



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:05 AM GMT

PDB ID : 3O3J
Title : Crystal structure of Arabidopsis thaliana peptide deformylase 1B (AtPDF1B)
in complex with inhibitor 6b
Authors : Fieulaine, S.; Meinnel, T.; Giglione, C.
Deposited on : 2010-07-24
Resolution : 3.00 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

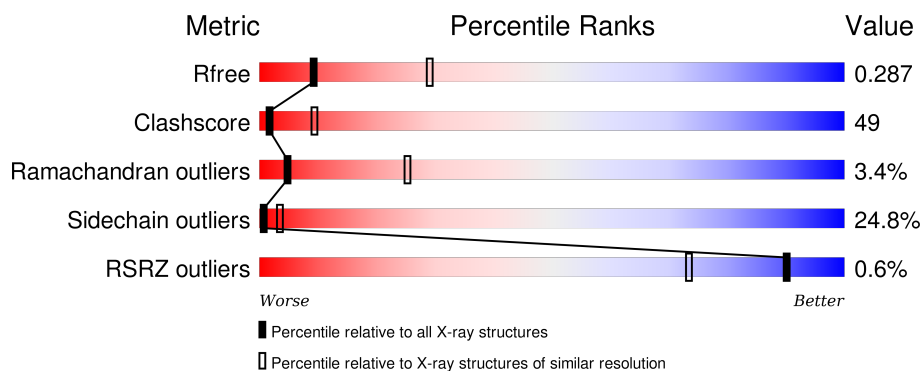
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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	193	<div> <div></div> <div>23%37%28%6%7%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1482 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 Peptide deformylase 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	180	Total	C	N	O	S	0	0	0
			1377	880	221	270	6			

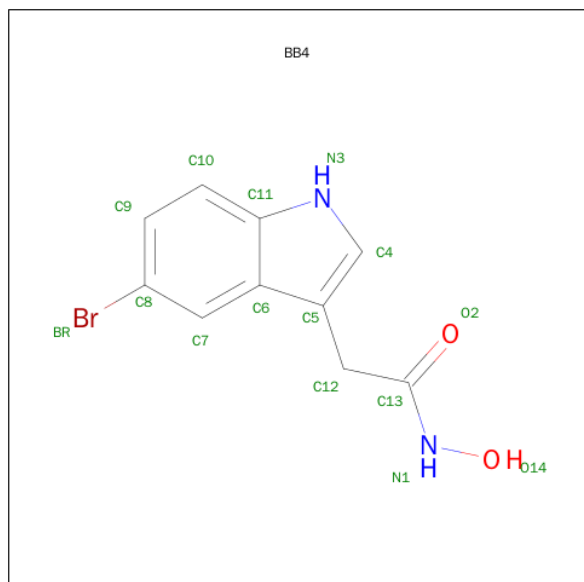
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP Q9FUZ2
A	2	GLU	-	EXPRESSION TAG	UNP Q9FUZ2

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	6	Total	Zn	0	0
			6	6		

- Molecule 3 is 2-(5-BROMO-1H-INDOL-3-YL)-N-HYDROXYACETAMIDE (three-letter code: BB4) (formula: C₁₀H₉BrN₂O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	Br	C	N	O	0	0
			15	1	10	2	2		

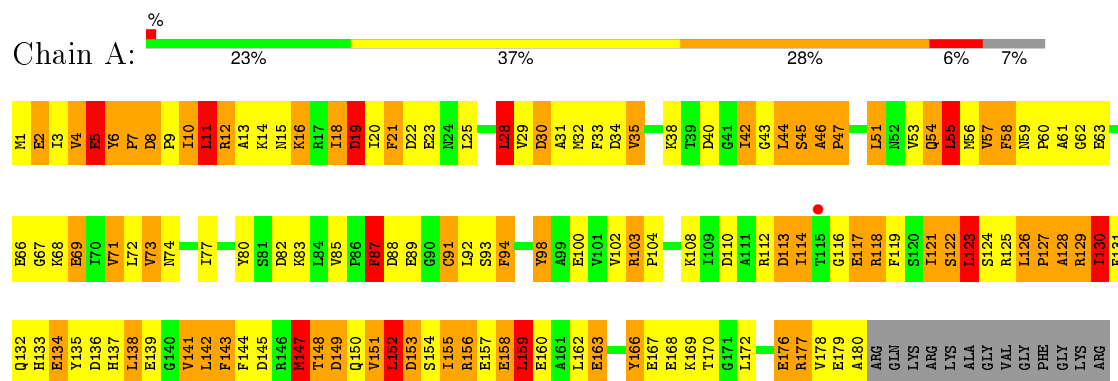
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	84	Total	O	0	0
			84	84		

