



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 02:32 pm GMT

PDB ID : 3ZH8  
Title : A novel small molecule aPKC inhibitor  
Authors : Kjaer, S.; Purkiss, A.G.; Kostecky, B.; Knowles, P.P.; Soriano, E.; Murray-Rust, J.; McDonald, N.Q.  
Deposited on : 2012-12-20  
Resolution : 2.74 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 : trunk28620  
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) : recalc28949

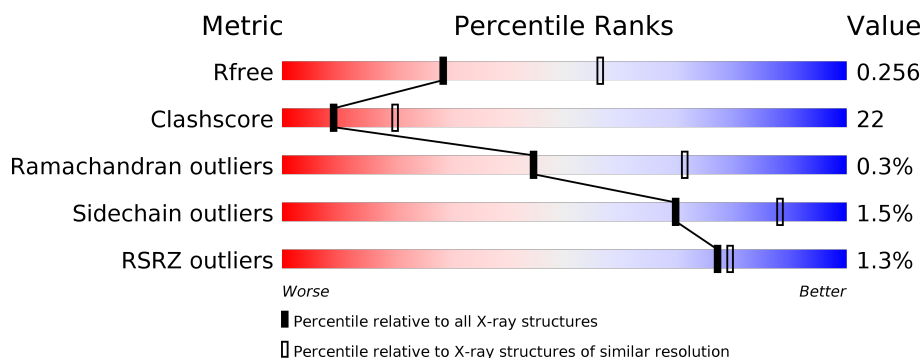
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.74 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	3342 (2.78-2.70)
Clashscore	112137	3731 (2.78-2.70)
Ramachandran outliers	110173	3670 (2.78-2.70)
Sidechain outliers	110143	3671 (2.78-2.70)
RSRZ outliers	101464	3362 (2.78-2.70)

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	349	<div> <div>2%</div> <div> <div></div> <div>62%</div> <div>28%</div> <div>• 8%</div> </div> </div>
1	B	349	<div> <div>%</div> <div> <div></div> <div>59%</div> <div>31%</div> <div>• 9%</div> </div> </div>
1	C	349	<div> <div>%</div> <div> <div></div> <div>57%</div> <div>33%</div> <div>• 10%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	IOD	A	904	-	-	X	-
2	IOD	B	904	-	-	X	-
2	IOD	C	904	-	-	X	-
5	EDO	A	1584	-	-	-	X
5	EDO	B	1582	-	-	-	X
5	EDO	B	1583	-	-	-	X
5	EDO	B	1584	-	-	-	X
5	EDO	B	1585	-	-	-	X
5	EDO	C	1581	-	-	-	X
5	EDO	C	1582	-	-	-	X
5	EDO	C	1583	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7849 atoms, of which 135 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 PROTEIN KINASE C IOTA TYPE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	P	S	0	1	0
			2508	1618	408	467	2	13			
1	B	319	Total	C	N	O	P	S	0	1	0
			2552	1639	419	480	2	12			
1	C	314	Total	C	N	O	P	S	0	1	0
			2436	1569	400	452	2	13			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	586	SER	CYS	ENGINEERED MUTATION	UNP P41743
B	586	SER	CYS	ENGINEERED MUTATION	UNP P41743
C	586	SER	CYS	ENGINEERED MUTATION	UNP P41743

- Molecule 2 is IODIDE ION (three-letter code: IOD) (formula: I).

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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

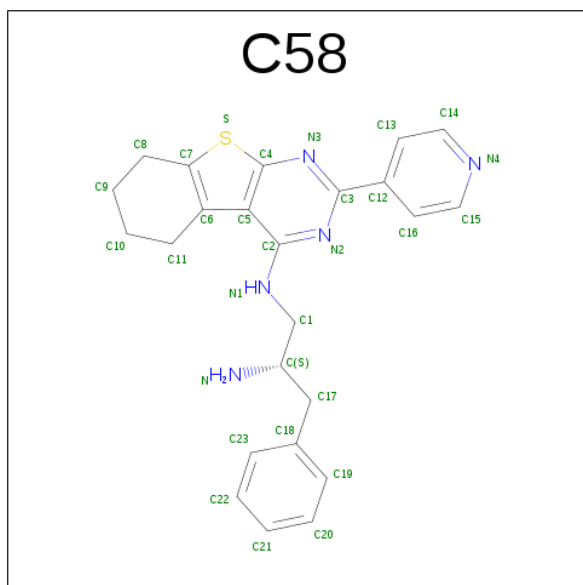
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	A	1	Total	Cl	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total Cl 1 1	0	0

