

# wwPDB X-ray Structure Validation Summary Report (i)

Jan 29, 2024 – 12:25 am GMT

PDB ID : 6FHH

Title : Crystal structure of bat influenza A/H17N10 polymerase with viral RNA pro-

moter bound to a 22-mer modified Pol II CTD peptide with serine 5 thiophos-

phorylated.

Authors : Lukarska, M.; Cusack, S.

Deposited on : 2018-01-14

Resolution : 2.70 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
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

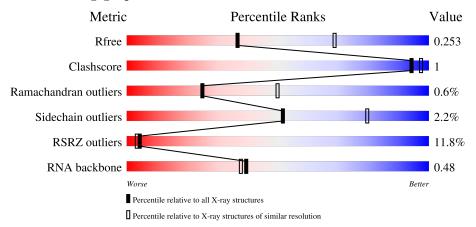
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 2.70 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)
RNA backbone	3102	1159 (3.00-2.40)

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 >=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 <=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		700	21%	
1	A	738	89%	6% • •
9	D	776	6%	
2	В	776	91%	6% •
		000	8%	
3	C	809	86%	• 10%
	_			
4	R	18	67% 6%	28%



Mol	Chain	Length				Quality o	f chain	
5	V	16	6%		69%	, 5		31%
6	X	22		27%	5%		68%	
6	Y	22		41%	o .	5%	5	5%



# 2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 18457 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 Polymerase acidic protein.

$\mathbf{Mol}$	Chain	Residues		$\mathbf{A}^{\dagger}$	toms			ZeroOcc	AltConf	Trace
1	A	709	Total 5770	C 3665	N 971	O 1097	S 37	0	0	0

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	GLY	-	expression tag	UNP H6QM92
A	-12	SER	-	expression tag	UNP H6QM92
A	-11	HIS	-	expression tag	UNP H6QM92
A	-10	HIS	-	expression tag	UNP H6QM92
A	-9	HIS	-	expression tag	UNP H6QM92
A	-8	HIS	-	expression tag	UNP H6QM92
A	-7	HIS	-	expression tag	UNP H6QM92
A	-6	HIS	_	expression tag	UNP H6QM92
A	-5	HIS	-	expression tag	UNP H6QM92
A	-4	HIS	-	expression tag	UNP H6QM92
A	-3	GLY	-	expression tag	UNP H6QM92
A	-2	SER	-	expression tag	UNP H6QM92
A	-1	GLY	-	expression tag	UNP H6QM92
A	0	SER	-	expression tag	UNP H6QM92
A	714	GLY	_	expression tag	UNP H6QM92
A	715	SER	-	expression tag	UNP H6QM92
A	716	GLY	_	expression tag	UNP H6QM92
A	717	SER	-	expression tag	UNP H6QM92
A	718	GLY	-	expression tag	UNP H6QM92
A	719	GLU	-	expression tag	UNP H6QM92
A	720	ASN	-	expression tag	UNP H6QM92
A	721	LEU	-	expression tag	UNP H6QM92
A	722	TYR	-	expression tag	UNP H6QM92
A	723	PHE	-	expression tag	UNP H6QM92
A	724	GLN	-	expression tag	UNP H6QM92

• Molecule 2 is a protein called RNA-directed RNA polymerase catalytic subunit.



$\mathbf{Mol}$	Chain	Residues		$\mathbf{A}$	toms			ZeroOcc	AltConf	Trace
2	В	750	Total 5986	C 3766	N 1062	O 1118	S 40	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	-8	GLY	-	expression tag	UNP H6QM91
В	-7	SER	-	expression tag	UNP H6QM91
В	-6	GLY	-	expression tag	UNP H6QM91
В	-5	SER	-	expression tag	UNP H6QM91
В	-4	GLY	-	expression tag	UNP H6QM91
В	-3	SER	-	expression tag	UNP H6QM91
В	-2	GLY	-	expression tag	UNP H6QM91
В	-1	SER	-	expression tag	UNP H6QM91
В	0	GLY	-	expression tag	UNP H6QM91
В	757	GLY	-	expression tag	UNP H6QM91
В	758	SER	-	expression tag	UNP H6QM91
В	759	GLY	-	expression tag	UNP H6QM91
В	760	SER	-	expression tag	UNP H6QM91
В	761	GLY	-	expression tag	UNP H6QM91
В	762	GLU	-	expression tag	UNP H6QM91
В	763	ASN	-	expression tag	UNP H6QM91
В	764	LEU	-	expression tag	UNP H6QM91
В	765	TYR	-	expression tag	UNP H6QM91
В	766	PHE	-	expression tag	UNP H6QM91
В	767	GLN	_	expression tag	UNP H6QM91

• Molecule 3 is a protein called Polymerase basic protein 2.

