



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 10:15 PM UTC

PDB ID : 2VME / pdb\_00002vme  
Title : Structure of the wild-type discoidin II from Dictyostelium discoideum  
Authors : Aragao, K.S.; Satre, M.; Imberty, A.; Varrot, A.  
Deposited on : 2008-01-25  
Resolution : 2.45 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
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

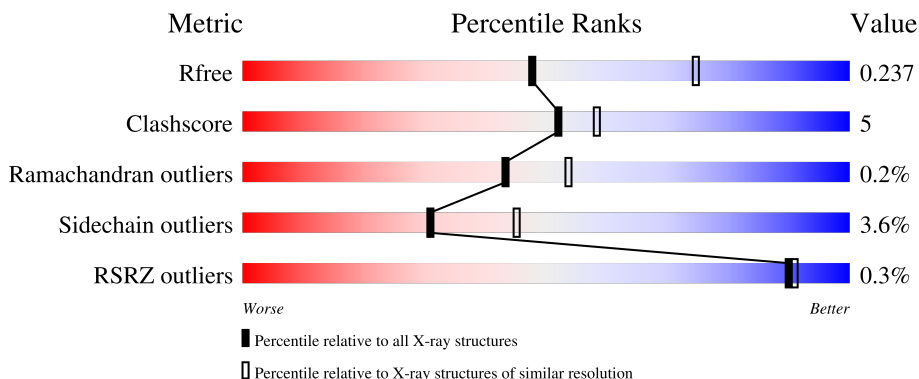
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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.



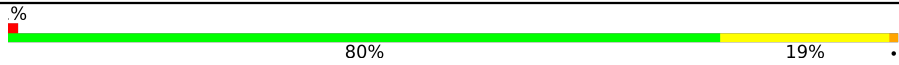
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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  $\geq 3$ , 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	257	
1	B	257	
1	C	257	
1	D	257	
1	E	257	

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Mol	Chain	Length	Quality of chain
1	F	257	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into two segments: a green segment on the left labeled '80%' and a yellow segment on the right labeled '19%'. A small red square is at the beginning of the bar, and a small black dot is at the end. A '%' symbol is positioned above the start of the bar.</p>

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 12771 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 DISCOIDIN-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	257	2027	1268	356	399	1	3	0	2	1
1	B	257	2017	1262	354	397	1	3	0	0	1
1	C	256	2015	1263	354	394	1	3	0	1	1
1	D	257	2024	1267	356	397	1	3	0	1	1
1	E	257	2017	1262	354	397	1	3	0	0	1
1	F	256	2015	1263	354	394	1	3	0	1	1

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		
2	C	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		
2	E	1	Total	Ca	0	0
			1	1		
2	F	1	Total	Ca	0	0
			1	1		

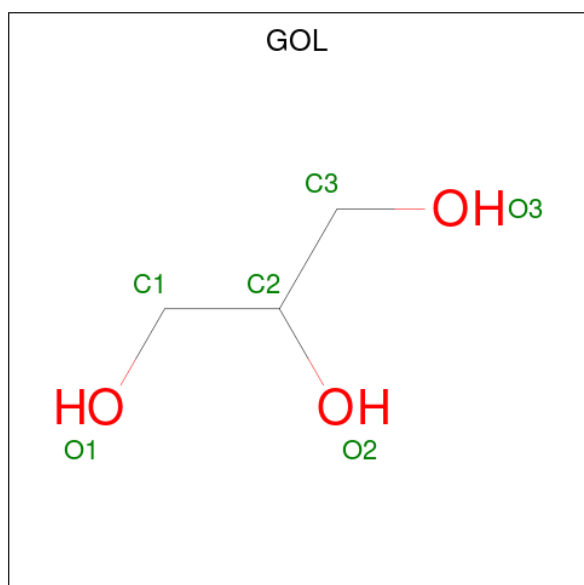
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Zn 1 1	0	0
3	D	1	Total Zn 1 1	0	0

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cl 1 1	0	0
4	D	1	Total Cl 1 1	0	0

