



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 26, 2017 – 03:52 PM EDT

PDB ID : 4MJM  
Title : Crystal Structure of the Inosine 5'-monophosphate Dehydrogenase, with a Short Internal Deletion of CBS Domain from Bacillus anthracis str. Ames  
Authors : Kim, Y.; Makowska-Grzyska, M.; Gu, M.; Anderson, W.F.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : unknown  
Resolution : 2.25 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029824
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20029824

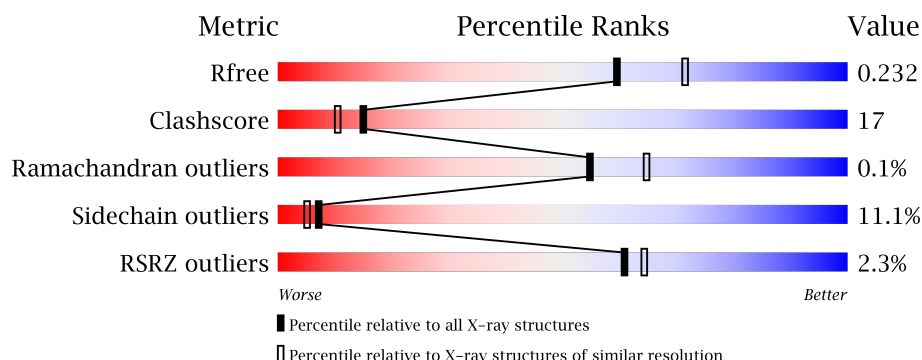
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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))
$R_{free}$	100719	1062 (2.26-2.26)
Clashscore	112137	1178 (2.26-2.26)
Ramachandran outliers	110173	1145 (2.26-2.26)
Sidechain outliers	110143	1146 (2.26-2.26)
RSRZ outliers	101464	1066 (2.26-2.26)

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  $\geq 3$ , 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	385	<div> <div>2%</div> <div> <div></div> <div>59%</div> <div>23%</div> <div>•</div> <div>15%</div> </div> </div>
1	B	385	<div> <div>•</div> <div> <div></div> <div>53%</div> <div>28%</div> <div>•</div> <div>15%</div> </div> </div>
1	C	385	<div> <div>3%</div> <div> <div></div> <div>52%</div> <div>29%</div> <div>•</div> <div>15%</div> </div> </div>
1	D	385	<div> <div>2%</div> <div> <div></div> <div>52%</div> <div>29%</div> <div>•</div> <div>15%</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EDO	B	501	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10136 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 Inosine-5'-monophosphate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	1	0
			2411	1514	421	463	13			
1	B	328	Total	C	N	O	S	0	0	0
			2408	1514	419	461	14			
1	C	329	Total	C	N	O	S	0	0	0
			2412	1517	419	462	14			
1	D	328	Total	C	N	O	S	0	0	0
			2409	1514	422	460	13			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	EXPRESSION TAG	UNP Q81W29
A	-1	ASN	-	EXPRESSION TAG	UNP Q81W29
A	0	ALA	-	EXPRESSION TAG	UNP Q81W29
A	95	GLY	-	LINKER	UNP Q81W29
B	-2	SER	-	EXPRESSION TAG	UNP Q81W29
B	-1	ASN	-	EXPRESSION TAG	UNP Q81W29
B	0	ALA	-	EXPRESSION TAG	UNP Q81W29
B	200	GLY	-	LINKER	UNP Q81W29
C	-2	SER	-	EXPRESSION TAG	UNP Q81W29
C	-1	ASN	-	EXPRESSION TAG	UNP Q81W29
C	0	ALA	-	EXPRESSION TAG	UNP Q81W29
C	95	GLY	-	LINKER	UNP Q81W29
D	-2	SER	-	EXPRESSION TAG	UNP Q81W29
D	-1	ASN	-	EXPRESSION TAG	UNP Q81W29
D	0	ALA	-	EXPRESSION TAG	UNP Q81W29
D	200	GLY	-	LINKER	UNP Q81W29

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).

