

Full wwPDB X-ray Structure Validation Report (i)

Jan 7, 2024 – 01:05 pm GMT

PDB ID : 5NNA

Title: Isatin hydrolase A (IHA) from Labrenzia aggregata bound to benzyl benzoate

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Deposited on : 2017-04-08

Resolution : 1.50 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 (i) 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 (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

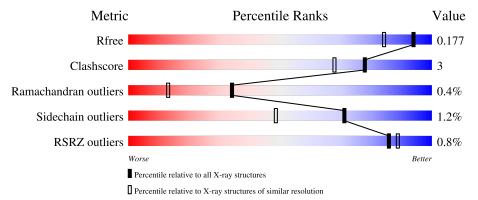
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 1.50 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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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 <=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	264	92%	
1	В	264	91%	5% • •
1	С	264	90%	7% •
1	D	264	92%	8%



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 9195 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 isatin hydrolase A.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	255	Total	С	N	О	S	0	9	0
1	A	255	2001	1272	346	374	9	0	9	
1	В	256	Total	С	N	О	S	0	6	0
1	Б	250	1996	1264	345	378	9	0		
1	С	257	Total	С	N	О	S	0	8	0
1		201	2014	1280	347	378	9	0	0	
1	D	264	Total	С	N	О	S	0	4	0
1		204	2054	1297	367	381	9		4	U

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	SER	-	expression tag	UNP A0P0F0
A	-5	HIS	-	expression tag	UNP A0P0F0
A	-4	HIS	-	expression tag	UNP A0P0F0
A	-3	HIS	-	expression tag	UNP A0P0F0
A	-2	HIS	-	expression tag	UNP A0P0F0
A	-1	HIS	-	expression tag	UNP A0P0F0
A	0	HIS	-	expression tag	UNP A0P0F0
A	1	ALA	-	expression tag	UNP A0P0F0
В	-6	SER	-	expression tag	UNP A0P0F0
В	-5	HIS	-	expression tag	UNP A0P0F0
В	-4	HIS	-	expression tag	UNP A0P0F0
В	-3	HIS	_	expression tag	UNP A0P0F0
В	-2	HIS	-	expression tag	UNP A0P0F0
В	-1	HIS	_	expression tag	UNP A0P0F0
В	0	HIS	-	expression tag	UNP A0P0F0
В	1	ALA	-	expression tag	UNP A0P0F0
С	-6	SER	-	expression tag	UNP A0P0F0
С	-5	HIS	-	expression tag	UNP A0P0F0
С	-4	HIS	-	expression tag	UNP A0P0F0
С	-3	HIS	-	expression tag	UNP A0P0F0
С	-2	HIS	-	expression tag	UNP A0P0F0

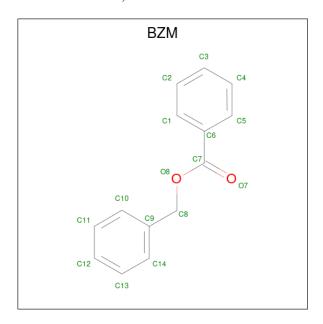
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Chain	Residue	Modelled	Actual	Comment	Reference
С	-1	HIS	=	expression tag	UNP A0P0F0
С	0	HIS	-	expression tag	UNP A0P0F0
С	1	ALA	-	expression tag	UNP A0P0F0
D	-6	SER	-	expression tag	UNP A0P0F0
D	-5	HIS	-	expression tag	UNP A0P0F0
D	-4	HIS	-	expression tag	UNP A0P0F0
D	-3	HIS	-	expression tag	UNP A0P0F0
D	-2	HIS	-	expression tag	UNP A0P0F0
D	-1	HIS	-	expression tag	UNP A0P0F0
D	0	HIS	-	expression tag	UNP A0P0F0
D	1	ALA	-	expression tag	UNP A0P0F0

• Molecule 2 is BENZOIC ACID PHENYLMETHYLESTER (three-letter code: BZM) (formula: $C_{14}H_{12}O_2$).



