

# Full wwPDB X-ray Structure Validation Report (i)

#### May 23, 2020 - 03:18 am BST

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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 following versions of software and data (see references (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
$\mathrm{EDS}$	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11
EDS Percentile statistics Ideal geometry (proteins) Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)	::	NOT EXECUTED 20191225.v01 (using entries in the PDB archive December 25th 2019) Engh & Huber (2001) Parkinson et al. (1996) 2.11

# 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 1.80 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain					
1	А	250	72%	20%	6% •			
1	В	250	73%	19%	6% •			

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	DMS	В	252	-	-	Х	-



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3948 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.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace
1	А	250	Total 1891	C 1202	N 332	O 351	S 6	0	0	0
1	В	249	Total 1883	C 1197	N 331	O 350	S 5	0	0	0

• Molecule 1 is a protein called TRIOSEPHOSPHATE ISOMERASE.

• Molecule 2 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C<sub>2</sub>H<sub>6</sub>OS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{cccc} \text{Total} & \text{C} & \text{O} & \text{S} \\ 4 & 2 & 1 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{cccc} \text{Total} & \text{C} & \text{O} & \text{S} \\ 4 & 2 & 1 & 1 \end{array}$	0	0
2	В	1	$\begin{array}{cccc} \text{Total} & \text{C} & \text{O} & \text{S} \\ 4 & 2 & 1 & 1 \end{array}$	0	0
2	В	1	$\begin{array}{cccc} \text{Total} & \text{C} & \text{O} & \text{S} \\ 4 & 2 & 1 & 1 \end{array}$	0	0



• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	75	Total O 75 75	0	0
3	В	83	Total O 83 83	0	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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 colorcoded 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: TRIOSEPHOSPHATE ISOMERASE



# 4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants	48.08Å 53.45Å 64.71Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$92.27^{\circ}$ $74.63^{\circ}$ $116.74^{\circ}$	Depositor
Resolution (Å)	32.00 - 1.80	Depositor
% Data completeness	(Not available) $(32.00-1.80)$	Depositor
(in resolution range)	(1101 available) (52.00 1.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	TNT, X-PLOR	Depositor
$R, R_{free}$	0.199 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3948	wwPDB-VP
Average B, all atoms $(Å^2)$	24.0	wwPDB-VP



# 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: DMS

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	Bo	nd lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.80	11/1925~(0.6%)	1.26	17/2609~(0.7%)	
1	В	0.82	9/1917~(0.5%)	1.30	22/2599~(0.8%)	
All	All	0.81	20/3842~(0.5%)	1.28	39/5208~(0.7%)	

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$\operatorname{Ideal}(\operatorname{\AA})$
1	В	167	GLU	CD-OE2	7.74	1.34	1.25
1	А	133	GLU	CD-OE1	6.99	1.33	1.25
1	В	241	GLU	CD-OE2	6.53	1.32	1.25
1	В	77	GLU	CD-OE2	6.41	1.32	1.25
1	В	107	GLU	CD-OE2	6.37	1.32	1.25
1	А	53	GLU	CD-OE1	6.16	1.32	1.25
1	А	23	GLU	CD-OE2	6.00	1.32	1.25
1	А	185	GLU	CD-OE1	5.94	1.32	1.25
1	А	129	GLU	CD-OE2	5.85	1.32	1.25
1	В	185	GLU	CD-OE1	5.83	1.32	1.25
1	А	205	GLU	CD-OE2	5.73	1.31	1.25
1	А	107	GLU	CD-OE2	5.67	1.31	1.25
1	А	104	GLU	CD-OE2	5.64	1.31	1.25
1	В	53	GLU	CD-OE2	5.51	1.31	1.25
1	В	135	GLU	CD-OE2	5.44	1.31	1.25
1	А	135	GLU	CD-OE2	5.43	1.31	1.25
1	А	167	GLU	CD-OE2	5.34	1.31	1.25
1	А	241	GLU	CD-OE2	5.25	1.31	1.25
1	В	23	GLU	CD-OE2	5.23	1.31	1.25
1	В	133	GLU	CD-OE2	5.11	1.31	1.25