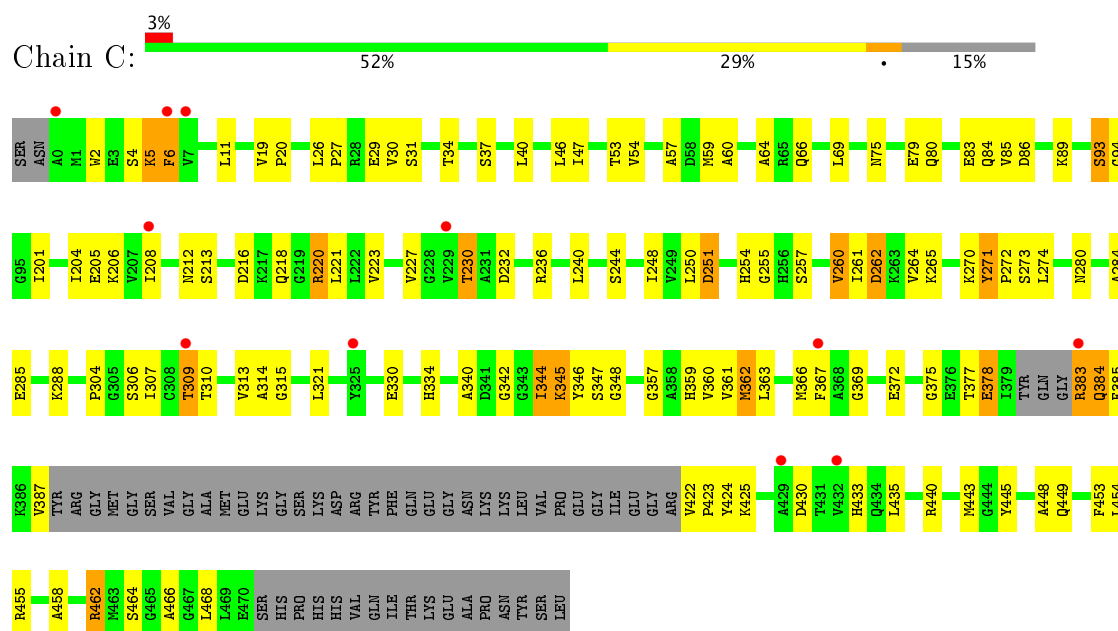


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0

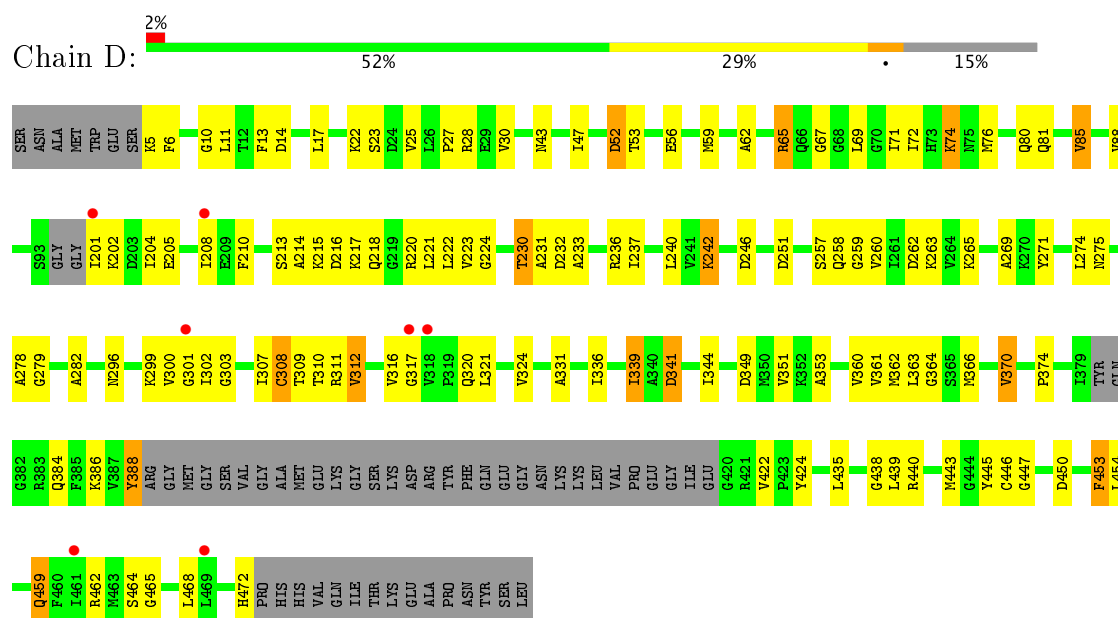
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	113	Total O 113 113	0	0
3	B	106	Total O 106 106	0	0
3	C	108	Total O 108 108	0	0
3	D	137	Total O 137 137	0	0