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: Peptide deformylase 1B



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	57.50 Å 57.50 Å 144.84 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.75 – 3.00 28.75 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (28.75-3.00) 99.3 (28.75-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.88 (at 3.00 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.200 , 0.285 0.228 , 0.287	Depositor DCC
R_{free} test set	263 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	65.8	Xtriage
Anisotropy	0.689	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 74.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 5261 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	1482	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.13% 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: ZN, BB4

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	2.23	65/1405 (4.6%)	2.01	43/1913 (2.2%)

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	1

All (65) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	16	LYS	CD-CE	13.81	1.85	1.51
1	A	134	GLU	CD-OE2	9.73	1.36	1.25
1	A	69	GLU	CG-CD	9.40	1.66	1.51
1	A	34	ASP	CG-OD1	9.22	1.46	1.25
1	A	110	ASP	CG-OD1	9.01	1.46	1.25
1	A	166	TYR	CE2-CZ	7.94	1.48	1.38
1	A	134	GLU	CD-OE1	7.77	1.34	1.25
1	A	141	VAL	CA-CB	-7.63	1.38	1.54
1	A	85	VAL	CB-CG2	-7.37	1.37	1.52
1	A	2	GLU	CD-OE2	7.31	1.33	1.25
1	A	5	GLU	CB-CG	-7.30	1.38	1.52
1	A	152	LEU	CG-CD1	7.25	1.78	1.51
1	A	58	PHE	CE2-CZ	7.18	1.51	1.37
1	A	83	LYS	CA-CB	7.18	1.69	1.53
1	A	68	LYS	CA-CB	7.10	1.69	1.53
1	A	157	GLU	CD-OE1	7.07	1.33	1.25
1	A	163	GLU	CD-OE1	7.04	1.33	1.25
1	A	71	VAL	CB-CG2	-7.03	1.38	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	94	PHE	CB-CG	6.98	1.63	1.51
1	A	7	PRO	C-O	6.97	1.37	1.23
1	A	87	PHE	CE1-CZ	6.95	1.50	1.37
1	A	89	GLU	CD-OE1	6.93	1.33	1.25
1	A	91	CYS	CB-SG	-6.78	1.70	1.82
1	A	2	GLU	CD-OE1	6.74	1.33	1.25
1	A	151	VAL	CA-CB	6.69	1.68	1.54
1	A	58	PHE	CD2-CE2	6.43	1.52	1.39
1	A	82	ASP	CA-CB	6.33	1.67	1.53
1	A	40	ASP	CB-CG	6.32	1.65	1.51
1	A	58	PHE	CB-CG	-6.28	1.40	1.51
1	A	149	ASP	CB-CG	6.26	1.65	1.51
1	A	5	GLU	CD-OE1	6.26	1.32	1.25
1	A	10	ILE	CA-CB	-6.26	1.40	1.54
1	A	176	GLU	CD-OE1	6.23	1.32	1.25
1	A	4	VAL	CB-CG2	-6.21	1.39	1.52
1	A	46	ALA	CA-CB	-6.17	1.39	1.52
1	A	63	GLU	CD-OE1	6.17	1.32	1.25
1	A	69	GLU	N-CA	6.16	1.58	1.46
1	A	143	PHE	CE2-CZ	-6.16	1.25	1.37
1	A	21	PHE	CB-CG	-6.14	1.41	1.51
1	A	141	VAL	CB-CG1	-6.08	1.40	1.52
1	A	30	ASP	CB-CG	-6.06	1.39	1.51
1	A	98	TYR	CB-CG	-6.04	1.42	1.51
1	A	14	LYS	CB-CG	6.00	1.68	1.52
1	A	100	GLU	CG-CD	5.98	1.60	1.51
1	A	69	GLU	CB-CG	5.92	1.63	1.52
1	A	87	PHE	CE2-CZ	5.86	1.48	1.37
1	A	57	VAL	CA-CB	-5.71	1.42	1.54
1	A	98	TYR	CE1-CZ	5.66	1.46	1.38
1	A	45	SER	CB-OG	5.58	1.49	1.42
1	A	167	GLU	CD-OE1	5.56	1.31	1.25
1	A	66	GLU	CB-CG	-5.54	1.41	1.52
1	A	83	LYS	N-CA	5.54	1.57	1.46
1	A	30	ASP	CG-OD1	5.52	1.38	1.25
1	A	158	GLU	CD-OE1	5.52	1.31	1.25
1	A	87	PHE	CG-CD2	5.46	1.47	1.38
1	A	179	GLU	CD-OE2	5.43	1.31	1.25
1	A	12	ARG	CB-CG	-5.37	1.38	1.52
1	A	6	TYR	CD2-CE2	5.35	1.47	1.39
1	A	34	ASP	CG-OD2	5.21	1.37	1.25
1	A	2	GLU	CG-CD	5.19	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	94	PHE	CG-CD1	5.18	1.46	1.38
1	A	18	ILE	CA-C	5.17	1.66	1.52
1	A	148	THR	CB-CG2	5.12	1.69	1.52
1	A	23	GLU	CD-OE2	5.07	1.31	1.25
1	A	54	GLN	CB-CG	-5.07	1.38	1.52

