



# Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 08:24 pm BST

PDB ID : 6CGO  
Title : Molecular basis for condensation domain-mediated chain release from the enacyloxin polyketide synthase  
Authors : Valentic, T.R.; Tsai, S.C.; Challis, G.L.; Lewandowski, J.R.; Kosol, S.; Gallo, A.; Griffiths, D.; Masschelein, J.L.; Jenner, M.; De los Santos, E.  
Deposited on : 2018-02-20  
Resolution : 2.00 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](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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 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) : 2.11

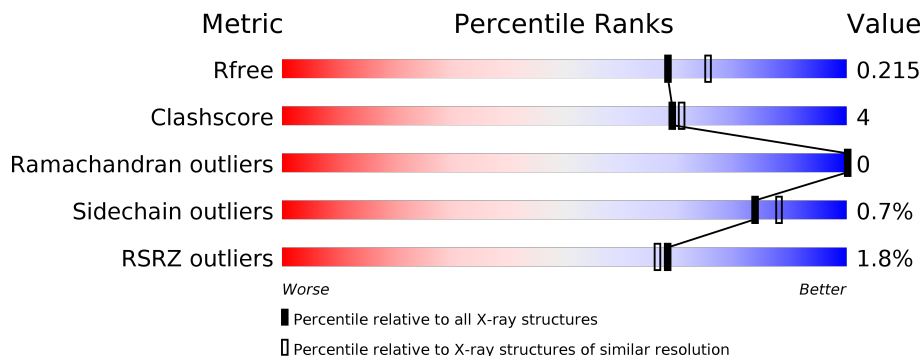
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 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	545	 89% 6% 5%
1	B	545	 84% 9% 7%

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	PO4	B	601	-	-	X	-

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 9033 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 Condensation domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	520	4013	2567	717	719	10	0	0	0
1	B	508	3942	2520	705	707	10	0	0	0

There are 66 discrepancies between the modelled and reference sequences:

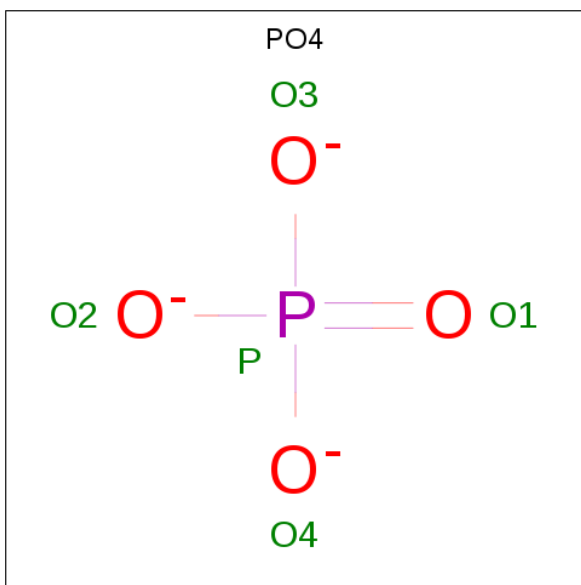
Chain	Residue	Modelled	Actual	Comment	Reference
A	-32	MET	-	initiating methionine	UNP Q0B313
A	-31	HIS	-	expression tag	UNP Q0B313
A	-30	HIS	-	expression tag	UNP Q0B313
A	-29	HIS	-	expression tag	UNP Q0B313
A	-28	HIS	-	expression tag	UNP Q0B313
A	-27	HIS	-	expression tag	UNP Q0B313
A	-26	HIS	-	expression tag	UNP Q0B313
A	-25	GLY	-	expression tag	UNP Q0B313
A	-24	LYS	-	expression tag	UNP Q0B313
A	-23	PRO	-	expression tag	UNP Q0B313
A	-22	ILE	-	expression tag	UNP Q0B313
A	-21	PRO	-	expression tag	UNP Q0B313
A	-20	ASN	-	expression tag	UNP Q0B313
A	-19	PRO	-	expression tag	UNP Q0B313
A	-18	LEU	-	expression tag	UNP Q0B313
A	-17	LEU	-	expression tag	UNP Q0B313
A	-16	GLY	-	expression tag	UNP Q0B313
A	-15	LEU	-	expression tag	UNP Q0B313
A	-14	ASP	-	expression tag	UNP Q0B313
A	-13	SER	-	expression tag	UNP Q0B313
A	-12	THR	-	expression tag	UNP Q0B313
A	-11	GLU	-	expression tag	UNP Q0B313
A	-10	ASN	-	expression tag	UNP Q0B313
A	-9	LEU	-	expression tag	UNP Q0B313
A	-8	TYR	-	expression tag	UNP Q0B313