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



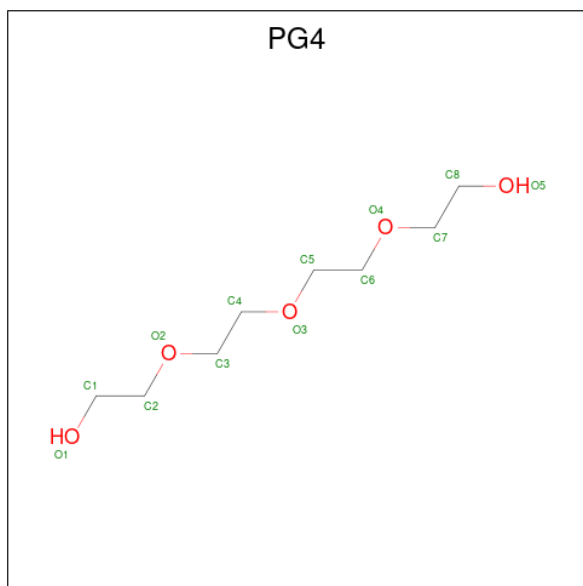
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	C	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		
5	E	1	Total	C	O	0	0
			6	3	3		
5	E	1	Total	C	O	0	0
			6	3	3		
5	E	1	Total	C	O	0	0
			6	3	3		
5	F	1	Total	C	O	0	0
			6	3	3		
5	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			13	8	5		

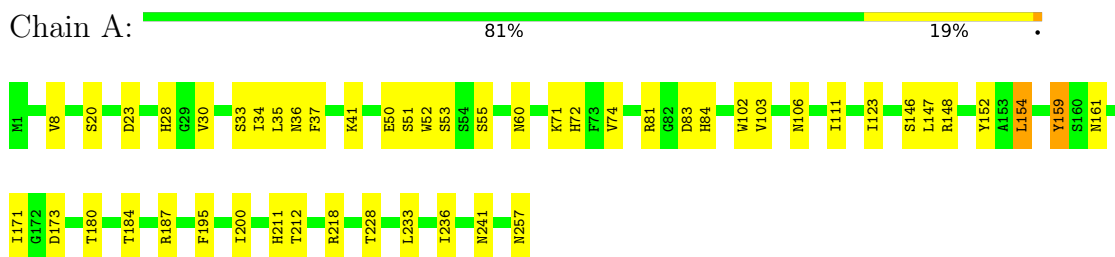
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	107	Total 107	O 107	0	0
7	B	120	Total 120	O 120	0	0
7	C	110	Total 110	O 110	0	0
7	D	87	Total 87	O 87	0	0
7	E	60	Total 60	O 60	0	0
7	F	59	Total 59	O 59	0	0

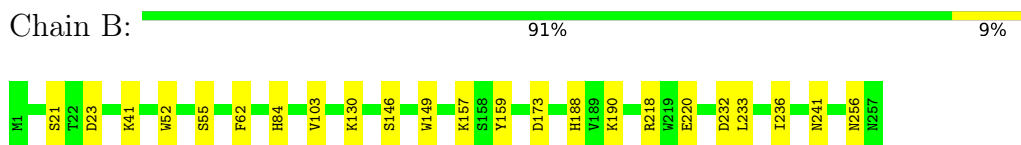
### 3 Residue-property plots [i](#)

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.