- Molecule 4 is (2S)-3-PHENYL-N 1 -[2-(PYRIDIN-4-YL)-5,6,7,8-TETRAHYDRO[1]BENZOTHIENO[2,3-D]PYRIMIDIN-4-YL]PROPANE-1,2-DIAMINE (three-letter code: C58) (formula: C<sub>24</sub>H<sub>25</sub>N<sub>5</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C H N S 55 24 25 5 1	0	0
4	B	1	Total C H N S 55 24 25 5 1	0	0
4	C	1	Total C H N S 55 24 25 5 1	0	0

- Molecule 5 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
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	B	1	Total	C	H	O	0	0
			10	2	6	2		
5	B	1	Total	C	H	O	0	0
			10	2	6	2		
5	B	1	Total	C	H	O	0	0
			10	2	6	2		
5	C	1	Total	C	H	O	0	0
			10	2	6	2		
5	C	1	Total	C	H	O	0	0
			10	2	6	2		
5	C	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	22	Total	O	0	0
			22	22		
6	B	29	Total	O	0	0
			29	29		

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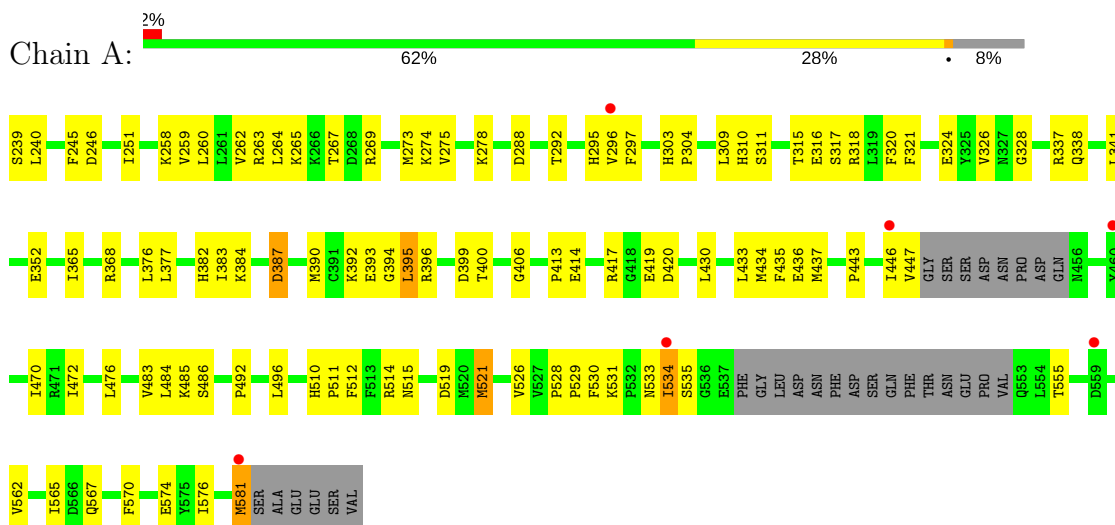
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	22	Total	O	0	0
			22	22		

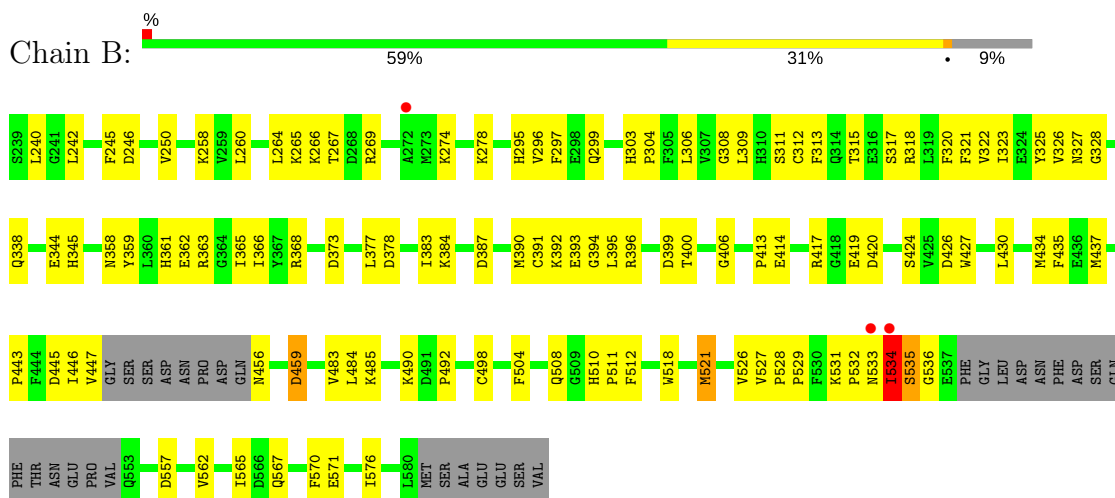
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: PROTEIN KINASE C IOTA TYPE