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	PHE	-	expression tag	UNP Q0B313
A	-6	GLN	-	expression tag	UNP Q0B313
A	-5	GLY	-	expression tag	UNP Q0B313
A	-4	ILE	-	expression tag	UNP Q0B313
A	-3	ASP	-	expression tag	UNP Q0B313
A	-2	PRO	-	expression tag	UNP Q0B313
A	-1	PHE	-	expression tag	UNP Q0B313
A	0	THR	-	expression tag	UNP Q0B313
B	-32	MET	-	initiating methionine	UNP Q0B313
B	-31	HIS	-	expression tag	UNP Q0B313
B	-30	HIS	-	expression tag	UNP Q0B313
B	-29	HIS	-	expression tag	UNP Q0B313
B	-28	HIS	-	expression tag	UNP Q0B313
B	-27	HIS	-	expression tag	UNP Q0B313
B	-26	HIS	-	expression tag	UNP Q0B313
B	-25	GLY	-	expression tag	UNP Q0B313
B	-24	LYS	-	expression tag	UNP Q0B313
B	-23	PRO	-	expression tag	UNP Q0B313
B	-22	ILE	-	expression tag	UNP Q0B313
B	-21	PRO	-	expression tag	UNP Q0B313
B	-20	ASN	-	expression tag	UNP Q0B313
B	-19	PRO	-	expression tag	UNP Q0B313
B	-18	LEU	-	expression tag	UNP Q0B313
B	-17	LEU	-	expression tag	UNP Q0B313
B	-16	GLY	-	expression tag	UNP Q0B313
B	-15	LEU	-	expression tag	UNP Q0B313
B	-14	ASP	-	expression tag	UNP Q0B313
B	-13	SER	-	expression tag	UNP Q0B313
B	-12	THR	-	expression tag	UNP Q0B313
B	-11	GLU	-	expression tag	UNP Q0B313
B	-10	ASN	-	expression tag	UNP Q0B313
B	-9	LEU	-	expression tag	UNP Q0B313
B	-8	TYR	-	expression tag	UNP Q0B313
B	-7	PHE	-	expression tag	UNP Q0B313
B	-6	GLN	-	expression tag	UNP Q0B313
B	-5	GLY	-	expression tag	UNP Q0B313
B	-4	ILE	-	expression tag	UNP Q0B313
B	-3	ASP	-	expression tag	UNP Q0B313
B	-2	PRO	-	expression tag	UNP Q0B313
B	-1	PHE	-	expression tag	UNP Q0B313
B	0	THR	-	expression tag	UNP Q0B313

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0

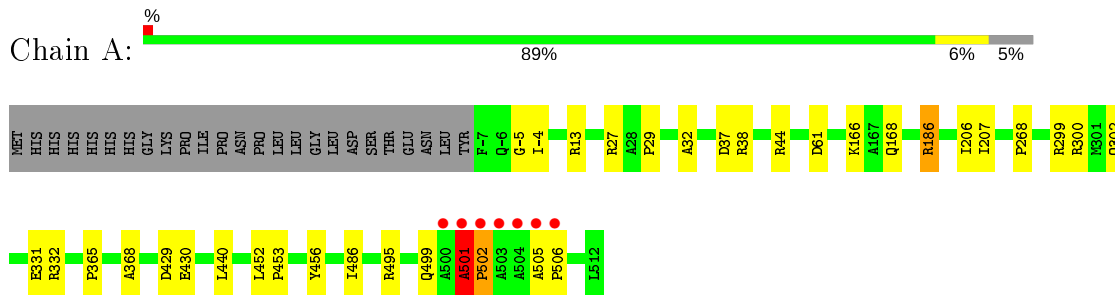
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	662	Total O 662 662	0	0
3	B	406	Total O 406 406	0	0

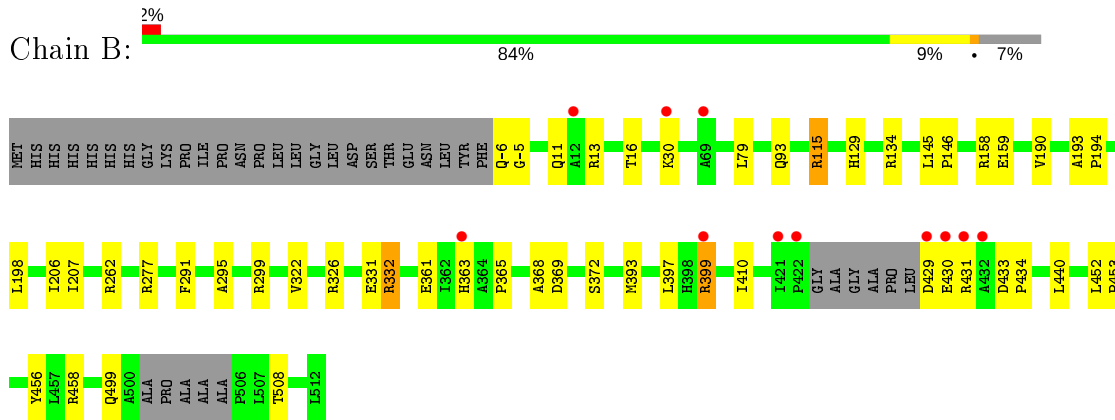
### 3 Residue-property plots i

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 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: Condensation domain protein