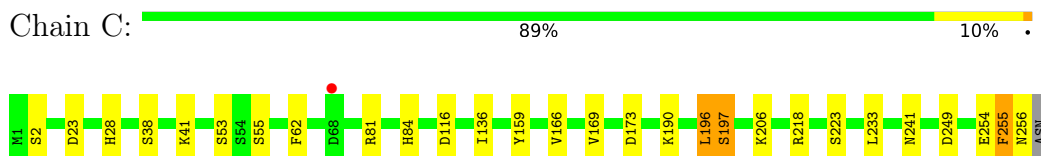
- Molecule 1: DISCOIDIN-2



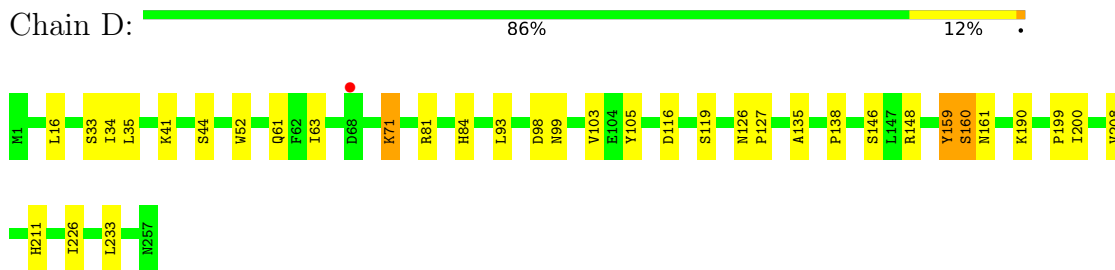
- Molecule 1: DISCOIDIN-2



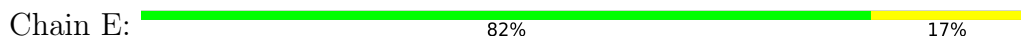
- Molecule 1: DISCOIDIN-2

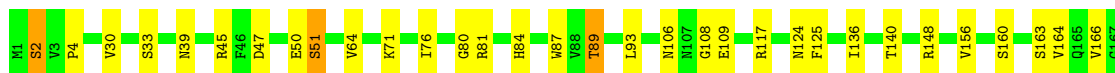


- Molecule 1: DISCOIDIN-2

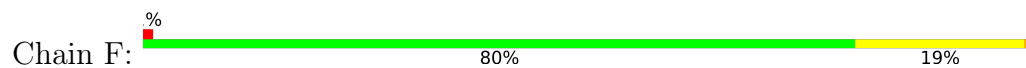


- Molecule 1: DISCOIDIN-2





• Molecule 1: DISCOIDIN-2



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	287.88Å 56.28Å 123.67Å 90.00° 109.10° 90.00°	Depositor
Resolution (Å)	26.80 – 2.45 26.80 – 2.45	Depositor EDS
% Data completeness (in resolution range)	95.9 (26.80-2.45) 95.8 (26.80-2.45)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.86 (at 2.44Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.181 , 0.238 0.180 , 0.237	Depositor DCC
$R_{free}$ test set	3380 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.5	Xtrriage
Anisotropy	0.444	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 33.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12771	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, PG4, CA, CL, GOL, HIP

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	0.85	0/2063	0.93	2/2803 (0.1%)
1	B	0.88	0/2047	0.95	1/2781 (0.0%)
1	C	0.86	0/2049	0.94	0/2785
1	D	0.84	0/2058	0.98	1/2796 (0.0%)
1	E	0.83	0/2047	0.92	1/2781 (0.0%)
1	F	0.82	0/2049	0.95	0/2785
All	All	0.85	0/12313	0.95	5/16731 (0.0%)

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	F	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	171	ILE	N-CA-C	-5.95	104.71	110.72
1	A	60	ASN	N-CA-C	5.39	119.55	112.92
1	D	160	SER	N-CA-C	5.35	118.28	109.72
1	E	117	ARG	N-CA-C	5.21	116.65	110.97
1	B	149	TRP	N-CA-C	5.07	116.01	108.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	255	PHE	Peptide

## 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	2027	0	1948	33	0
1	B	2017	0	1936	9	0
1	C	2015	0	1937	12	0
1	D	2024	0	1943	24	0
1	E	2017	0	1936	21	0
1	F	2015	0	1937	31	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
5	A	12	0	16	1	0
5	B	18	0	24	0	0
5	C	12	0	16	1	0
5	D	12	0	16	0	0
5	E	18	0	24	1	0
5	F	18	0	24	1	0
6	C	13	0	18	1	0
7	A	107	0	0	0	0
7	B	120	0	0	0	0
7	C	110	0	0	0	0
7	D	87	0	0	0	0
7	E	60	0	0	2	0
7	F	59	0	0	2	0
All	All	12771	0	11775	122	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 5.

The worst 5 of 122 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:D:161:ASN:ND2	1:F:161:ASN:HD22	1.72	0.88
1:D:161:ASN:HD21	1:F:161:ASN:HD22	1.24	0.82
1:D:200:ILE:HD12	1:D:200:ILE:O	1.79	0.82
1:D:126:ASN:HD22	1:D:127:PRO:HA	1.46	0.81
1:D:200:ILE:HD12	1:D:200:ILE:C	2.08	0.78

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	256/257 (100%)	243 (95%)	13 (5%)	0	100	100
1	B	254/257 (99%)	244 (96%)	10 (4%)	0	100	100
1	C	254/257 (99%)	245 (96%)	9 (4%)	0	100	100
1	D	255/257 (99%)	244 (96%)	11 (4%)	0	100	100
1	E	254/257 (99%)	242 (95%)	10 (4%)	2 (1%)	16	20
1	F	254/257 (99%)	240 (94%)	13 (5%)	1 (0%)	30	37
All	All	1527/1542 (99%)	1458 (96%)	66 (4%)	3 (0%)	43	54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	2	SER
1	E	51	SER
1	F	145	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	227/226 (100%)	220 (97%)	7 (3%)	35	50
1	B	225/226 (100%)	220 (98%)	5 (2%)	45	60
1	C	225/226 (100%)	214 (95%)	11 (5%)	22	33
1	D	226/226 (100%)	219 (97%)	7 (3%)	35	50
1	E	225/226 (100%)	215 (96%)	10 (4%)	25	37
1	F	225/226 (100%)	217 (96%)	8 (4%)	31	45
All	All	1353/1356 (100%)	1305 (96%)	48 (4%)	31	46