All (39) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	244	ASP	CB-CG-OD1	-9.14	110.08	118.30
1	В	36	ASP	CB-CG-OD1	-8.83	110.36	118.30
1	В	220	ARG	NE-CZ-NH2	-8.58	116.01	120.30
1	В	36	ASP	CB-CG-OD2	8.25	125.72	118.30
1	А	36	ASP	CB-CG-OD1	-8.11	111.00	118.30
1	А	220	ARG	NE-CZ-NH1	7.95	124.28	120.30
1	А	244	ASP	CB-CG-OD1	-7.65	111.42	118.30
1	В	111	ASP	CB-CG-OD2	-7.54	111.51	118.30
1	В	244	ASP	CB-CG-OD2	7.40	124.96	118.30
1	В	226	ARG	NE-CZ-NH1	7.16	123.88	120.30
1	В	227	ASP	CB-CG-OD2	-6.93	112.07	118.30
1	А	36	ASP	CB-CG-OD2	6.88	124.49	118.30
1	В	220	ARG	NE-CZ-NH1	6.78	123.69	120.30
1	А	244	ASP	CB-CG-OD2	6.72	124.35	118.30
1	В	165	ALA	N-CA-CB	6.41	119.07	110.10
1	А	165	ALA	N-CA-CB	6.26	118.86	110.10
1	А	111	ASP	CB-CG-OD2	-6.03	112.87	118.30
1	В	201	ASP	CB-CG-OD2	-6.01	112.89	118.30
1	В	158	ASP	CB-CG-OD1	-5.99	112.91	118.30
1	В	85	ASP	CB-CG-OD2	-5.91	112.98	118.30
1	А	158	ASP	CB-CG-OD2	-5.87	113.02	118.30
1	А	227	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	В	158	ASP	CB-CG-OD2	5.81	123.53	118.30
1	В	30	SER	CB-CA-C	-5.73	99.21	110.10
1	В	3	LYS	N-CA-CB	5.67	120.80	110.60
1	В	223	TYR	CB-CG-CD1	-5.59	117.64	121.00
1	А	227	ASP	CB-CG-OD1	5.57	123.31	118.30
1	А	98	ARG	NE-CZ-NH1	5.53	123.07	120.30
1	В	111	ASP	CB-CG-OD1	5.44	123.19	118.30
1	А	26	ASP	CB-CG-OD1	-5.29	113.54	118.30
1	В	130	THR	CA-CB-CG2	-5.28	105.01	112.40
1	В	26	ASP	CB-CG-OD2	-5.26	113.57	118.30
1	В	176	LYS	CB-CA-C	-5.21	99.97	110.40
1	A	134	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	А	141	VAL	CB-CA-C	-5.08	101.74	111.40
1	A	192	SER	N-CA-CB	5.06	118.09	110.50
1	A	201	ASP	CB-CG-OD2	-5.04	113.76	118.30
1	А	30	SER	N-CA-CB	-5.02	102.97	110.50
1	В	63	ALA	N-CA-CB	-5.01	103.09	110.10

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	А	1891	0	1929	34	0
1	В	1883	0	1917	42	0
2	А	8	0	12	0	0
2	В	8	0	12	5	0
3	А	75	0	0	0	0
3	В	83	0	0	0	0
All	All	3948	0	3870	76	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 10.

All (76) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash	
Atom-1	Atom-2	${ m distance}~({ m \AA})$	overlap (Å)	
1:B:226:ARG:HH11	1:B:226:ARG:HG3	1.34	0.92	
1:B:19:GLN:HE21	1:B:19:GLN:HA	1.34	0.91	
1:B:97:GLU:HA	2:B:252:DMS:H21	1.61	0.82	
1:A:51:THR:HG22	1:A:62:ILE:HD11	1.65	0.76	
1:B:97:GLU:HA	2:B:252:DMS:C2	2.17	0.74	
1:A:24:LEU:HD21	1:A:28:PHE:CZ	2.22	0.73	
1:B:226:ARG:NH1	1:B:226:ARG:HG3	2.00	0.73	
1:B:197:LYS:C	1:B:198:ILE:HD13	2.08	0.72	
1:B:10:ALA:HB1	1:B:237:SER:HB2	1.74	0.70	
1:A:185:GLU:O	1:A:189:LEU:HD23	1.94	0.67	
1:B:220:ARG:NH2	1:B:250:GLN:OXT	2.29	0.66	
1:B:220:ARG:HH21	1:B:223:TYR:HD2	1.45	0.65	
1:A:10:ALA:HB1	1:A:237:SER:HB2	1.79	0.64	
1:A:186:ALA:HA	1:A:189:LEU:CD2	2.30	0.61	
1:A:3:LYS:NZ	1:A:223:TYR:O	2.33	0.61	
1:B:97:GLU:CA	2:B:252:DMS:H21	2.29	0.61	
1:B:19:GLN:HE21	1:B:19:GLN:CA	2.08	0.61	
1:A:51:THR:HG22	1:A:62:ILE:CD1	2.32	0.60	
1:A:174:THR:O	1:A:176:LYS:NZ	2.30	0.58	
1:B:154:LEU:HB3	1:B:158:ASP:HB2	1.85	0.58	
1:A:186:ALA:HA	1:A:189:LEU:HD21	1.86	0.57	