- Molecule 1: Condensation domain protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.63Å 58.77Å 107.00Å 90.00° 104.96° 90.00°	Depositor
Resolution (Å)	51.69 – 2.00 51.69 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (51.69-2.00) 99.4 (51.69-2.00)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.90 (at 2.00Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.180 , 0.215 0.180 , 0.215	Depositor DCC
$R_{free}$ test set	1995 reflections (2.37%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.5	Xtrriage
Anisotropy	0.158	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 47.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.016 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9033	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% 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: PO4

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	0.64	1/4113 (0.0%)	0.74	7/5621 (0.1%)
1	B	0.50	1/4037 (0.0%)	0.69	7/5511 (0.1%)
All	All	0.57	2/8150 (0.0%)	0.72	14/11132 (0.1%)

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	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	502	PRO	N-CD	13.74	1.67	1.47
1	B	399	ARG	CB-CG	-5.38	1.38	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	115	ARG	NE-CZ-NH2	-10.50	115.05	120.30
1	A	501	ALA	CB-CA-C	-9.55	95.77	110.10
1	B	115	ARG	NE-CZ-NH1	9.20	124.90	120.30
1	A	502	PRO	CA-N-CD	-7.55	100.93	111.50
1	B	399	ARG	CB-CA-C	-7.38	95.65	110.40
1	A	501	ALA	C-N-CA	7.06	151.64	122.00
1	B	399	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	B	399	ARG	NE-CZ-NH2	-6.41	117.10	120.30
1	A	501	ALA	C-N-CD	-6.00	107.39	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	277	ARG	CA-CB-CG	5.97	126.53	113.40
1	A	44	ARG	NE-CZ-NH1	-5.72	117.44	120.30
1	B	115	ARG	CG-CD-NE	-5.20	100.87	111.80
1	A	186	ARG	NE-CZ-NH1	-5.02	117.79	120.30
1	A	429	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	501	ALA	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	4013	0	4077	27	0
1	B	3942	0	4006	38	0
2	A	5	0	0	0	0
2	B	5	0	0	2	0
3	A	662	0	0	7	0
3	B	406	0	0	7	0
All	All	9033	0	8083	59	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 4.