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	34	ASP	CB-CG-OD2	-21.80	98.68	118.30
1	A	30	ASP	CB-CG-OD2	-19.86	100.43	118.30
1	A	69	GLU	OE1-CD-OE2	-10.44	110.78	123.30
1	A	8	ASP	CB-CG-OD1	9.99	127.29	118.30
1	A	16	LYS	CD-CE-NZ	-9.66	89.49	111.70
1	A	55	LEU	CB-CG-CD2	-9.12	95.49	111.00
1	A	6	TYR	C-N-CD	-8.68	101.51	120.60
1	A	34	ASP	OD1-CG-OD2	8.53	139.51	123.30
1	A	129	ARG	NE-CZ-NH1	8.48	124.54	120.30
1	A	30	ASP	CB-CG-OD1	8.37	125.83	118.30
1	A	40	ASP	CB-CG-OD2	8.29	125.76	118.30
1	A	51	LEU	CA-CB-CG	-8.15	96.55	115.30
1	A	134	GLU	OE1-CD-OE2	7.76	132.62	123.30
1	A	147	MET	CG-SD-CE	7.67	112.47	100.20
1	A	16	LYS	CG-CD-CE	-7.67	88.89	111.90
1	A	118	ARG	NE-CZ-NH2	7.48	124.04	120.30
1	A	8	ASP	CB-CG-OD2	-7.46	111.58	118.30
1	A	138	LEU	CA-CB-CG	-7.10	98.97	115.30
1	A	141	VAL	CB-CA-C	-7.02	98.06	111.40
1	A	142	LEU	CA-CB-CG	-7.01	99.18	115.30
1	A	28	LEU	CB-CG-CD2	-6.58	99.82	111.00
1	A	130	ILE	CB-CA-C	-6.55	98.51	111.60
1	A	69	GLU	CG-CD-OE1	6.51	131.31	118.30
1	A	123	LEU	CA-CB-CG	-6.41	100.55	115.30
1	A	6	TYR	C-N-CA	6.36	148.70	122.00
1	A	19	ASP	CB-CG-OD1	-6.28	112.65	118.30
1	A	11	LEU	CB-CG-CD1	6.26	121.64	111.00
1	A	159	LEU	CB-CG-CD1	-6.08	100.67	111.00
1	A	40	ASP	OD1-CG-OD2	-6.01	111.88	123.30
1	A	11	LEU	CA-CB-CG	-5.75	102.08	115.30
1	A	72	LEU	CA-CB-CG	-5.69	102.21	115.30
1	A	103	ARG	NE-CZ-NH1	-5.64	117.48	120.30
1	A	162	LEU	CB-CG-CD2	-5.48	101.69	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	152	LEU	CB-CG-CD1	5.47	120.31	111.00
1	A	129	ARG	NE-CZ-NH2	-5.45	117.58	120.30
1	A	35	VAL	CB-CA-C	-5.42	101.11	111.40
1	A	163	GLU	CG-CD-OE2	-5.41	107.48	118.30
1	A	134	GLU	CG-CD-OE2	-5.34	107.62	118.30
1	A	153	ASP	CB-CG-OD2	-5.33	113.51	118.30
1	A	30	ASP	OD1-CG-OD2	5.15	133.09	123.30
1	A	55	LEU	CB-CG-CD1	5.15	119.76	111.00
1	A	88	ASP	N-CA-C	-5.12	97.17	111.00
1	A	110	ASP	CB-CG-OD1	5.07	122.86	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	ARG	Sidechain

