



# Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 03:36 pm BST

PDB ID : 3V0G  
Title : Crystal structure of Ciona intestinalis voltage sensor-containing phosphatase (Ci-VSP), residues 241-576(C363S), form III  
Authors : Liu, L.; Kohout, S.C.; Xu, Q.; Muller, S.; Kimberlin, C.; Isacoff, E.Y.; Minor, D.L.  
Deposited on : 2011-12-08  
Resolution : 1.60 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

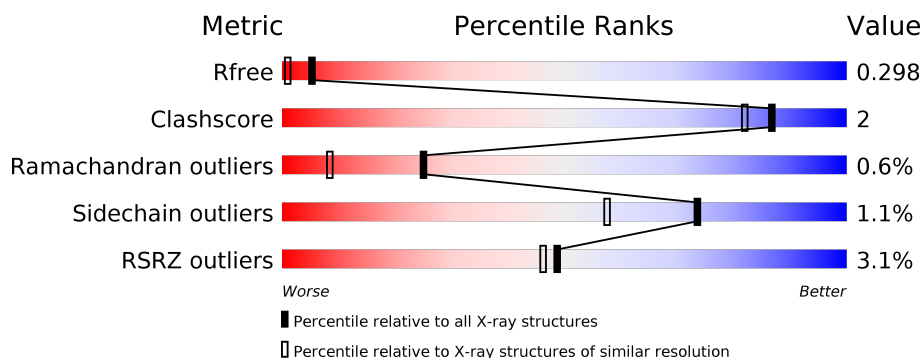
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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	339	 3% 91% 8%
1	B	339	 4% 88% 10%
1	C	339	 3% 91% 8%
1	D	339	 0% 87% 13%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11885 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 Voltage-sensor containing phosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	0	0
			2630	1668	453	496	13			
1	B	334	Total	C	N	O	S	0	8	0
			2716	1723	465	514	14			
1	C	324	Total	C	N	O	S	0	5	0
			2642	1683	454	492	13			
1	D	325	Total	C	N	O	S	3	12	0
			2683	1707	457	503	16			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	238	GLY	-	EXPRESSION TAG	UNP Q4W8A1
A	239	HIS	-	EXPRESSION TAG	UNP Q4W8A1
A	240	MET	-	EXPRESSION TAG	UNP Q4W8A1
A	363	SER	CYS	ENGINEERED MUTATION	UNP Q4W8A1
B	238	GLY	-	EXPRESSION TAG	UNP Q4W8A1
B	239	HIS	-	EXPRESSION TAG	UNP Q4W8A1
B	240	MET	-	EXPRESSION TAG	UNP Q4W8A1
B	363	SER	CYS	ENGINEERED MUTATION	UNP Q4W8A1
C	238	GLY	-	EXPRESSION TAG	UNP Q4W8A1
C	239	HIS	-	EXPRESSION TAG	UNP Q4W8A1
C	240	MET	-	EXPRESSION TAG	UNP Q4W8A1
C	363	SER	CYS	ENGINEERED MUTATION	UNP Q4W8A1
D	238	GLY	-	EXPRESSION TAG	UNP Q4W8A1
D	239	HIS	-	EXPRESSION TAG	UNP Q4W8A1
D	240	MET	-	EXPRESSION TAG	UNP Q4W8A1
D	363	SER	CYS	ENGINEERED MUTATION	UNP Q4W8A1

- 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	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	272	Total	O	0	0
			272	272		
3	B	284	Total	O	0	0
			284	284		
3	C	275	Total	O	0	0
			275	275		

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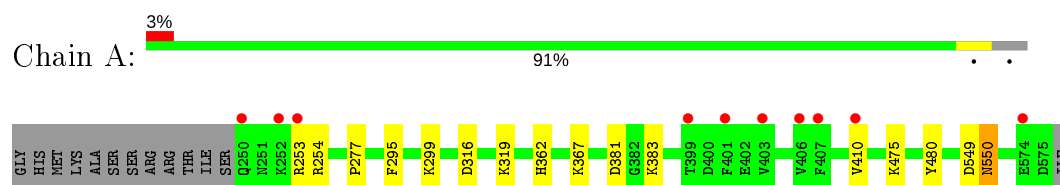
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	338	Total	O	0	0
			338	338		