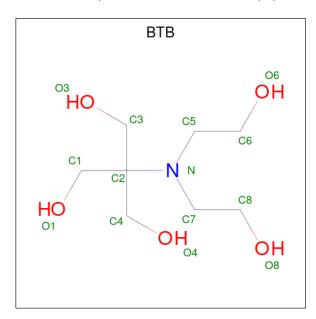
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 16 14 2	0	0
2	В	1	Total C O 16 14 2	0	0
2	С	1	Total C O 16 14 2	0	0
2	D	1	Total C O 16 14 2	0	0

• Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mn 1 1	0	0
3	В	1	Total Mn 1 1	0	0
3	С	1	Total Mn 1 1	0	0
3	D	1	Total Mn 1 1	0	0

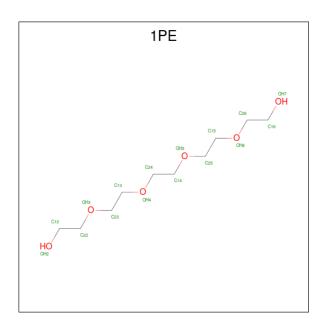
• Molecule 4 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (three-letter code: BTB) (formula: $C_8H_{19}NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 14	C 8	N 1	O 5	0	0

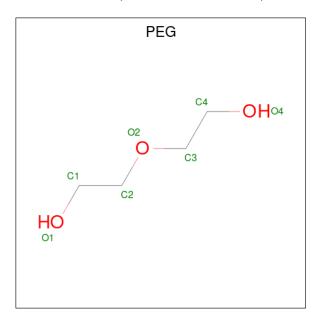
• Molecule 5 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	В	1	Total 16	C 10	O 6	0	0

 $\bullet \ \ Molecule \ 6 \ is \ DI(HYDROXYETHYL)ETHER \ (three-letter \ code: \ PEG) \ (formula: \ C_4H_{10}O_3).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	В	1	Total C O 7 4 3	0	0

• Molecule 7 is water.



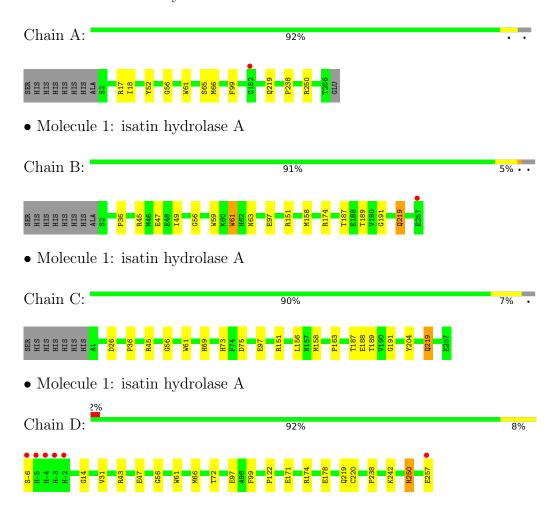
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	270	Total O 271 271	0	1
7	В	260	Total O 261 261	0	1
7	С	262	Total O 263 263	0	1
7	D	229	Total O 230 230	0	1



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: isatin hydrolase A





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	37.69Å 70.67Å 92.92Å	Donositon
a, b, c, α , β , γ	108.23° 95.94° 101.48°	Depositor
Resolution (Å)	63.54 - 1.50	Depositor
Resolution (A)	86.85 - 1.50	EDS
% Data completeness	96.1 (63.54-1.50)	Depositor
(in resolution range)	96.1 (86.85-1.50)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.56 (at 1.50Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.148 , 0.177	Depositor
it, it _{free}	0.148 , 0.177	DCC
R_{free} test set	6636 reflections $(4.91%)$	wwPDB-VP
Wilson B-factor (Å ²)	11.2	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 47.0	EDS
L-test for twinning ²	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.004 for -h,-k,h+k+l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9195	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.68% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: BZM, MN, PEG, BTB, 1PE

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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.51	0/2090	0.71	$2/2852 \ (0.1\%)$	
1	В	0.54	0/2068	0.73	0/2822	
1	С	0.51	0/2093	0.69	$1/2856 \ (0.0\%)$	
1	D	0.47	0/2129	0.68	2/2903~(0.1%)	
All	All	0.51	0/8380	0.70	5/11433 (0.0%)	

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	D	66	MET	CG-SD-CE	-6.02	90.56	100.20
1	D	250	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	A	66	MET	CG-SD-CE	-5.80	90.92	100.20
1	С	75	ASP	CB-CG-OD1	5.40	123.16	118.30
1	A	250	ARG	NE-CZ-NH1	5.22	122.91	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	2001	0	1951	3	0
1	В	1996	0	1929	18	0

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Mol	Chain		H(model)	H(added)	Clashes	Symm-Clashes
1	С	2014	0	1957	17	0
1	D	2054	0	1975	12	0
2	A	16	0	12	1	0
2	В	16	0	12	0	0
2	С	16	0	12	2	0
2	D	16	0	12	0	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
3	С	1	0	0	0	0
3	D	1	0	0	0	0
4	A	14	0	19	0	0
5	В	16	0	22	1	0
6	В	7	0	10	3	0
7	A	271	0	0	0	3
7	В	261	0	0	9	1
7	С	263	0	0	8	1
7	D	230	0	0	4	2
All	All	9195	0	7911	46	4

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 3.