#### • Molecule 1: PROTEIN KINASE C IOTA TYPE



#### • Molecule 1: PROTEIN KINASE C IOTA TYPE





SER	GLY	GLU	PHE	GLY	LEU	ASP	ASN	PHE	ASP	SER	GLN	PHE	THR	ASN	GLU	PRO	VAL	D553	L554	T555	P556	D557	D558	D559	D560	I561	V562	R563	K564	I565	E569	F570	F573	L579	LEU	MET	SER	ALA	GLU	GLU	SER	VAL				
R441	S442	D445	I446	V447	GLY	SER	SER	ASP	ASN	PRO	ASP	GLN	R456	L466	I470	R471	I472	L476	A481	S482	V483	L484	K485	S486	F487	K490	D491	P492	L496	G497	G503	Q508	G509	H510	P511	F512	W518	D519	H520	H521	E522	Q525	P528	P529	N533	ILE
M335	R339	L355	Y369	L360	H361	E362	R363	G364	I365	I366	Y367	R368	D369	L370	K371	L372	D373	N374	V375	L376	I383	K384	L385	T386	D387	M390	C391	K392	E393	G394	L395	R396	D399	C405	Y410	P413	E414	I415	L416	R417	F423	L430	M434	M437		
S239	L242	F245	V250	I251	G252	R253	Y256	V259	L260	L261	L264	K265	K266	T267	D268	R269	I270	Y271	K274	V290	K294	H295	V296	F297	E298	Q299	H303	P304	F305	L306	V307	G308	L309	H310	S311	T315	L319	F320	F321	V322	Y325	V326	N327	D330	L331	

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	113.58Å 113.58Å 82.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.23 – 2.74 49.18 – 2.74	Depositor EDS
% Data completeness (in resolution range)	100.0 (42.23-2.74) 100.0 (49.18-2.74)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.85 (at 2.73Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8.1_1168)	Depositor
R, $R_{free}$	0.210 , 0.257 0.206 , 0.256	Depositor DCC
$R_{free}$ test set	1576 reflections (5.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	53.1	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.039 for -h,-k,l 0.308 for h,-h-k,-l 0.043 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7849	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, IOD, C58, EDO, CL

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	0.23	0/2544	0.40	0/3441
1	B	0.25	0/2588	0.40	0/3497
1	C	0.23	0/2471	0.40	0/3349
All	All	0.24	0/7603	0.40	0/10287

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	2508	0	2363	106	0
1	B	2552	0	2436	120	0
1	C	2436	0	2250	101	0
2	A	4	0	0	5	0
2	B	4	0	0	5	0
2	C	4	0	0	4	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	30	25	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	30	25	25	1	0
4	C	30	25	25	1	0
5	A	12	18	18	2	0
5	B	16	24	24	5	0
5	C	12	18	18	4	0
6	A	22	0	0	1	0
6	B	29	0	0	4	0
6	C	22	0	0	1	0
All	All	7714	135	7184	329	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 22.

The worst 5 of 329 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:387:ASP:HA	2:B:904:IOD:I	2.16	1.16
1:A:387:ASP:HA	2:A:904:IOD:I	2.30	1.00
1:B:366:ILE:HD11	1:B:395:LEU:CD2	1.91	0.99
1:B:366:ILE:HD11	1:B:395:LEU:HD21	1.48	0.95
1:B:390:MET:HE1	1:B:406:GLY:N	1.82	0.94

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	312/349 (89%)	299 (96%)	11 (4%)	2 (1%)	28	54
1	B	311/349 (89%)	302 (97%)	8 (3%)	1 (0%)	44	71
1	C	306/349 (88%)	299 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	929/1047 (89%)	900 (97%)	26 (3%)	3 (0%)	44 71

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	534	ILE
1	A	534	ILE
1	A	387	ASP

