CA-CB-CG	-6.89	105.71	112.60
1	A	71(A)	ASN	CA-CB-CG	-6.87	105.73	112.60
1	A	29	ASN	CB-CA-C	-6.69	102.18	111.41
1	A	80(A)	ASN	CA-CB-CG	-6.65	105.95	112.60
1	A	307	HIS	CA-CB-CG	-6.56	107.24	113.80
1	A	14(A)	ARG	NE-CZ-NH1	6.56	128.06	121.50
1	A	84	ARG	CD-NE-CZ	-6.47	115.34	124.40
1	A	29	ASN	CA-CB-CG	-6.29	106.31	112.60
1	A	215	ASN	N-CA-CB	-6.16	99.61	110.39
1	A	34(A)	GLN	CA-C-N	6.15	130.68	122.93
1	A	34(A)	GLN	C-N-CA	6.15	130.68	122.93
1	A	110	VAL	CA-C-N	-6.13	112.11	120.44
1	A	110	VAL	C-N-CA	-6.13	112.11	120.44
1	A	44(A)	THR	CA-CB-CG2	6.03	120.75	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	262	GLY	CA-C-N	-6.00	114.98	122.48
1	A	262	GLY	C-N-CA	-6.00	114.98	122.48
1	A	55(A)	ARG	NE-CZ-NH2	-5.95	113.84	119.20
1	A	232	SER	CB-CA-C	-5.91	101.61	110.88
1	A	214	GLU	CA-C-N	5.88	132.82	121.18
1	A	214	GLU	C-N-CA	5.88	132.82	121.18
1	A	54	LYS	O-C-N	5.83	126.45	121.20
1	A	72(A)	GLU	CA-C-N	-5.77	115.09	122.77
1	A	72(A)	GLU	C-N-CA	-5.77	115.09	122.77
1	A	191	ALA	O-C-N	5.70	129.77	123.33
1	A	61(A)	ILE	CA-C-O	-5.67	115.37	121.27
1	A	84(A)	SER	CB-CA-C	-5.59	101.86	110.81
1	A	61(A)	ILE	N-CA-CB	5.58	116.71	110.51
1	A	68(A)	LEU	N-CA-C	-5.58	105.28	111.36
1	A	85	ASP	CA-CB-CG	-5.55	107.05	112.60
1	A	273	ASP	CA-C-N	-5.52	113.82	122.49
1	A	273	ASP	C-N-CA	-5.52	113.82	122.49
1	A	102	ASN	CA-CB-CG	-5.49	107.11	112.60
1	A	232	SER	CA-CB-OG	-5.45	100.21	111.10
1	A	215	ASN	OD1-CG-ND2	5.42	128.02	122.60
1	A	279	PHE	CA-CB-CG	-5.41	108.39	113.80
1	A	219	LEU	CA-C-N	-5.39	112.63	120.29
1	A	219	LEU	C-N-CA	-5.39	112.63	120.29
1	A	46	ASN	CA-C-N	-5.37	115.76	122.48
1	A	46	ASN	C-N-CA	-5.37	115.76	122.48
1	A	10(A)	GLU	CB-CG-CD	-5.37	103.47	112.60
1	A	27	SER	CA-CB-OG	-5.37	100.36	111.10
1	A	287	GLN	OE1-CD-NE2	5.34	127.94	122.60
1	A	7	HIS	ND1-CG-CD2	5.32	111.42	106.10
1	A	224	LYS	CA-C-N	5.32	125.84	119.94
1	A	224	LYS	C-N-CA	5.32	125.84	119.94
1	A	45	ASP	CA-CB-CG	-5.22	107.38	112.60
1	A	29	ASN	CA-C-O	-5.20	115.99	121.29
1	A	189	ILE	N-CA-CB	-5.20	105.05	110.82
1	A	288	ALA	O-C-N	5.19	127.48	122.09
1	A	93	GLU	CA-C-N	5.17	128.58	120.82
1	A	93	GLU	C-N-CA	5.17	128.58	120.82
1	A	130	ARG	NE-CZ-NH2	-5.16	114.56	119.20
1	A	244	SER	CB-CA-C	-5.14	102.81	110.88
1	A	95	HIS	CA-CB-CG	-5.10	108.70	113.80
1	A	17(A)	VAL	N-CA-C	5.05	115.12	107.80
1	A	175	GLU	O-C-N	5.00	127.22	122.07