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	190	LYS
1	E	166	VAL
1	D	233	LEU
1	E	64	VAL
1	E	223	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	214	ASN
1	F	13	ASN
1	F	142	ASN
1	B	256	ASN
1	B	142	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains

6 non-standard protein/DNA/RNA residues 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
1	HIP	F	84	1	10,14,15	2.00	2 (20%)	4,20,22	1.40	0
1	HIP	C	84	1	10,14,15	1.97	2 (20%)	4,20,22	1.19	0
1	HIP	B	84	1	10,14,15	2.33	2 (20%)	4,20,22	1.06	0
1	HIP	A	84	1	10,14,15	2.24	2 (20%)	4,20,22	1.39	1 (25%)
1	HIP	D	84	1	10,14,15	2.13	2 (20%)	4,20,22	1.54	1 (25%)
1	HIP	E	84	1	10,14,15	2.06	2 (20%)	4,20,22	0.96	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
1	HIP	F	84	1	-	2/5/12/14	0/1/1/1
1	HIP	C	84	1	-	2/5/12/14	0/1/1/1
1	HIP	B	84	1	-	2/5/12/14	0/1/1/1
1	HIP	A	84	1	-	2/5/12/14	0/1/1/1
1	HIP	D	84	1	-	2/5/12/14	0/1/1/1
1	HIP	E	84	1	-	2/5/12/14	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	84	HIP	P-O1P	6.17	1.55	1.46
1	A	84	HIP	P-O1P	5.73	1.54	1.46
1	F	84	HIP	P-O1P	4.87	1.53	1.46
1	D	84	HIP	P-O1P	4.85	1.53	1.46
1	C	84	HIP	P-O1P	4.74	1.53	1.46

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	84	HIP	O3P-P-O1P	-2.16	107.64	112.95
1	A	84	HIP	O3P-P-O1P	-2.02	107.98	112.95

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	84	HIP	C-CA-CB-CG
1	B	84	HIP	C-CA-CB-CG
1	C	84	HIP	C-CA-CB-CG
1	D	84	HIP	C-CA-CB-CG
1	E	84	HIP	C-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	F	84	HIP	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 10 are monoatomic - leaving 16 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	$\# Z  > 2$
5	GOL	B	504	-	5,5,5	0.61	0	5,5,5	0.83	0
5	GOL	F	503	-	5,5,5	0.45	0	5,5,5	0.41	0
6	PG4	C	505	-	12,12,12	0.67	0	11,11,11	0.62	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	GOL	E	506	-	5,5,5	0.34	0	5,5,5	0.46	0
5	GOL	E	507	-	5,5,5	0.41	0	5,5,5	0.71	0
5	GOL	F	506	-	5,5,5	0.25	0	5,5,5	0.55	0
5	GOL	E	504	-	5,5,5	0.29	0	5,5,5	0.58	0
5	GOL	A	503	-	5,5,5	0.42	0	5,5,5	0.48	0
5	GOL	A	504	-	5,5,5	0.46	0	5,5,5	0.39	0
5	GOL	D	504	-	5,5,5	0.55	0	5,5,5	0.63	0
5	GOL	C	504	-	5,5,5	0.58	0	5,5,5	0.35	0
5	GOL	F	504	-	5,5,5	0.53	0	5,5,5	0.82	0
5	GOL	C	506	-	5,5,5	0.32	0	5,5,5	0.35	0
5	GOL	B	506	-	5,5,5	0.46	0	5,5,5	0.95	0
5	GOL	B	503	-	5,5,5	0.47	0	5,5,5	0.84	0
5	GOL	D	506	-	5,5,5	0.51	0	5,5,5	0.49	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	GOL	B	504	-	-	2/4/4/4	-
5	GOL	F	503	-	-	0/4/4/4	-
6	PG4	C	505	-	-	6/10/10/10	-
5	GOL	E	506	-	-	4/4/4/4	-
5	GOL	E	507	-	-	1/4/4/4	-
5	GOL	F	506	-	-	0/4/4/4	-
5	GOL	E	504	-	-	2/4/4/4	-
5	GOL	A	503	-	-	4/4/4/4	-
5	GOL	A	504	-	-	2/4/4/4	-
5	GOL	D	504	-	-	2/4/4/4	-
5	GOL	C	504	-	-	0/4/4/4	-
5	GOL	F	504	-	-	2/4/4/4	-
5	GOL	C	506	-	-	1/4/4/4	-
5	GOL	B	506	-	-	2/4/4/4	-
5	GOL	B	503	-	-	0/4/4/4	-
5	GOL	D	506	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	503	GOL	O1-C1-C2-O2
5	A	503	GOL	O1-C1-C2-C3
5	A	503	GOL	C1-C2-C3-O3
5	A	504	GOL	C1-C2-C3-O3
5	B	506	GOL	C1-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	505	PG4	1	0
5	E	506	GOL	1	0
5	A	503	GOL	1	0
5	F	504	GOL	1	0
5	C	506	GOL	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 [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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	256/257 (99%)	-0.56	0 <a href="#">100</a> <a href="#">100</a>	13, 24, 37, 46	3 (1%)
1	B	256/257 (99%)	-0.78	0 <a href="#">100</a> <a href="#">100</a>	14, 21, 28, 34	1 (0%)
1	C	255/257 (99%)	-0.64	1 (0%) <a href="#">88</a> <a href="#">89</a>	13, 23, 33, 44	2 (0%)
1	D	256/257 (99%)	-0.50	1 (0%) <a href="#">88</a> <a href="#">89</a>	13, 26, 38, 47	2 (0%)
1	E	256/257 (99%)	-0.44	0 <a href="#">100</a> <a href="#">100</a>	14, 27, 42, 50	1 (0%)
1	F	255/257 (99%)	-0.26	2 (0%) <a href="#">82</a> <a href="#">83</a>	18, 31, 44, 49	2 (0%)
All	All	1534/1542 (99%)	-0.53	4 (0%) <a href="#">90</a> <a href="#">91</a>	13, 25, 39, 50	11 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	68	ASP	2.6
1	D	68	ASP	2.5
1	F	188[A]	HIS	2.4
1	F	256	ASN	2.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [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<sup>th</sup> 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(Å <sup>2</sup> )	Q<0.9
1	HIP	F	84	14/15	0.84	0.12	38,44,48,51	0
1	HIP	A	84	14/15	0.85	0.13	36,43,47,49	0
1	HIP	D	84	14/15	0.86	0.13	35,42,47,48	0
1	HIP	B	84	14/15	0.89	0.10	28,34,39,39	0
1	HIP	E	84	14/15	0.91	0.10	38,48,53,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
1	HIP	C	84	14/15	0.91	0.10	29,38,44,45	0