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	1377	0	1306	133	1
2	A	6	0	0	1	0
3	A	15	0	8	2	0
4	A	84	0	0	4	0
All	All	1482	0	1314	133	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 49.

All (133) 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:152:LEU:CD1	1:A:152:LEU:CG	1.78	1.58
1:A:121:ILE:CD1	1:A:121:ILE:CG1	1.74	1.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:LYS:CE	1:A:16:LYS:CD	1.85	1.52
1:A:1:MET:CE	1:A:35:VAL:CG2	2.31	1.09
1:A:42:ILE:HG13	1:A:130:ILE:HD13	1.36	1.06
1:A:1:MET:CE	1:A:35:VAL:HG23	1.86	1.05
1:A:16:LYS:CG	1:A:16:LYS:CE	2.42	0.97
1:A:19:ASP:OD1	1:A:19:ASP:N	1.92	0.97
1:A:1:MET:HE1	1:A:35:VAL:HG23	1.47	0.93
1:A:121:ILE:HG23	1:A:123:LEU:HD12	1.51	0.90
1:A:158:GLU:HG2	4:A:256:HOH:O	1.71	0.89
1:A:103:ARG:HG3	1:A:129:ARG:NH1	1.91	0.86
1:A:1:MET:HE3	1:A:35:VAL:CG2	2.07	0.83
1:A:152:LEU:CD1	1:A:152:LEU:HG	2.07	0.83
1:A:126:LEU:O	1:A:127:PRO:O	1.98	0.82
1:A:16:LYS:NZ	1:A:16:LYS:CD	2.43	0.81
1:A:1:MET:HE1	1:A:35:VAL:CG2	2.06	0.78
1:A:54:GLN:HA	1:A:138:LEU:HD22	1.65	0.78
1:A:178:VAL:HG22	1:A:178:VAL:O	1.84	0.77
1:A:12:ARG:HD2	1:A:176:GLU:OE2	1.83	0.77
1:A:1:MET:CE	1:A:35:VAL:HG21	2.16	0.75
1:A:113:ASP:HB3	1:A:119:PHE:HE1	1.52	0.74
1:A:127:PRO:O	1:A:128:ALA:C	2.26	0.74
1:A:155:ILE:HG13	1:A:159:LEU:CD1	2.19	0.73
1:A:1:MET:HE3	1:A:35:VAL:HG21	1.69	0.72
1:A:121:ILE:CG2	1:A:123:LEU:HD12	2.20	0.72
1:A:114:ILE:O	1:A:114:ILE:HG13	1.89	0.72
1:A:1:MET:SD	1:A:31:ALA:HB1	2.30	0.71
1:A:32:MET:HB3	1:A:44:LEU:HD23	1.73	0.70
1:A:113:ASP:OD1	1:A:113:ASP:C	2.30	0.70
1:A:144:PHE:HA	1:A:147:MET:CG	2.23	0.69
1:A:5:GLU:HA	1:A:93:SER:HB3	1.75	0.69
1:A:104:PRO:HD2	1:A:132:GLN:HE22	1.58	0.68
1:A:144:PHE:HA	1:A:147:MET:HG3	1.75	0.68
1:A:113:ASP:HB3	1:A:119:PHE:CE1	2.29	0.67
1:A:33:PHE:CZ	1:A:69:GLU:HB3	2.30	0.67
1:A:136:ASP:HB3	1:A:141:VAL:HB	1.76	0.66
1:A:160:GLU:OE2	2:A:203:ZN:ZN	1.43	0.66
1:A:155:ILE:HG13	1:A:159:LEU:HD12	1.76	0.66
1:A:92:LEU:N	3:A:300:BB4:O2	2.22	0.65