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	103	LEU	Mainchain,Peptide
1	A	157	SER	Mainchain
1	A	188(A)	SER	Mainchain
1	A	215	ASN	Mainchain
1	A	240	TYR	Sidechain
1	A	247	ILE	Mainchain
1	A	248	TYR	Sidechain
1	A	264	LYS	Mainchain
1	A	267	PHE	Mainchain
1	A	299	TYR	Sidechain
1	A	37	ALA	Mainchain
1	A	51	LYS	Mainchain
1	A	74(A)	GLN	Mainchain
1	A	84	ARG	Sidechain
1	A	88(A)	ALA	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	3174	0	3000	51	0
2	A	1	0	0	0	0
3	A	27	0	22	3	0
4	A	204	0	0	3	0
All	All	3406	0	3022	52	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 9.

All (52) 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:8:SER:HB3	1:A:11:LYS:HG2	1.46	0.93
1:A:201:MET:HE1	1:A:247:ILE:HD11	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9(A):GLY:H	1:A:81(A):ASN:HD21	1.36	0.73
1:A:14(A):ARG:HD3	1:A:53(A):ASP:OD1	1.93	0.68
1:A:40(A):PRO:HD2	1:A:52(A):VAL:HG13	1.81	0.62
1:A:39(A):LYS:HB2	4:A:552:HOH:O	2.00	0.61
1:A:56(A):VAL:HG12	1:A:61(A):ILE:CD1	2.32	0.60
1:A:72:GLU:O	1:A:75:SER:HB3	2.03	0.58
1:A:253:GLY:HA3	3:A:1:BEN:HN21	1.71	0.56
1:A:25(A):GLU:HG2	1:A:73(A):LEU:HD21	1.86	0.56
3:A:3:BEN:H6	4:A:697:HOH:O	2.07	0.55
1:A:70:ALA:HB1	1:A:119:THR:HG23	1.89	0.54
1:A:8(A):GLU:OE1	1:A:83(A):ARG:HD2	2.08	0.53
1:A:233:LEU:HD13	1:A:234:TYR:CE2	2.44	0.53
1:A:18:ILE:O	1:A:22:THR:HG23	2.09	0.51
1:A:14(A):ARG:HD2	1:A:51(A):THR:HG23	1.93	0.51
1:A:45(A):GLN:HE22	1:A:155:GLY:HA2	1.77	0.50
1:A:190:LYS:HG3	1:A:308:LEU:CD2	2.43	0.49
1:A:56(A):VAL:HG12	1:A:61(A):ILE:HD13	1.94	0.48
1:A:160:PRO:HA	1:A:165:TYR:CG	2.48	0.48
1:A:9(A):GLY:H	1:A:81(A):ASN:ND2	2.08	0.48
1:A:41:THR:HG21	1:A:113:ILE:HB	1.95	0.48
1:A:89:THR:HB	1:A:93:GLU:HG3	1.95	0.48
1:A:233:LEU:HB3	1:A:234:TYR:CD2	2.49	0.47
1:A:150:GLY:O	1:A:251:ALA:HB1	2.14	0.47
1:A:253:GLY:HA3	3:A:1:BEN:N2	2.29	0.47
1:A:6:GLY:O	1:A:11:LYS:HE3	2.15	0.46
1:A:14(A):ARG:HD2	1:A:51(A):THR:CG2	2.45	0.46
1:A:36:SER:O	1:A:48:TYR:HA	2.16	0.46
1:A:35(A):ILE:HG23	1:A:54(A):PHE:HB2	1.99	0.45
1:A:130:ARG:CZ	1:A:139:THR:HG21	2.47	0.45
1:A:57(A):LYS:O	1:A:61(A):ILE:HD13	2.17	0.45
1:A:207:SER:O	1:A:249:PRO:HA	2.18	0.44
1:A:32:LEU:HD12	1:A:32:LEU:HA	1.86	0.44
1:A:28:LYS:C	1:A:30:PRO:HD3	2.43	0.44
1:A:33:ILE:HD11	1:A:87:VAL:CG1	2.47	0.44
1:A:14(A):ARG:HB2	1:A:78(A):LEU:HD13	2.01	0.43
1:A:82(A):LEU:HD12	1:A:82(A):LEU:HA	1.78	0.43
1:A:22(A):ASP:O	1:A:25(A):GLU:HB3	2.19	0.43
1:A:33(A):ARG:HB2	1:A:35(A):ILE:HD13	2.01	0.43
1:A:29:ASN:HB2	1:A:33:ILE:HD12	2.01	0.43
1:A:148:ASN:HD22	1:A:148:ASN:HA	1.62	0.42
1:A:29:ASN:N	1:A:30:PRO:HD3	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:VAL:HB	1:A:105:PHE:HB2	2.02	0.41
1:A:111:LEU:HD13	1:A:179:LEU:HD12	2.02	0.41
1:A:127:ARG:NH2	1:A:163:GLU:O	2.53	0.41
1:A:13(A):PHE:O	1:A:53(A):ASP:HA	2.21	0.41
1:A:203:LEU:HD22	1:A:243:GLY:HA2	2.03	0.41
1:A:42:PHE:HB2	4:A:584:HOH:O	2.20	0.40
1:A:54:LYS:HD3	1:A:54:LYS:HA	1.74	0.40
1:A:159:ASN:HD22	1:A:160:PRO:HD2	1.87	0.40
1:A:7(A):PHE:HD2	1:A:86(A):LEU:HD13	1.87	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	393/395 (100%)	376 (96%)	14 (4%)	3 (1%)	16 20