• Molecule 1: Inosine-5'-monophosphate dehydrogenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	84.33Å 84.25Å 84.31Å 110.01° 109.22° 109.19°	Depositor
Resolution (Å)	48.83 – 2.25 48.83 – 2.25	Depositor EDS
% Data completeness (in resolution range)	94.1 (48.83-2.25) 76.3 (48.83-2.25)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.29 (at 2.24Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.206 , 0.232 0.206 , 0.232	Depositor DCC
$R_{free}$ test set	3948 reflections (4.98%)	DCC
Wilson B-factor (Å <sup>2</sup> )	40.4	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 70.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.22$	Xtriage

*Continued on next page...*

<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.



*Continued from previous page...*

Property	Value	Source
Estimated twinning fraction	0.077 for -k,-l,h+k+l 0.077 for h+k+l,-h,-k 0.457 for -l,-h,h+k+l 0.457 for -k,h+k+l,-h 0.078 for h+k+l,-l,-h 0.078 for -l,h+k+l,-k 0.078 for -h-k-l,k,h 0.078 for l,k,-h-k-l 0.078 for l,h,k 0.078 for k,l,h 0.078 for k,-h-k-l,l 0.078 for -h-k-l,h,l 0.078 for h,-h-k-l,k 0.078 for h,l,-h-k-l 0.377 for l,-h-k-l,h 0.077 for -h,h+k+l,-l 0.458 for -h-k-l,l,k 0.377 for -h,-l,-k 0.377 for k,h,-h-k-l 0.078 for -h,-k,h+k+l 0.077 for -l,-k,-h 0.377 for h+k+l,-k,-l 0.079 for -k,-h,-l	Xtriage
Reported twinning fraction	0.500 for -h-k-l,l,k	Depositor
Outliers	0 of 79280 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10136	wwPDB-VP
Average B, all atoms ( $\text{\AA}^2$ )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% of the height of the origin peak. No significant pseudotranslation is detected.*

## 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: EDO

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	0.27	1/2438 (0.0%)	0.46	1/3290 (0.0%)
1	B	0.26	1/2436 (0.0%)	0.47	1/3287 (0.0%)
1	C	0.26	1/2440 (0.0%)	0.46	1/3294 (0.0%)
1	D	0.27	0/2436	0.46	1/3286 (0.0%)
All	All	0.27	3/9750 (0.0%)	0.46	4/13157 (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	C	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	211	PRO	N-CD	5.31	1.55	1.47
1	C	272	PRO	N-CD	5.29	1.55	1.47
1	B	272	PRO	N-CD	5.13	1.55	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	303	GLY	C-N-CD	5.99	140.99	128.40
1	B	271	TYR	C-N-CD	5.75	140.47	128.40
1	C	271	TYR	C-N-CD	5.51	139.97	128.40
1	A	210	PHE	C-N-CD	5.38	139.71	128.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	230	THR	Peptide

## 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	2411	0	2482	86	0
1	B	2408	0	2475	94	0
1	C	2412	0	2487	86	0
1	D	2409	0	2482	86	0
2	A	12	0	18	0	0
2	B	4	0	6	0	0
2	C	4	0	6	0	0
2	D	12	0	18	1	0
3	A	113	0	0	6	0
3	B	106	0	0	18	0
3	C	108	0	0	13	0
3	D	137	0	0	9	0
All	All	10136	0	9974	331	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 17.