### 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	253/311 (81%)	249 (98%)	4 (2%)	68 87
1	B	267/311 (86%)	262 (98%)	5 (2%)	62 85
1	C	238/311 (76%)	236 (99%)	2 (1%)	85 94
All	All	758/933 (81%)	747 (98%)	11 (2%)	70 88

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	338	GLN
1	B	459	ASP
1	B	535	SER
1	A	581	MET
1	B	534	ILE

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

Mol	Chain	Res	Type
1	B	358	ASN
1	C	327	ASN

### 5.3.3 RNA ⓘ

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	TPO	A	403	1	9,10,11	1.21	0	10,14,16	1.15	1 (10%)
1	TPO	A	555	1	9,10,11	1.17	1 (11%)	10,14,16	1.06	2 (20%)
1	TPO	B	403	1	9,10,11	1.17	1 (11%)	10,14,16	1.08	1 (10%)
1	TPO	B	555	1	9,10,11	1.25	1 (11%)	10,14,16	0.99	0
1	TPO	C	403	1	9,10,11	1.12	0	10,14,16	0.94	0
1	TPO	C	555	1	9,10,11	1.29	1 (11%)	10,14,16	0.99	1 (10%)

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	TPO	A	403	1	-	0/8/11/13	0/0/0/0
1	TPO	A	555	1	-	0/8/11/13	0/0/0/0
1	TPO	B	403	1	-	0/8/11/13	0/0/0/0
1	TPO	B	555	1	-	0/8/11/13	0/0/0/0
1	TPO	C	403	1	-	0/8/11/13	0/0/0/0
1	TPO	C	555	1	-	0/8/11/13	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	555	TPO	CA-C	2.02	1.52	1.50
1	B	403	TPO	CA-C	2.16	1.53	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	555	TPO	CA-C	2.27	1.53	1.50
1	C	555	TPO	CA-C	2.53	1.53	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	403	TPO	CG2-CB-CA	-2.50	108.58	113.22
1	B	403	TPO	CG2-CB-CA	-2.33	108.88	113.22
1	A	555	TPO	CG2-CB-CA	-2.17	109.20	113.22
1	A	555	TPO	O-C-CA	-2.10	120.24	125.15
1	C	555	TPO	O-C-CA	-2.01	120.46	125.15

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	555	TPO	1	0
1	C	555	TPO	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 15 are monoatomic - leaving 13 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	$\# Z  > 2$
4	C58	A	1582	-	31,34,34	0.72	1 (3%)	31,47,47	0.71	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	EDO	A	1583	-	3,3,3	0.47	0	2,2,2	0.30	0
5	EDO	A	1584	-	3,3,3	0.45	0	2,2,2	0.32	0
5	EDO	A	1585	-	3,3,3	0.47	0	2,2,2	0.30	0
4	C58	B	1581	-	31,34,34	0.70	1 (3%)	31,47,47	1.14	0
5	EDO	B	1582	-	3,3,3	0.49	0	2,2,2	0.18	0
5	EDO	B	1583	-	3,3,3	0.49	0	2,2,2	0.27	0
5	EDO	B	1584	-	3,3,3	0.47	0	2,2,2	0.24	0
5	EDO	B	1585	-	3,3,3	0.47	0	2,2,2	0.29	0
4	C58	C	1580	-	31,34,34	0.67	1 (3%)	31,47,47	1.12	0
5	EDO	C	1581	-	3,3,3	0.42	0	2,2,2	0.37	0
5	EDO	C	1582	-	3,3,3	0.46	0	2,2,2	0.29	0
5	EDO	C	1583	-	3,3,3	0.45	0	2,2,2	0.31	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
4	C58	A	1582	-	-	0/13/20/20	0/5/5/5
5	EDO	A	1583	-	-	0/1/1/1	0/0/0/0
5	EDO	A	1584	-	-	0/1/1/1	0/0/0/0
5	EDO	A	1585	-	-	0/1/1/1	0/0/0/0
4	C58	B	1581	-	-	0/13/20/20	0/5/5/5
5	EDO	B	1582	-	-	0/1/1/1	0/0/0/0
5	EDO	B	1583	-	-	0/1/1/1	0/0/0/0
5	EDO	B	1584	-	-	0/1/1/1	0/0/0/0
5	EDO	B	1585	-	-	0/1/1/1	0/0/0/0
4	C58	C	1580	-	-	0/13/20/20	0/5/5/5
5	EDO	C	1581	-	-	0/1/1/1	0/0/0/0
5	EDO	C	1582	-	-	0/1/1/1	0/0/0/0
5	EDO	C	1583	-	-	0/1/1/1	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1581	C58	C6-C5	2.53	1.46	1.41
4	A	1582	C58	C6-C5	2.56	1.46	1.41
4	C	1580	C58	C6-C5	2.63	1.46	1.41

There are no bond angle outliers.