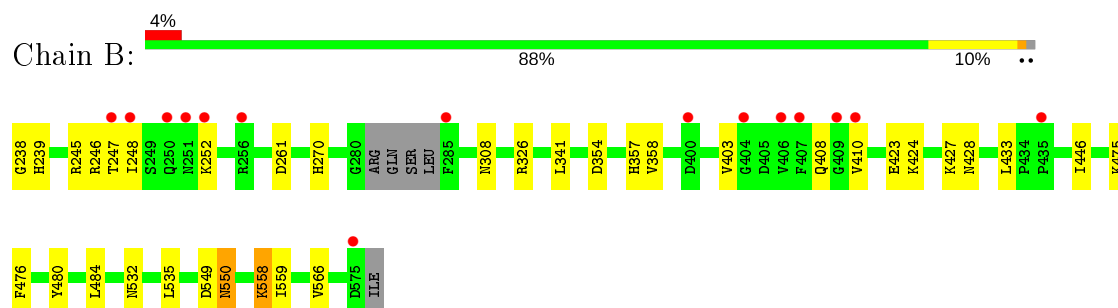
### 3 Residue-property plots [i](#)

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.

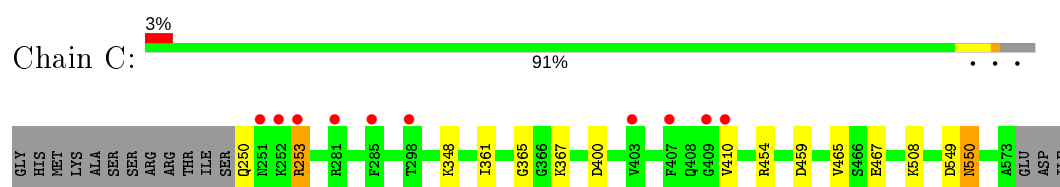
- Molecule 1: Voltage-sensor containing phosphatase



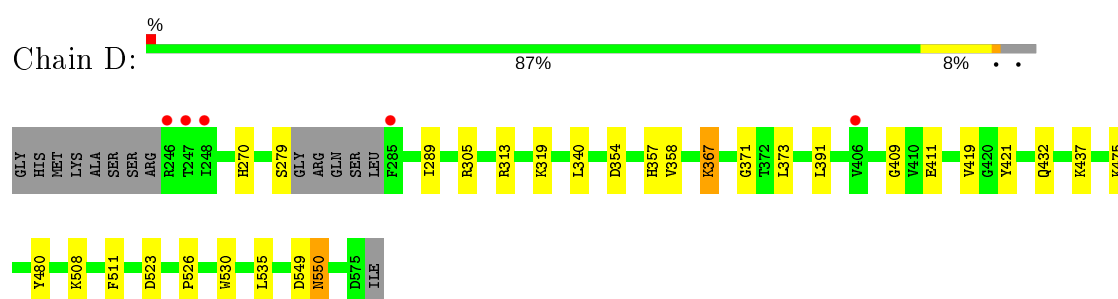
- Molecule 1: Voltage-sensor containing phosphatase



- Molecule 1: Voltage-sensor containing phosphatase



- Molecule 1: Voltage-sensor containing phosphatase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.86Å 83.86Å 83.60Å 86.55° 89.55° 89.38°	Depositor
Resolution (Å)	83.71 – 1.60 43.67 – 1.50	Depositor EDS
% Data completeness (in resolution range)	80.1 (83.71-1.60) 80.1 (43.67-1.50)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.47 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.256 , 0.298 0.256 , 0.298	Depositor DCC
$R_{free}$ test set	8947 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.8	Xtriage
Anisotropy	0.399	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 30.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.079 for h,-k,-l 0.079 for -h,l,k 0.079 for -h,-l,-k	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	11885	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% 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	0.35	0/2690	0.50	0/3628
1	B	0.36	0/2800	0.50	0/3771
1	C	0.35	0/2717	0.50	0/3661
1	D	0.36	0/2778	0.51	0/3744
All	All	0.36	0/10985	0.50	0/14804

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 [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	2630	0	2573	9	0
1	B	2716	0	2676	16	0
1	C	2642	0	2619	7	0
1	D	2683	0	2659	15	0
2	A	5	0	0	0	0
2	B	15	0	0	0	0
2	C	15	0	0	0	0
2	D	10	0	0	0	0
3	A	272	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	284	0	0	0	0
3	C	275	0	0	0	0
3	D	338	0	0	0	0
All	All	11885	0	10527	44	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 2.