All (46) 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:C:187[B]:THR:HG22	1:C:189:THR:H	1.40	0.84
1:B:187[B]:THR:HG22	1:B:189:THR:H	1.43	0.82
1:B:174:ARG:NH1	7:B:402:HOH:O	2.16	0.78
1:A:65:SER:HB2	6:B:304:PEG:H11	1.66	0.78
1:D:14:GLY:O	7:D:401:HOH:O	2.04	0.75
1:D:-6:SER:N	7:D:402:HOH:O	2.22	0.72
1:B:219[A]:GLN:OE1	7:B:401:HOH:O	2.09	0.71
1:D:174:ARG:NH1	1:D:178:GLU:OE1	2.24	0.69
1:C:219[B]:GLN:OE1	7:C:401:HOH:O	2.09	0.69
1:C:97[A]:GLU:HG2	7:C:527:HOH:O	1.92	0.69
1:B:47:GLU:HG2	6:B:304:PEG:H41	1.77	0.66
1:B:45:ARG:HD3	1:D:47:GLU:OE1	1.97	0.65
1:B:158[B]:MET:HG2	1:C:36:PRO:HG3	1.80	0.64
1:B:151:ARG:NH1	7:B:403:HOH:O	2.31	0.64
1:C:156[A]:LEU:HD11	7:C:454:HOH:O	2.01	0.59
1:B:36:PRO:HG3	1:C:158[B]:MET:HG2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:GLY:HA2	7:B:401:HOH:O	2.04	0.57
1:C:187[B]:THR:HG23	7:C:597:HOH:O	2.08	0.54
1:B:63:ASN:HB3	6:B:304:PEG:H21	1.91	0.52
1:C:204[A]:TYR:CD1	2:C:301:BZM:H81	2.44	0.52
1:C:26:ASP:OD2	1:D:242:LYS:HD2	2.11	0.51
1:B:219[B]:GLN:OE1	7:B:584[B]:HOH:O	2.19	0.50
1:D:257:GLU:HG3	7:D:401:HOH:O	2.12	0.49
1:C:151:ARG:NH1	7:C:405:HOH:O	2.44	0.49
1:B:47:GLU:HG2	1:B:63:ASN:HB2	1.95	0.48
1:C:187[A]:THR:HG21	7:C:475:HOH:O	2.12	0.48
1:C:45:ARG:NH1	7:C:411:HOH:O	2.47	0.47
1:B:187[B]:THR:HG23	7:B:602:HOH:O	2.14	0.47
1:C:187[B]:THR:HG22	1:C:188:GLU:N	2.30	0.47
1:B:187[A]:THR:HG21	7:B:501:HOH:O	2.15	0.46
1:C:191:GLY:HA2	7:C:401:HOH:O	2.16	0.45
1:D:250:ARG:NH2	7:D:404:HOH:O	2.34	0.45
1:D:31:VAL:HG22	1:D:43:ARG:HD3	1.98	0.44
1:A:18:ILE:HD12	1:B:97:GLU:HA	1.99	0.44
1:C:158[A]:MET:SD	1:C:163:PRO:HB3	2.58	0.43
1:C:69:HIS:HA	1:C:73:HIS:CD2	2.54	0.42
1:A:99:PHE:CE1	1:A:238:PRO:HD2	2.54	0.42
2:A:301:BZM:H11	1:B:59:TRP:CE2	2.55	0.42
1:D:122:PRO:HG2	1:D:171:GLU:HG3	2.00	0.42
5:B:303:1PE:H232	7:B:612:HOH:O	2.20	0.41
1:B:49:ILE:HB	1:B:61:TRP:CD1	2.55	0.41
1:C:204[B]:TYR:CD1	2:C:301:BZM:H81	2.55	0.41
1:D:97:GLU:H	1:D:97:GLU:CD	2.24	0.41
1:B:187[B]:THR:HG21	7:B:501:HOH:O	2.20	0.40
1:D:72:THR:HA	1:D:220:CYS:HB2	2.04	0.40
1:D:99:PHE:CE1	1:D:238:PRO:HD2	2.57	0.40