### 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, 95<sup>th</sup> 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(Å <sup>2</sup> )	Q<0.9
5	GOL	E	507	6/6	0.81	0.15	50,53,54,54	0
6	PG4	C	505	13/13	0.83	0.14	29,40,45,46	0
5	GOL	F	506	6/6	0.86	0.10	39,41,42,43	0
5	GOL	E	504	6/6	0.87	0.09	32,38,41,43	0
5	GOL	C	506	6/6	0.87	0.13	46,48,48,49	0
5	GOL	D	506	6/6	0.88	0.11	45,46,47,48	0
5	GOL	E	506	6/6	0.89	0.12	50,51,51,51	0
5	GOL	B	506	6/6	0.89	0.10	33,36,37,40	0
5	GOL	B	503	6/6	0.90	0.08	33,39,41,44	0
5	GOL	F	503	6/6	0.91	0.09	44,45,46,47	0
5	GOL	B	504	6/6	0.92	0.09	19,22,23,25	0
5	GOL	A	503	6/6	0.92	0.08	34,36,37,37	0
5	GOL	F	504	6/6	0.93	0.09	29,33,33,34	0
5	GOL	A	504	6/6	0.94	0.09	28,29,30,32	0
5	GOL	C	504	6/6	0.95	0.07	23,23,25,25	0
5	GOL	D	504	6/6	0.95	0.07	24,28,29,32	0
2	CA	D	500	1/1	0.97	0.07	26,26,26,26	0
2	CA	F	500	1/1	0.97	0.04	25,25,25,25	0
2	CA	A	500	1/1	0.97	0.05	25,25,25,25	0
2	CA	E	500	1/1	0.98	0.07	31,31,31,31	0
4	CL	D	502	1/1	0.98	0.15	26,26,26,26	0
4	CL	A	502	1/1	0.99	0.12	15,15,15,15	0
2	CA	C	500	1/1	0.99	0.05	21,21,21,21	0
2	CA	B	500	1/1	0.99	0.04	19,19,19,19	0
3	ZN	A	501	1/1	1.00	0.09	14,14,14,14	0
3	ZN	D	501	1/1	1.00	0.08	16,16,16,16	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.