All (44) 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:245:ARG:HH12	1:C:467:GLU:HB3	1.69	0.58
1:B:424:LYS:HG3	1:B:428:ASN:HD22	1.70	0.56
1:D:421:TYR:CD2	1:D:535[B]:LEU:HD22	2.43	0.54
1:A:475:LYS:HB2	1:A:480:TYR:HB3	1.91	0.53
1:B:341:LEU:HD12	1:B:433:LEU:HG	1.91	0.51
1:B:354:ASP:HB3	1:B:357:HIS:CG	2.47	0.50
1:B:558:LYS:HD2	1:B:559:ILE:HG13	1.93	0.49
1:D:354:ASP:HB3	1:D:357:HIS:CG	2.47	0.49
1:B:247:THR:HG21	1:D:305:ARG:NH2	2.28	0.48
1:D:313[B]:ARG:HB2	1:D:313[B]:ARG:CZ	2.44	0.47
1:D:508:LYS:HD2	1:D:530:TRP:CZ2	2.50	0.47
1:D:367:LYS:HE3	1:D:409:GLY:O	2.14	0.47
1:D:340:LEU:HD13	1:D:373[A]:LEU:HD22	1.97	0.47
1:D:391:LEU:HD21	1:D:419:VAL:HG21	1.97	0.46
1:A:549:ASP:O	1:A:550:ASN:HB2	2.16	0.46
1:D:549:ASP:O	1:D:550:ASN:HB2	2.15	0.46
1:C:365:GLY:HA3	1:C:367:LYS:HZ2	1.81	0.46
1:C:454:ARG:HD3	1:C:459:ASP:HB3	1.97	0.46
1:B:476:PHE:HB3	1:B:484:LEU:HD22	1.97	0.46
1:B:261:ASP:HB3	1:D:432:GLN:NE2	2.31	0.45
1:B:446:ILE:HG12	1:B:566:VAL:HG22	1.98	0.45
1:D:289:ILE:HG12	1:D:319:LYS:HD2	1.98	0.45
1:B:270:HIS:HA	1:B:358:VAL:HG12	1.99	0.44
1:B:423:GLU:HG2	1:B:427:LYS:HE2	2.00	0.44
1:C:465:VAL:HB	1:C:508:LYS:HB3	1.99	0.44
1:B:308:ASN:HB3	1:B:326:ARG:HG2	1.99	0.44
1:C:250:GLN:HA	1:C:253:ARG:HE	1.81	0.44
1:C:549:ASP:O	1:C:550:ASN:HB2	2.18	0.44
1:D:371:GLY:HA3	1:D:411:GLU:OE1	2.18	0.43
1:B:549:ASP:O	1:B:550:ASN:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:316:ASP:HB3	1:A:319:LYS:HE2	2.00	0.42
1:D:511:PHE:O	1:D:526:PRO:HD2	2.18	0.42
1:A:253:ARG:HH22	1:A:254:ARG:HH11	1.68	0.42
1:D:270:HIS:HA	1:D:358:VAL:HG12	2.02	0.42
1:C:361:ILE:N	1:C:361:ILE:HD12	2.35	0.41
1:B:238:GLY:HA3	1:B:239:HIS:HA	1.79	0.41
1:B:532:ASN:HB3	1:B:535:LEU:HD23	2.03	0.41
1:A:277:PRO:HD2	1:A:362:HIS:CE1	2.54	0.41
1:A:475:LYS:HB2	1:A:480:TYR:CB	2.51	0.41
1:B:475:LYS:HB2	1:B:480:TYR:HB3	2.03	0.41
1:A:381:ASP:OD1	1:A:383:LYS:NZ	2.53	0.41
1:A:295:PHE:CE1	1:A:299:LYS:HD2	2.56	0.40
1:A:475:LYS:H	1:A:480:TYR:HB3	1.85	0.40
1:D:475:LYS:HB2	1:D:480:TYR:HB3	2.03	0.40

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	324/339 (96%)	313 (97%)	9 (3%)	2 (1%)	25	8
1	B	338/339 (100%)	322 (95%)	13 (4%)	3 (1%)	17	4
1	C	327/339 (96%)	315 (96%)	10 (3%)	2 (1%)	25	8
1	D	333/339 (98%)	325 (98%)	7 (2%)	1 (0%)	41	21
All	All	1322/1356 (98%)	1275 (96%)	39 (3%)	8 (1%)	25	8

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	550	ASN

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Mol	Chain	Res	Type
1	B	550	ASN
1	C	410	VAL
1	C	550	ASN
1	D	550	ASN
1	B	410	VAL
1	A	410	VAL
1	B	403	VAL