All (4) 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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
7:A:402:HOH:O	7:A:570:HOH:O[1_655]	1.97	0.23
7:A:619:HOH:O	7:C:605:HOH:O[1_444]	2.09	0.11
7:B:605:HOH:O	7:D:617:HOH:O[1_554]	2.09	0.11
7:A:542:HOH:O	7:D:470:HOH:O[1_455]	2.13	0.07



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	Perce	ntiles
1	A	263/264 (100%)	259 (98%)	3 (1%)	1 (0%)	34	13
1	В	260/264~(98%)	256 (98%)	3 (1%)	1 (0%)	34	13
1	С	263/264 (100%)	259 (98%)	3 (1%)	1 (0%)	34	13
1	D	266/264 (101%)	261 (98%)	4 (2%)	1 (0%)	34	13
All	All	$1052/1056\ (100\%)$	1035 (98%)	13 (1%)	4 (0%)	34	13

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	56	GLY
1	В	56	GLY
1	С	56	GLY
1	D	56	GLY

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	215/213 (101%)	210 (98%)	5 (2%)	50 20
1	В	212/213 (100%)	209 (99%)	3 (1%)	67 42
1	С	214/213 (100%)	211 (99%)	3 (1%)	67 42
1	D	217/213 (102%)	214 (99%)	3 (1%)	67 42
All	All	858/852 (101%)	844 (98%)	14 (2%)	71 36



All	(14)	residues	with	a	non-rotameric	sid	lechain	are	listed	below:

Mol	Chain	Res	Type
1	A	17	ARG
1	A	52	TYR
1	A	61	TRP
1	A	219[A]	GLN
1	A	219[B]	GLN
1	В	61	TRP
1	В	219[A]	GLN
1	В	219[B]	GLN
1	С	61	TRP
1	С	219[A]	GLN
1	С	219[B]	GLN
1	D	61	TRP
1	D	219[A]	GLN
1	D	219[B]	GLN

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 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	Mol Type Chain		Res Link		Bo	ond leng	ths	Bond angles		
IVIOI	$\operatorname{Mol} \mid \operatorname{Type} \mid \operatorname{Chain} \mid$	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
5	1PE	В	303	-	15,15,15	0.54	0	14,14,14	0.46	0
2	BZM	D	301	-	17,17,17	1.88	3 (17%)	21,21,21	1.53	3 (14%)
2	BZM	С	301	-	17,17,17	1.93	2 (11%)	21,21,21	2.66	3 (14%)
2	BZM	A	301	-	17,17,17	1.94	3 (17%)	21,21,21	1.79	4 (19%)
2	BZM	В	301	-	17,17,17	1.83	2 (11%)	21,21,21	2.83	5 (23%)
4	BTB	A	303	-	13,13,13	0.52	0	7,16,16	0.45	0
6	PEG	В	304	-	6,6,6	0.44	0	5,5,5	0.36	0

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
5	1PE	В	303	-	-	6/13/13/13	-
2	BZM	D	301	-	-	2/9/9/9	0/2/2/2
2	BZM	С	301	-	-	3/9/9/9	0/2/2/2
2	BZM	A	301	-	-	3/9/9/9	0/2/2/2
2	BZM	В	301	-	-	4/9/9/9	0/2/2/2
4	BTB	A	303	-	-	0/21/21/21	-
6	PEG	В	304	-	-	2/4/4/4	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
2	A	301	BZM	O7-C7	6.90	1.41	1.22
2	D	301	BZM	O7-C7	6.49	1.40	1.22
2	В	301	BZM	O7-C7	6.47	1.40	1.22
2	С	301	BZM	O7-C7	6.40	1.40	1.22
2	С	301	BZM	O8-C8	-3.83	1.37	1.45
2	В	301	BZM	O8-C8	-3.15	1.39	1.45
2	D	301	BZM	O8-C8	-2.78	1.40	1.45
2	A	301	BZM	O8-C8	-2.59	1.40	1.45
2	A	301	BZM	O8-C7	2.31	1.39	1.33
2	D	301	BZM	O8-C7	2.20	1.39	1.33