The worst 5 of 331 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:B:281:VAL:HG21	1:B:287:THR:HG23	1.48	0.94
1:B:455:ARG:HD3	3:B:704:HOH:O	1.77	0.83
1:D:76:MET:HB2	1:D:80:GLN:HG3	1.62	0.81
1:A:387:VAL:O	1:A:388:TYR:HB2	1.84	0.76
1:A:470:GLU:OE2	1:B:12:THR:HG21	1.86	0.75

There are no symmetry-related clashes.

## 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	323/385 (84%)	299 (93%)	24 (7%)	0	100	100
1	B	320/385 (83%)	292 (91%)	28 (9%)	0	100	100
1	C	323/385 (84%)	298 (92%)	25 (8%)	0	100	100
1	D	320/385 (83%)	296 (92%)	23 (7%)	1 (0%)	44	50
All	All	1286/1540 (84%)	1185 (92%)	100 (8%)	1 (0%)	55	65

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	364	GLY

### 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	253/299 (85%)	233 (92%)	20 (8%)	14	12
1	B	252/299 (84%)	222 (88%)	30 (12%)	6	4
1	C	253/299 (85%)	219 (87%)	34 (13%)	4	2
1	D	253/299 (85%)	225 (89%)	28 (11%)	7	5
All	All	1011/1196 (84%)	899 (89%)	112 (11%)	7	5

5 of 112 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	4	SER
1	C	220	ARG
1	D	316	VAL
1	C	6	PHE
1	C	83	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	457	ASN
1	C	81	GLN
1	D	457	ASN
1	C	66	GLN
1	C	212	ASN

### 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](#)

8 ligands 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
2	EDO	A	501	-	3,3,3	0.41	0	2,2,2	1.00	0
2	EDO	A	502	-	3,3,3	0.33	0	2,2,2	0.48	0
2	EDO	A	503	-	3,3,3	0.45	0	2,2,2	0.10	0
2	EDO	B	501	-	3,3,3	0.45	0	2,2,2	0.36	0
2	EDO	C	501	-	3,3,3	0.26	0	2,2,2	0.63	0
2	EDO	D	501	-	3,3,3	0.35	0	2,2,2	0.79	0
2	EDO	D	502	-	3,3,3	0.36	0	2,2,2	0.30	0
2	EDO	D	503	-	3,3,3	0.31	0	2,2,2	0.26	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
2	EDO	A	501	-	-	0/1/1/1	0/0/0/0
2	EDO	A	502	-	-	0/1/1/1	0/0/0/0
2	EDO	A	503	-	-	0/1/1/1	0/0/0/0
2	EDO	B	501	-	-	0/1/1/1	0/0/0/0
2	EDO	C	501	-	-	0/1/1/1	0/0/0/0
2	EDO	D	501	-	-	0/1/1/1	0/0/0/0
2	EDO	D	502	-	-	0/1/1/1	0/0/0/0
2	EDO	D	503	-	-	0/1/1/1	0/0/0/0

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 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	502	EDO	1	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, 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	328/385 (85%)	-0.09	9 (2%) 55 58	24, 41, 77, 128	0
1	B	328/385 (85%)	-0.12	3 (0%) 84 85	24, 43, 79, 143	0
1	C	329/385 (85%)	0.03	11 (3%) 47 51	29, 49, 91, 141	0
1	D	328/385 (85%)	-0.08	7 (2%) 64 67	27, 45, 82, 161	0
All	All	1313/1540 (85%)	-0.07	30 (2%) 61 64	24, 45, 84, 161	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	201	ILE	6.6
1	A	293	ALA	5.2
1	C	309	THR	5.0
1	C	7	VAL	5.0
1	B	379	ILE	4.8

### 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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	EDO	B	501	4/4	0.82	0.19	8.67	82,83,87,89	0
2	EDO	C	501	4/4	0.95	0.10	-	41,42,43,45	0
2	EDO	A	503	4/4	0.93	0.12	-	44,47,48,52	0
2	EDO	A	502	4/4	0.91	0.11	-	57,60,63,65	0
2	EDO	D	501	4/4	0.90	0.14	-	39,45,47,49	0
2	EDO	D	502	4/4	0.96	0.10	-	35,36,41,42	0
2	EDO	A	501	4/4	0.97	0.13	-	40,41,43,46	0
2	EDO	D	503	4/4	0.97	0.12	-	38,39,40,40	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.