Mol	Chain	Residues		A	toms			ZeroOcc	AltConf	Trace
3	С	725	Total 5753	C 3631	N 1015	O 1075	S 32	0	0	0

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	-8	GLY	-	expression tag	UNP H6QM90
С	-7	SER	-	expression tag	UNP H6QM90
С	-6	GLY	-	expression tag	UNP H6QM90
С	-5	SER	-	expression tag	UNP H6QM90
С	-4	GLY	-	expression tag	UNP H6QM90
С	-3	SER	-	expression tag	UNP H6QM90
С	-2	GLY	-	expression tag	UNP H6QM90



Chain	Residue	Modelled	Actual	Comment	Reference
С	-1	SER	-	expression tag	UNP H6QM90
С	0	GLY	-	expression tag	UNP H6QM90
С	761	GLY	-	expression tag	UNP H6QM90
С	762	TRP	-	expression tag	UNP H6QM90
С	763	SER	-	expression tag	UNP H6QM90
С	764	HIS	-	expression tag	UNP H6QM90
С	765	PRO	-	expression tag	UNP H6QM90
С	766	GLN	-	expression tag	UNP H6QM90
С	767	PHE	-	expression tag	UNP H6QM90
С	768	GLU	-	expression tag	UNP H6QM90
С	769	LYS	-	expression tag	UNP H6QM90
С	770	GLY	-	expression tag	UNP H6QM90
С	771	GLY	-	expression tag	UNP H6QM90
С	772	GLY	-	expression tag	UNP H6QM90
С	773	SER	-	expression tag	UNP H6QM90
С	774	GLY	-	expression tag	UNP H6QM90
С	775	GLY	-	expression tag	UNP H6QM90
С	776	GLY	-	expression tag	UNP H6QM90
С	777	SER	-	expression tag	UNP H6QM90
С	778	GLY	-	expression tag	UNP H6QM90
С	779	GLY	-	expression tag	UNP H6QM90
С	780	SER	-	expression tag	UNP H6QM90
С	781	ALA	-	expression tag	UNP H6QM90
С	782	TRP	-	expression tag	UNP H6QM90
С	783	SER	-	expression tag	UNP H6QM90
С	784	HIS	-	expression tag	UNP H6QM90
С	785	PRO	-	expression tag	UNP H6QM90
С	786	GLN	-	expression tag	UNP H6QM90
С	787	PHE	-	expression tag	UNP H6QM90
С	788	GLU	-	expression tag	UNP H6QM90
С	789	LYS	-	expression tag	UNP H6QM90
С	790	GLY	-	expression tag	UNP H6QM90
С	791	ARG	-	expression tag	UNP H6QM90
С	792	SER	-	expression tag	UNP H6QM90
С	793	GLY	-	expression tag	UNP H6QM90
С	794	GLY	-	expression tag	UNP H6QM90
С	795	GLU	-	expression tag	UNP H6QM90
С	796	ASN	-	expression tag	UNP H6QM90
С	797	LEU	-	expression tag	UNP H6QM90
С	798	TYR	-	expression tag	UNP H6QM90
С	799	PHE	-	expression tag	UNP H6QM90
С	800	GLN	-	expression tag	UNP H6QM90



• Molecule 4 is a RNA chain called RNA (5'-R(\*UP\*AP\*UP\*AP\*CP\*CP\*UP\*CP\*UP\*GP\*CP\*UP\*U)-3').

$\mathbf{M}$	ol	Chain	Residues		$\mathbf{At}$	oms			ZeroOcc	AltConf	Trace
4		R	13	Total 247	C 111	N 37	O 87	P 12	0	0	0

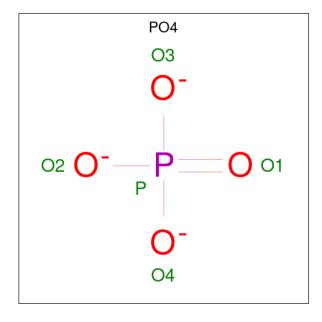
• Molecule 5 is a RNA chain called RNA (5'-R(P\*AP\*GP\*UP\*AP\*GP\*UP\*AP\*AP\*CP\*AP \*AP\*GP\*AP\*GP\*GP\*G)-3').

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
5	V	16	Total 353	C 157	N 72	O 108	P 16	0	0	0

 $\bullet$  Molecule 6 is a protein called TYR-SER-PRO-THR-TPS-PRO-SER.