All (15) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	301	BZM	O8-C7-O7	-10.60	102.18	123.67
2	С	301	BZM	O8-C7-O7	-10.56	102.25	123.67
2	A	301	BZM	O8-C7-O7	-6.15	111.20	123.67
2	D	301	BZM	O8-C7-O7	-4.84	113.85	123.67
2	В	301	BZM	C8-O8-C7	-4.33	108.26	115.91
2	С	301	BZM	O8-C7-C6	-3.75	105.61	112.14
2	A	301	BZM	O7-C7-C6	-2.83	112.80	122.09
2	С	301	BZM	O7-C7-C6	-2.79	112.95	122.09
2	В	301	BZM	C10-C9-C14	2.63	122.31	118.17
2	В	301	BZM	O8-C7-C6	-2.61	107.60	112.14
2	D	301	BZM	O7-C7-C6	-2.42	114.17	122.09
2	A	301	BZM	O8-C7-C6	-2.22	108.27	112.14
2	D	301	BZM	O8-C8-C9	-2.16	104.21	109.39
2	A	301	BZM	C10-C9-C14	2.13	121.52	118.17
2	В	301	BZM	O8-C8-C9	-2.01	104.56	109.39

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	301	BZM	C1-C6-C7-O8
2	В	301	BZM	C5-C6-C7-O8
2	С	301	BZM	O7-C7-O8-C8
2	В	301	BZM	O7-C7-O8-C8
2	A	301	BZM	O7-C7-O8-C8
5	В	303	1PE	ОН4-С13-С23-ОН3
2	D	301	BZM	O7-C7-O8-C8
2	С	301	BZM	C1-C6-C7-O7
5	В	303	1PE	ОН7-С16-С26-ОН6
2	С	301	BZM	C5-C6-C7-O7
5	В	303	1PE	OH5-C14-C24-OH4
6	В	304	PEG	O2-C3-C4-O4
2	A	301	BZM	C5-C6-C7-O7
2	A	301	BZM	C1-C6-C7-O7
5	В	303	1PE	C24-C14-OH5-C25
5	В	303	1PE	C12-C22-OH3-C23
6	В	304	PEG	O1-C1-C2-O2
5	В	303	1PE	C23-C13-OH4-C24
2	В	301	BZM	C9-C8-O8-C7
2	D	301	BZM	C1-C6-C7-O7

There are no ring outliers.

4 monomers are involved in 7 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	В	303	1PE	1	0
2	С	301	BZM	2	0
2	A	301	BZM	1	0
6	В	304	PEG	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 (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, 95^{th} 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>	$\# \mathrm{RSRZ} {>} 2$	$OWAB(A^2)$	Q<0.9
1	A	255/264~(96%)	-0.42	1 (0%) 92 94	6, 10, 23, 34	0
1	В	256/264~(96%)	-0.46	1 (0%) 92 94	6, 10, 25, 46	0
1	С	257/264 (97%)	-0.38	0 100 100	6, 11, 28, 48	0
1	D	264/264 (100%)	-0.29	6 (2%) 60 65	7, 13, 31, 56	0
All	All	1032/1056~(97%)	-0.39	8 (0%) 86 89	6, 11, 27, 56	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	-5	HIS	3.5
1	D	257	GLU	2.7
1	D	-4	HIS	2.7
1	D	-3	HIS	2.6
1	A	152	GLY	2.5
1	D	-6	SER	2.1
1	D	-2	HIS	2.1
1	В	257	GLU	2.1

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 monosaccharides 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, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
6	PEG	В	304	7/7	0.88	0.22	25,31,39,40	0
5	1PE	В	303	16/16	0.90	0.13	21,33,43,50	0
2	BZM	D	301	16/16	0.92	0.12	12,19,24,26	0
2	BZM	С	301	16/16	0.93	0.10	10,17,33,35	0
2	BZM	В	301	16/16	0.93	0.10	10,15,29,34	0
2	BZM	A	301	16/16	0.96	0.10	11,17,25,25	0
4	BTB	A	303	14/14	0.97	0.07	12,13,17,18	0
3	MN	D	302	1/1	0.99	0.06	12,12,12,12	1
3	MN	В	302	1/1	1.00	0.04	6,6,6,6	1
3	MN	С	302	1/1	1.00	0.04	6,6,6,6	1
3	MN	A	302	1/1	1.00	0.04	10,10,10,10	1

6.5 Other polymers (i)

There are no such residues in this entry.