1:A:57:VAL:HG12	1:A:71:VAL:HG22	1.79	0.65
1:A:134:GLU:OE1	3:A:300:BB4:N1	2.26	0.65
1:A:6:TYR:HB2	1:A:94:PHE:CE2	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:ILE:CG1	1:A:159:LEU:HD11	2.29	0.63
1:A:178:VAL:O	1:A:178:VAL:CG2	2.47	0.62
1:A:113:ASP:OD1	1:A:114:ILE:N	2.31	0.62
1:A:150:GLN:O	1:A:153:ASP:HB2	1.98	0.62
1:A:6:TYR:CB	1:A:94:PHE:CE2	2.83	0.62
1:A:57:VAL:O	1:A:58:PHE:HB3	1.99	0.61
1:A:123:LEU:HD23	1:A:127:PRO:HB2	1.83	0.61
1:A:15:ASN:HD21	1:A:47:PRO:HG3	1.67	0.60
1:A:123:LEU:HD23	1:A:128:ALA:H	1.67	0.60
1:A:123:LEU:HD23	1:A:128:ALA:N	2.18	0.59
1:A:148:THR:OG1	1:A:151:VAL:HG23	2.02	0.59
1:A:155:ILE:CG1	1:A:159:LEU:CD1	2.81	0.58
1:A:42:ILE:CG1	1:A:130:ILE:HD13	2.22	0.58
1:A:33:PHE:CE1	1:A:69:GLU:HB3	2.39	0.58
1:A:177:ARG:O	1:A:180:ALA:HB3	2.04	0.58
1:A:126:LEU:O	1:A:127:PRO:C	2.41	0.57
1:A:1:MET:HE2	1:A:35:VAL:HG23	1.85	0.56
1:A:77:ILE:HD12	1:A:135:TYR:CD2	2.41	0.55
1:A:77:ILE:HD13	1:A:80:TYR:CZ	2.41	0.55
1:A:6:TYR:CG	1:A:94:PHE:CE2	2.94	0.55
1:A:16:LYS:CE	1:A:16:LYS:HG2	2.34	0.54
1:A:147:MET:HE1	1:A:155:ILE:HD13	1.89	0.54
1:A:59:ASN:C	1:A:59:ASN:OD1	2.43	0.53
1:A:147:MET:HE1	1:A:155:ILE:CD1	2.39	0.53
1:A:113:ASP:CB	1:A:119:PHE:HE1	2.22	0.53
1:A:11:LEU:HD23	1:A:11:LEU:N	2.22	0.53
1:A:123:LEU:CD2	1:A:128:ALA:N	2.72	0.52
1:A:77:ILE:HD12	1:A:135:TYR:CE2	2.45	0.52
1:A:136:ASP:O	1:A:137:HIS:C	2.48	0.51
1:A:7:PRO:O	1:A:8:ASP:C	2.49	0.51
1:A:127:PRO:O	1:A:129:ARG:N	2.43	0.50
1:A:128:ALA:O	1:A:131:PHE:HB3	2.12	0.50
1:A:104:PRO:HD2	1:A:132:GLN:NE2	2.24	0.49
1:A:116:GLY:O	1:A:117:GLU:C	2.51	0.49
1:A:61:ALA:HB2	1:A:67:GLY:HA3	1.95	0.49
1:A:61:ALA:HB2	1:A:67:GLY:CA	2.43	0.48
1:A:6:TYR:CD2	1:A:6:TYR:C	2.87	0.47
1:A:166:TYR:CE1	1:A:170:THR:HG21	2.50	0.47
1:A:46:ALA:HB2	1:A:55:LEU:HD23	1.97	0.47
1:A:142:LEU:N	1:A:145:ASP:OD1	2.41	0.46
1:A:42:ILE:O	1:A:58:PHE:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:ASN:ND2	1:A:47:PRO:HG3	2.31	0.46
1:A:20:ILE:HG12	1:A:22:ASP:OD2	2.15	0.46
1:A:73:VAL:HG23	1:A:74:ASN:N	2.30	0.46