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		Interatomic	Clash	
Atom-1	Atom-2	distance $(Å)$	overlap (Å)	
1:A:220:ARG:NH2	1:A:250:GLN:O	2.35	0.57	
1:A:247:LYS:O	1:A:250:GLN:HG2	2.04	0.57	
1:B:27:LEU:CD2	1:B:240:PRO:HB3	2.34	0.56	
1:B:3:LYS:NZ	1:B:223:TYB:0	2.39	0.55	
1:A:201:ASP:N	1:A:201:ASP:OD1	2.39	0.53	
1:B:220:ABG:NH2	1:B:223:TYB:HD2	2.07	0.53	
1:B:198:ILE:HD13	1:B:198:ILE:N	2.3	0.53	
1:B:80:LEU:HB2	1:B:81:PRO:HD3	1.92	0.52	
1:A:198:ILE:HD13	1:A:198:ILE:N	2.25	0.52	
1:A:104:GLU:OE2	1:A:112:LYS:NZ	2.40	0.51	
1:B:220:ABG:HG3	1:B:220:ABG:O	2.09	0.51	
1:B:27:LEU:HD21	1:B:240:PRO:HB3	1.93	0.50	
1:B:96:SEB:O	2:B:252:DMS:H23	2.11	0.50	
1:A:193:TBP:CE2	1:A:197:LYS:HG3	2.47	0.50	
1:B:52:LYS:HE2	1:B:86:PHE:CE2	2.47	0.49	
$1 \cdot A \cdot 220 \cdot A \text{ BG} \cdot \text{NH1}$	$1 \cdot A \cdot 250 \cdot GLN \cdot O$	2.45	0.49	
1.A.197.LYS.C	$1 \cdot A \cdot 198 \cdot ILE \cdot HD13$	2.33	0.19	
1·B·197·LYS·O	$1 \cdot B \cdot 198 \cdot ILE \cdot HD13$	2.33	0.48	
1:A:24:LEU:HD21	1:A:28:PHE:CE2	2.10	0.10	
1.A.117.VAL.HG11	1.A.158.ASP.HB3	1.97	0.47	
1:A:186:ALA:HA	1:A:189:LEU:HD23	1.97	0.47	
1:B:226:ARG:HH11	1:B:226:ARG:CG	2.15	0.46	
1:B:10:ALA:CB	1:B:237:SER:HB2	2.42	0.46	
1:A:80:LEU:HD13	1:A:116:ALA:HA	1.98	0.46	
1:A:111:ASP:OD1	1:A:153:LYS:HE3	2.17	0.45	
1:B:80:LEU:N	1:B:81:PRO:CD	2.80	0.45	
1:A:130:THR:OG1	1:A:133:GLU:HG3	2.17	0.44	
1:B:247:LYS:O	1:B:250:GLN:HG3	2.17	0.44	
1:B:220:ARG:NH1	1:B:250:GLN:OXT	2.51	0.44	
1:A:154:LEU:HB3	1:A:158:ASP:HB2	2.00	0.44	
1:B:26:ASP:OD1	1:B:54:ARG:NH2	2.50	0.44	
1:B:140:ALA:HA	1:B:189:LEU:HD21	1.99	0.43	
1:B:130:THR:OG1	1:B:133:GLU:HG3	2.19	0.43	
1:A:142:VAL:O	1:A:146:GLN:HG3	2.18	0.43	
1:A:128:GLY:HA3	1:A:167:GLU:O	2.19	0.43	
1:A:201:ASP:OD1	1:A:202:VAL:N	2.50	0.43	
1:B:51:THR:HG22	1:B:62:ILE:HG21	2.00	0.43	
1:A:149:ALA:O	1:A:152:LYS:HG2	2.19	0.43	
1:B:83:LEU:HA	1:B:83:LEU:HD23	1.89	0.43	
1:A:216:GLY:N	1:A:241:GLU:OE2	2.39	0.42	
1:B:97:GLU:N	2:B:252:DMS:H21	2.34	0.42	