There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1582	C58	1	0
5	A	1584	EDO	1	0
5	A	1585	EDO	1	0
4	B	1581	C58	1	0
5	B	1582	EDO	2	0
5	B	1585	EDO	3	0
4	C	1580	C58	1	0
5	C	1581	EDO	2	0
5	C	1582	EDO	1	0
5	C	1583	EDO	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	318/349 (91%)	-0.06	6 (1%) 67 70	32, 60, 87, 118	0
1	B	317/349 (90%)	-0.11	3 (0%) 84 86	25, 50, 82, 110	0
1	C	312/349 (89%)	0.06	3 (0%) 82 84	41, 65, 101, 121	0
All	All	947/1047 (90%)	-0.04	12 (1%) 77 79	25, 59, 91, 121	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	534	ILE	4.2
1	A	581	MET	4.1
1	A	446	ILE	3.8
1	C	259	VAL	2.5
1	C	322	VAL	2.4

### 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. 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(Å <sup>2</sup> )	Q<0.9
1	TPO	A	555	11/12	0.96	0.15	-	52,66,95,95	0
1	TPO	C	403	11/12	0.98	0.15	-	46,52,58,58	0
1	TPO	B	403	11/12	0.98	0.13	-	36,39,45,46	0
1	TPO	A	403	11/12	0.97	0.12	-	41,51,58,58	0
1	TPO	B	555	11/12	0.97	0.10	-	55,61,66,100	0
1	TPO	C	555	11/12	0.90	0.15	-	78,99,130,135	0

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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(Å <sup>2</sup> )	Q<0.9
5	EDO	C	1581	4/4	0.90	0.50	17.70	65,78,79,80	0
5	EDO	B	1582	4/4	0.68	0.36	12.72	61,74,75,75	0
5	EDO	C	1583	4/4	0.69	0.49	12.14	81,97,98,98	0
5	EDO	B	1583	4/4	0.79	0.40	10.23	66,79,80,80	0
5	EDO	C	1582	4/4	0.88	0.39	4.98	58,70,72,73	0
5	EDO	A	1584	4/4	0.88	0.30	3.79	70,84,85,85	0
5	EDO	B	1585	4/4	0.90	0.22	2.77	48,58,63,64	0
5	EDO	B	1584	4/4	0.82	0.25	2.53	52,63,67,69	0
4	C58	B	1581	30/30	0.95	0.21	0.67	35,43,53,54	0
4	C58	A	1582	30/30	0.96	0.23	0.65	38,47,56,58	0
5	EDO	A	1583	4/4	0.86	0.18	0.53	65,78,79,79	0
2	IOD	C	901	1/1	0.98	0.18	0.47	77,77,77,77	0
4	C58	C	1580	30/30	0.95	0.20	-0.34	61,75,98,99	0
2	IOD	C	902	1/1	0.99	0.16	-0.53	72,72,72,72	0
2	IOD	C	904	1/1	0.99	0.19	-0.75	63,63,63,63	1
2	IOD	B	901	1/1	0.99	0.15	-0.88	56,56,56,56	0
3	CL	C	912	1/1	0.89	0.10	-1.64	57,57,57,57	0
2	IOD	A	901	1/1	0.98	0.11	-1.69	61,61,61,61	0
2	IOD	B	904	1/1	0.99	0.09	-2.25	58,58,58,58	1
2	IOD	C	903[B]	1/1	0.97	0.09	-2.97	38,38,38,38	1
3	CL	B	912	1/1	0.94	0.10	-	58,58,58,58	0
3	CL	A	912	1/1	0.93	0.12	-	47,47,47,47	0
2	IOD	A	903[B]	1/1	0.99	0.06	-	29,29,29,29	1
2	IOD	A	904	1/1	0.99	0.06	-	53,53,53,53	1
2	IOD	B	903[B]	1/1	0.98	0.09	-	29,29,29,29	1
2	IOD	A	902	1/1	0.97	0.07	-	87,87,87,87	0
5	EDO	A	1585	4/4	0.75	0.17	-	77,92,94,94	0
2	IOD	B	902	1/1	0.99	0.12	-	70,70,70,70	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.