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	199	SER
1	A	280	VAL
1	A	247	ILE

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	344/344 (100%)	322 (94%)	22 (6%)	16	23

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16(A)	ASN
1	A	17(A)	VAL
1	A	35(A)	ILE
1	A	51(A)	THR
1	A	61(A)	ILE
1	A	73(A)	LEU
1	A	78(A)	LEU
1	A	4	THR
1	A	16	GLU
1	A	17	THR
1	A	35	ARG
1	A	51	LYS
1	A	58	ASN
1	A	73	TRP
1	A	78	PHE
1	A	132	THR
1	A	152	CYS
1	A	215	ASN
1	A	227	VAL
1	A	244	SER
1	A	276	ARG
1	A	305	LEU

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	45(A)	GLN
1	A	81(A)	ASN
1	A	46	ASN
1	A	102	ASN
1	A	112	ASN
1	A	148	ASN
1	A	159	ASN
1	A	185	ASN
1	A	215	ASN
1	A	287	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 ⓘ

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	$\# Z > 2$
3	BEN	A	2	-	9,9,9	1.44	1 (11%)	7,11,11	1.05	1 (14%)
3	BEN	A	1	-	9,9,9	2.14	1 (11%)	7,11,11	0.76	0
3	BEN	A	3	-	9,9,9	1.25	1 (11%)	7,11,11	0.91	1 (14%)

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
3	BEN	A	2	-	-	0/4/4/4	0/1/1/1
3	BEN	A	1	-	-	0/4/4/4	0/1/1/1
3	BEN	A	3	-	-	1/4/4/4	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	BEN	C1-C	-5.18	1.37	1.47
3	A	2	BEN	C1-C	-3.36	1.41	1.47
3	A	3	BEN	C-N1	2.35	1.37	1.27

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2	BEN	C1-C-N2	2.54	121.86	118.01
3	A	3	BEN	C1-C-N2	2.02	121.08	118.01

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	3	BEN	N1-C-C1-C2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	BEN	2	0
3	A	3	BEN	1	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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.