### 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	290/301 (96%)	289 (100%)	1 (0%)	92	87
1	B	303/301 (101%)	298 (98%)	5 (2%)	60	38
1	C	293/301 (97%)	290 (99%)	3 (1%)	76	61
1	D	302/301 (100%)	298 (99%)	4 (1%)	69	50
All	All	1188/1204 (99%)	1175 (99%)	13 (1%)	73	57

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	367	LYS
1	B	246	ARG
1	B	248	ILE
1	B	252	LYS
1	B	408	GLN
1	B	558	LYS
1	C	253	ARG
1	C	348	LYS
1	C	400	ASP
1	D	279	SER
1	D	367	LYS
1	D	437	LYS
1	D	523	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	250	GLN
1	A	323	HIS
1	A	332	HIS
1	A	408	GLN
1	A	432	GLN
1	B	428	ASN
1	D	251	ASN
1	D	540	HIS

### 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](#)

9 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	C	3	-	4,4,4	1.04	0	6,6,6	0.54	0
2	PO4	D	7	-	4,4,4	0.91	0	6,6,6	0.43	0
2	PO4	C	6	-	4,4,4	0.90	0	6,6,6	0.46	0
2	PO4	D	4	-	4,4,4	1.03	0	6,6,6	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	PO4	B	5	-	4,4,4	0.92	0	6,6,6	0.47	0
2	PO4	C	9	-	4,4,4	0.89	0	6,6,6	0.45	0
2	PO4	A	1	-	4,4,4	0.97	0	6,6,6	0.64	0
2	PO4	B	8	-	4,4,4	0.98	0	6,6,6	0.35	0
2	PO4	B	2	-	4,4,4	1.02	0	6,6,6	0.41	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.

No monomer is involved in short contacts.

## 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	326/339 (96%)	0.13	10 (3%) 49 46	16, 25, 41, 50	0
1	B	334/339 (98%)	0.11	15 (4%) 33 30	15, 24, 37, 42	0
1	C	324/339 (95%)	0.06	10 (3%) 49 46	14, 22, 37, 50	0
1	D	325/339 (95%)	-0.04	5 (1%) 73 73	14, 20, 33, 44	0
All	All	1309/1356 (96%)	0.06	40 (3%) 49 46	14, 23, 37, 50	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	247	THR	5.8
1	A	407	PHE	5.5
1	C	251	ASN	5.4
1	B	406	VAL	5.1
1	A	406	VAL	4.5
1	C	409	GLY	4.2
1	A	410	VAL	4.2
1	D	246	ARG	4.1
1	B	407	PHE	4.1
1	B	248	ILE	3.9
1	D	248	ILE	3.6
1	B	575	ASP	3.5
1	A	252	LYS	3.5
1	A	253	ARG	3.4
1	A	574	GLU	3.3
1	C	285	PHE	3.2
1	B	404	GLY	3.0
1	D	285	PHE	3.0
1	C	410	VAL	2.7
1	B	409	GLY	2.7
1	C	407	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	250	GLN	2.6
1	A	250	GLN	2.6
1	A	401	PHE	2.6
1	B	252	LYS	2.6
1	C	403	VAL	2.6
1	A	399	THR	2.4
1	B	247	THR	2.3
1	C	253	ARG	2.3
1	B	285	PHE	2.3
1	A	403	VAL	2.2
1	B	251	ASN	2.2
1	C	252	LYS	2.2
1	C	298	THR	2.2
1	B	256	ARG	2.2
1	D	406	VAL	2.2
1	B	400	ASP	2.2
1	C	281	ARG	2.1
1	B	410	VAL	2.0
1	B	435	PRO	2.0

## 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( $\text{\AA}^2$ )	Q<0.9
2	PO4	D	7	5/5	0.90	0.09	54,54,55,55	0
2	PO4	C	6	5/5	0.90	0.12	43,43,43,43	0
2	PO4	B	5	5/5	0.92	0.09	53,54,54,54	0
2	PO4	C	9	5/5	0.96	0.07	24,25,25,26	0

*Continued on next page...*

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	C	3	5/5	0.97	0.08	22,24,25,25	0
2	PO4	D	4	5/5	0.97	0.07	22,23,24,24	0
2	PO4	A	1	5/5	0.97	0.08	26,26,27,28	0
2	PO4	B	2	5/5	0.97	0.10	26,27,28,28	0
2	PO4	B	8	5/5	0.98	0.06	25,26,26,26	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.