All (59) 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:A:300:ARG:NE	1:A:501:ALA:O	1.92	1.01
1:B:458:ARG:NH2	2:B:601:PO4:O3	2.03	0.91
1:B:299:ARG:NH2	1:B:430:GLU:OE2	2.15	0.78
1:B:332:ARG:NH1	1:B:363:HIS:HB2	1.99	0.77
1:B:429:ASP:N	3:B:704:HOH:O	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:ARG:NE	1:B:361:GLU:OE2	2.17	0.74
1:A:300:ARG:HE	1:A:501:ALA:HB3	1.52	0.73
1:B:159:GLU:OE1	3:B:701:HOH:O	2.08	0.72
1:B:129:HIS:ND1	3:B:705:HOH:O	2.22	0.70
1:A:13:ARG:HD3	1:B:499:GLN:HB3	1.72	0.70
1:A:38:ARG:NH2	3:A:704:HOH:O	2.27	0.68
1:A:440:LEU:HD11	1:A:486:ILE:HG21	1.74	0.67
1:B:134:ARG:NH2	3:B:706:HOH:O	2.28	0.67
1:A:61:ASP:OD2	3:A:701:HOH:O	2.12	0.67
1:B:331:GLU:OE1	3:B:702:HOH:O	2.13	0.67
1:B:-6:GLN:HA	3:B:1018:HOH:O	1.95	0.65
1:B:399:ARG:HG3	1:B:399:ARG:O	1.94	0.65
1:B:206:ILE:HG23	1:B:207:ILE:HG12	1.80	0.63
1:B:332:ARG:HH12	1:B:363:HIS:HB2	1.61	0.62
1:A:505:ALA:HB1	1:A:506:PRO:HD2	1.83	0.59
1:A:29:PRO:HG2	1:A:32:ALA:HB2	1.84	0.59
2:B:601:PO4:O1	3:B:703:HOH:O	2.17	0.58
1:B:452:LEU:HD12	1:B:453:PRO:HD2	1.85	0.57
1:A:300:ARG:CD	1:A:501:ALA:O	2.52	0.57
1:A:186:ARG:HD3	3:A:714:HOH:O	2.05	0.56
1:A:168:GLN:NE2	3:A:709:HOH:O	2.37	0.56
1:A:331:GLU:OE2	3:A:702:HOH:O	2.18	0.56
1:A:365:PRO:HG2	1:A:368:ALA:HB2	1.86	0.56
1:B:369:ASP:N	1:B:369:ASP:OD1	2.34	0.56
1:B:11:GLN:OE1	1:B:16:THR:HG22	2.06	0.55
1:B:393:MET:HE1	1:B:410:ILE:HD12	1.89	0.55
1:A:206:ILE:HG23	1:A:207:ILE:HG12	1.87	0.55
1:A:166:LYS:HG3	3:A:760:HOH:O	2.05	0.55
1:B:291:PHE:HB3	1:B:440:LEU:HD12	1.92	0.51
1:B:158:ARG:HG2	1:B:158:ARG:HH11	1.75	0.51
1:A:-4:ILE:O	1:B:326:ARG:NH1	2.45	0.50
1:B:365:PRO:HG2	1:B:368:ALA:HB2	1.93	0.49
1:B:322:VAL:O	1:B:326:ARG:HG3	2.12	0.49
1:A:299:ARG:NH2	1:A:430:GLU:OE2	2.45	0.49
1:B:115:ARG:NH2	1:B:145:LEU:O	2.39	0.49
1:B:429:ASP:OD1	1:B:431:ARG:HG3	2.13	0.48
1:A:452:LEU:HD12	1:A:453:PRO:HD2	1.95	0.48
1:B:193:ALA:HB1	1:B:194:PRO:HD2	1.95	0.47
1:A:13:ARG:HH22	1:A:37:ASP:CG	2.17	0.47
1:A:501:ALA:N	1:A:502:PRO:HD2	2.31	0.45
1:B:295:ALA:O	1:B:299:ARG:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:ARG:NH2	1:B:-5:GLY:O	2.50	0.45
1:B:433:ASP:N	1:B:434:PRO:HD3	2.32	0.43
1:A:499:GLN:OE1	1:B:13:ARG:NH1	2.52	0.43
1:A:-5:GLY:HA2	1:B:369:ASP:HA	2.01	0.43
1:B:145:LEU:HD12	1:B:146:PRO:HD2	2.01	0.43
1:B:399:ARG:O	1:B:399:ARG:CG	2.60	0.43
1:B:190:VAL:HB	1:B:198:LEU:HB3	2.00	0.43
1:B:331:GLU:CD	1:B:365:PRO:HA	2.39	0.42
1:A:302:GLN:NE2	3:A:735:HOH:O	2.52	0.42
1:B:79:LEU:HD22	1:B:397:LEU:HD21	2.00	0.42
1:A:27:ARG:HA	1:B:508:THR:O	2.20	0.42
1:A:506:PRO:HD2	1:B:30:LYS:NZ	2.35	0.42
1:A:268:PRO:HD3	1:A:332:ARG:CZ	2.51	0.41

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	518/545 (95%)	511 (99%)	7 (1%)	0	100	100
1	B	502/545 (92%)	493 (98%)	9 (2%)	0	100	100
All	All	1020/1090 (94%)	1004 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	412/435 (95%)	411 (100%)	1 (0%)	93	95
1	B	408/435 (94%)	403 (99%)	5 (1%)	71	76
All	All	820/870 (94%)	814 (99%)	6 (1%)	84	88

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	456	TYR
1	B	93	GLN
1	B	262	ARG
1	B	332	ARG
1	B	372	SER
1	B	456	TYR

Some 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

2 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	PO4	B	601	-	4,4,4	1.21	0	6,6,6	0.49	0
2	PO4	A	601	-	4,4,4	1.34	0	6,6,6	0.51	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 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	PO4	2	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	520/545 (95%)	-0.32	7 (1%) 77 76	13, 23, 55, 127	0
1	B	508/545 (93%)	-0.31	11 (2%) 62 60	20, 34, 64, 114	0
All	All	1028/1090 (94%)	-0.31	18 (1%) 68 66	13, 30, 60, 127	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	503	ALA	12.0
1	A	504	ALA	6.1
1	B	432	ALA	4.0
1	B	430	GLU	3.5
1	B	399	ARG	3.2
1	B	429	ASP	3.1
1	B	431	ARG	3.1
1	B	421	ILE	2.8
1	B	422	PRO	2.7
1	A	505	ALA	2.7
1	B	30	LYS	2.5
1	B	363	HIS	2.5
1	A	501	ALA	2.5
1	A	502	PRO	2.5
1	A	500	ALA	2.3
1	A	506	PRO	2.3
1	B	69	ALA	2.2
1	B	12	ALA	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 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. 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
2	PO4	B	601	5/5	0.96	0.17	30,30,30,30	0
2	PO4	A	601	5/5	0.98	0.11	30,30,30,30	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.