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Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}~({ m \AA})$	overlap (Å)
1:B:220:ARG:NH2	1:B:223:TYR:CD2	2.85	0.42
1:A:144:LEU:HD22	1:A:193:TRP:CG	2.54	0.42
1:B:28:PHE:CD1	1:B:28:PHE:N	2.87	0.42
1:A:134:ARG:HD2	1:A:170:TRP:CD2	2.54	0.42
1:A:10:ALA:CB	1:A:237:SER:HB2	2.48	0.41
1:B:226:ARG:O	1:B:226:ARG:HD2	2.20	0.41
1:B:215:ASN:HB2	1:B:241:GLU:OE2	2.21	0.41
1:B:79:SER:HB2	1:B:81:PRO:HD2	2.01	0.41
1:A:35:HIS:N	1:A:35:HIS:ND1	2.66	0.41
1:B:19:GLN:NE2	1:B:19:GLN:CA	2.80	0.41
1:A:24:LEU:C	1:A:24:LEU:HD23	2.41	0.41
1:B:156:LYS:HE3	1:B:202:VAL:HG23	2.02	0.40
1:B:132:GLN:HB3	1:B:132:GLN:HE21	1.67	0.40
1:B:128:GLY:HA3	1:B:167:GLU:O	2.22	0.40

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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	А	248/250~(99%)	244~(98%)	4 (2%)	0	100 100
1	В	247/250~(99%)	241 (98%)	5(2%)	1 (0%)	34 21
All	All	495/500 (99%)	485(98%)	9 (2%)	1 (0%)	47 33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	3	LYS



#### 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	197/197~(100%)	175~(89%)	22 (11%)		6	1	
1	В	196/197~(100%)	175~(89%)	21 (11%)		6	1	
All	All	393/394~(100%)	350~(89%)	43 (11%)		6	1	

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	1	MET
1	А	30	SER
1	А	50	MET
1	А	53	GLU
1	А	54	ARG
1	А	55	LEU
1	А	134	ARG
1	А	138	ARG
1	А	141	VAL
1	А	152	LYS
1	А	155	LYS
1	А	176	LYS
1	А	189	LEU
1	А	192	SER
1	А	196	SER
1	А	205	GLU
1	А	207	ARG
1	А	217	LYS
1	А	220	ARG
1	А	221	THR
1	А	241	GLU
1	A	247	LYS
1	В	2	SER
1	В	19	GLN
1	В	24	LEU
1	В	50	MET
1	В	52	LYS

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Mol	Chain	Res	Type
1	В	53	GLU
1	В	55	LEU
1	В	62	ILE
1	В	70	LYS
1	В	107	GLU
1	В	131	LEU
1	В	132	GLN
1	В	134	ARG
1	В	138	ARG
1	В	147	ILE
1	В	152	LYS
1	В	176	LYS
1	В	197	LYS
1	В	220	ARG
1	В	226	ARG
1	В	239	LYS

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Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	В	19	GLN
1	В	132	GLN

#### 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 carbohydrates in this entry.

### 5.6 Ligand geometry (i)

4 ligands are modelled in this entry.



1TPF

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 True		Chain	Dog	Tinle	Bond lengths			E	Bond ang	gles
	Type	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
2	DMS	А	252	-	3,3,3	0.42	0	3,3,3	0.52	0
2	DMS	В	251	-	3,3,3	0.56	0	3,3,3	0.28	0
2	DMS	А	251	-	3,3,3	0.42	0	3,3,3	0.72	0
2	DMS	В	252	-	3,3,3	0.39	0	3,3,3	0.55	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	252	DMS	5	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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

## 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

## 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