1:A:147:MET:CE	1:A:155:ILE:CD1	2.93	0.46
1:A:32:MET:O	1:A:33:PHE:C	2.53	0.46
1:A:43:GLY:HA2	1:A:58:PHE:CB	2.46	0.46
1:A:144:PHE:HB3	1:A:147:MET:HE2	1.98	0.45
1:A:21:PHE:HB3	4:A:246:HOH:O	2.15	0.45
1:A:121:ILE:CD1	1:A:121:ILE:CB	2.82	0.45
1:A:144:PHE:H	1:A:144:PHE:HD2	1.63	0.45
1:A:87:PHE:HA	1:A:87:PHE:HD2	1.69	0.45
1:A:123:LEU:C	1:A:128:ALA:HB2	2.37	0.44
1:A:8:ASP:OD2	1:A:8:ASP:C	2.55	0.44
1:A:151:VAL:O	1:A:154:SER:N	2.51	0.44
1:A:91:CYS:HB2	1:A:133:HIS:HE1	1.81	0.44
1:A:130:ILE:O	1:A:131:PHE:C	2.53	0.44
1:A:177:ARG:O	1:A:180:ALA:CB	2.66	0.43
1:A:21:PHE:CE2	1:A:116:GLY:HA2	2.53	0.43
1:A:142:LEU:HA	1:A:142:LEU:HD23	1.57	0.43
1:A:152:LEU:O	1:A:155:ILE:N	2.49	0.43
1:A:28:LEU:O	1:A:29:VAL:C	2.56	0.43
1:A:98:TYR:CD1	1:A:98:TYR:N	2.86	0.43
1:A:148:THR:HG23	4:A:210:HOH:O	2.18	0.43
1:A:61:ALA:CB	1:A:67:GLY:HA3	2.49	0.43
1:A:53:VAL:O	1:A:53:VAL:CG2	2.67	0.43
1:A:32:MET:HE2	1:A:57:VAL:HG13	2.00	0.42
1:A:77:ILE:HD13	1:A:80:TYR:OH	2.19	0.42
1:A:163:GLU:OE1	1:A:177:ARG:HG2	2.19	0.42
1:A:147:MET:CE	1:A:155:ILE:HD13	2.49	0.42
1:A:155:ILE:O	1:A:156:ARG:C	2.58	0.42
1:A:152:LEU:O	1:A:153:ASP:C	2.57	0.42
1:A:148:THR:O	1:A:149:ASP:C	2.58	0.42
1:A:6:TYR:CG	1:A:94:PHE:HE2	2.36	0.42
1:A:108:LYS:HA	1:A:122:SER:HA	2.02	0.41
1:A:166:TYR:O	1:A:170:THR:HG23	2.20	0.41
1:A:138:LEU:HD23	1:A:138:LEU:HA	1.91	0.41
1:A:56:MET:CE	1:A:138:LEU:HD12	2.51	0.41
1:A:51:LEU:HA	1:A:51:LEU:HD23	1.94	0.41
1:A:1:MET:HG2	4:A:290:HOH:O	2.20	0.41
1:A:59:ASN:O	1:A:62:GLY:N	2.42	0.41
1:A:123:LEU:O	1:A:128:ALA:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:PRO:O	1:A:10:ILE:C	2.55	0.41
1:A:129:ARG:HG3	1:A:130:ILE:N	2.36	0.41
1:A:144:PHE:N	1:A:144:PHE:CD2	2.87	0.40
1:A:92:LEU:C	1:A:94:PHE:H	2.24	0.40
1:A:30:ASP:O	1:A:31:ALA:C	2.59	0.40
1:A:53:VAL:O	1:A:53:VAL:HG23	2.21	0.40
1:A:4:VAL:H	1:A:4:VAL:HG23	1.44	0.40
1:A:45:SER:HB3	1:A:134:GLU:OE2	2.21	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)
1:A:30:ASP:OD1	1:A:69:GLU:OE1[8_554]	1.62	0.58

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	178/193 (92%)	142 (80%)	30 (17%)	6 (3%)	5	25

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	LEU
1	A	127	PRO
1	A	13	ALA
1	A	128	ALA
1	A	117	GLU
1	A	125	ARG

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	145/169 (86%)	109 (75%)	36 (25%)	1 3

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	3	ILE
1	A	5	GLU
1	A	18	ILE
1	A	19	ASP
1	A	25	LEU
1	A	28	LEU
1	A	38	LYS
1	A	42	ILE
1	A	44	LEU
1	A	47	PRO
1	A	55	LEU
1	A	60	PRO
1	A	73	VAL
1	A	87	PHE
1	A	102	VAL
1	A	112	ARG
1	A	113	ASP
1	A	114	ILE
1	A	121	ILE
1	A	122	SER
1	A	123	LEU
1	A	124	SER
1	A	126	LEU
1	A	130	ILE
1	A	139	GLU
1	A	143	PHE
1	A	147	MET
1	A	152	LEU
1	A	155	ILE

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Mol	Chain	Res	Type
1	A	156	ARG
1	A	159	LEU
1	A	168	GLU
1	A	169	LYS
1	A	172	LEU
1	A	177	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 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	BB4	A	300	2	15,16,16	4.64	8 (53%)	15,22,22	4.37	7 (46%)

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	BB4	A	300	2	-	0/5/6/6	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	300	BB4	C11-N3	-2.68	1.30	1.38
3	A	300	BB4	C4-C5	-2.13	1.34	1.38
3	A	300	BB4	C10-C9	3.23	1.43	1.36
3	A	300	BB4	C9-C8	4.00	1.47	1.38
3	A	300	BB4	C12-C13	6.64	1.68	1.51
3	A	300	BB4	BR-C8	6.76	2.05	1.90
3	A	300	BB4	C7-C8	7.36	1.48	1.36
3	A	300	BB4	C13-N1	11.34	1.44	1.32

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	300	BB4	C7-C6-C11	-10.90	116.03	120.34
3	A	300	BB4	C9-C8-C7	-6.52	116.13	121.93
3	A	300	BB4	BR-C8-C7	-2.06	117.27	119.83
3	A	300	BB4	C10-C9-C8	2.95	122.23	119.25
3	A	300	BB4	BR-C8-C9	4.60	126.55	119.28
3	A	300	BB4	C5-C12-C13	5.77	123.95	112.40
3	A	300	BB4	O14-N1-C13	6.29	129.08	119.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	300	BB4	2	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	180/193 (93%)	-0.40	1 (0%) 90 73	15, 67, 145, 189	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	115	THR	2.6

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
3	BB4	A	300	15/15	0.95	0.17	-0.03	53,64,68,71	0
2	ZN	A	201	1/1	0.99	0.15	-0.21	53,53,53,53	0
2	ZN	A	203	1/1	0.98	0.08	-1.75	53,53,53,53	0
2	ZN	A	204	1/1	0.95	0.05	-1.93	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ZN	A	202	1/1	0.98	0.11	-	67,67,67,67	0
2	ZN	A	205	1/1	0.87	0.09	-	106,106,106,106	0
2	ZN	A	206	1/1	0.96	0.20	-	54,54,54,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.