Mo	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
6	v	7	7 Total C N O P S	Total C N O P	0	0	0				
0	$\Lambda$	1	55	32	7	14	1	1	U	U	0
6	V	10	Total	С	N	О	Р	S	0	0	0
0	ı	10	80	49	10	19	1	1			

• Molecule 7 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



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



 $Continued\ from\ previous\ page...$ 

Mol		Residues	Atoms	ZeroOcc	AltConf	
7	Λ	1	Total O P		0	
7	A	1	5   4   1	0		
7	A	1	Total O P	0	0	
'	A	1	5   4   1		0	
7	В	1	Total O P	0	0	
<b>'</b>	Б	1	5   4   1		0	
7	В	1	Total O P	0	0	
<b>'</b>	Б	1	5   4   1		0	
7	В	1	Total O P	0	0	
<b>'</b>	Б	1	5   4   1		U	
7	В	1	Total O P	0	0	
<b>'</b>	Б	1	5   4   1	0	0	
7	В	1	Total O P	0	0	
'	Ъ	1	5   4   1	0		
7	В	1	Total O P	1 11	0	
'	Ъ	1	5 4 1	U		
7	В	1	Total O P	0	0	
'	Ъ	1	5 4 1	0	0	
7	С	1	Total O P	0	0	
'		1	5   4   1		0	
7	С	1	Total O P	0	0	
'		1	5   4   1	0	0	
7	С	1	Total O P	0	0	
		1	5 4 1		U	
7	С	1	Total O P	1 (1)	0	
		1	5 4 1		U	
7	С	1	Total O P	1 11	0	
'		1	$\begin{vmatrix} 5 & 4 & 1 \end{vmatrix}$	0	0	

• Molecule 8 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	В	1	Total Zn 1 1	0	0

• Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	41	Total O 41 41	0	0
9	В	54	Total O 54 54	0	0



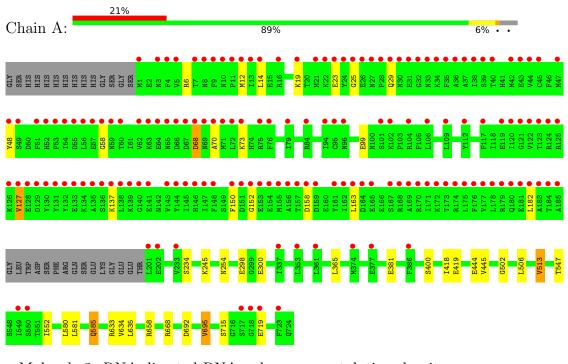
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	С	35	Total O 35 35	0	0
9	R	1	Total O 1 1	0	0
9	V	6	Total O 6 6	0	0



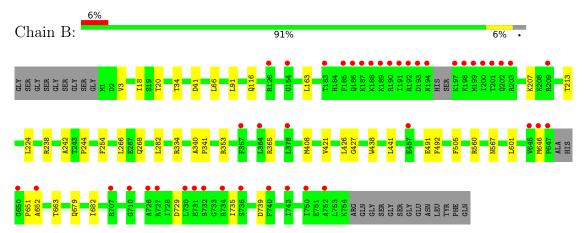
# 3 Residue-property plots (i)

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: Polymerase acidic protein

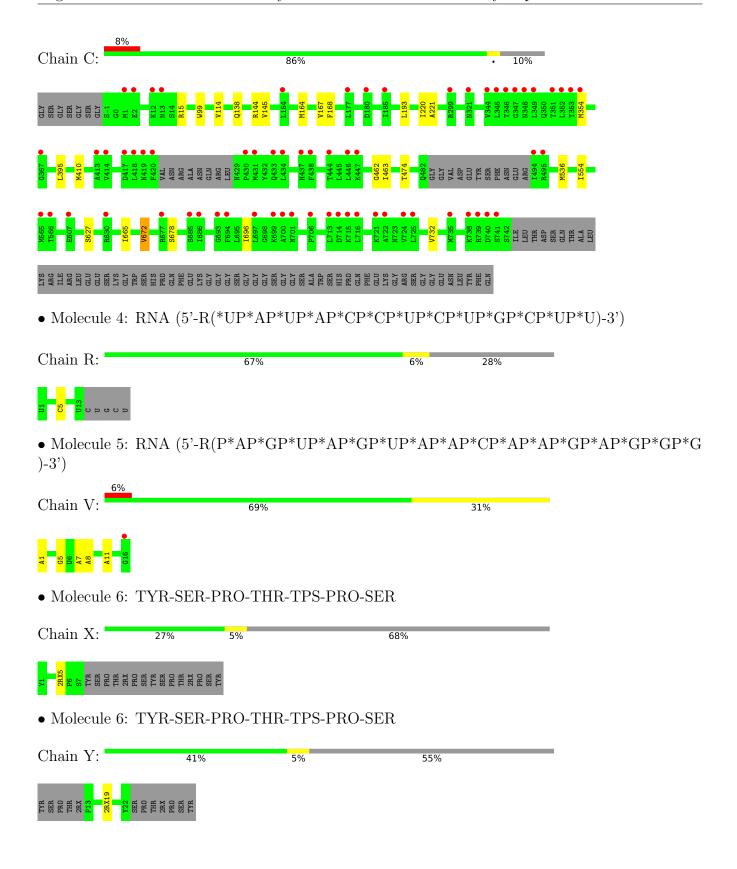


• Molecule 2: RNA-directed RNA polymerase catalytic subunit



• Molecule 3: Polymerase basic protein 2







# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	267.77Å 147.81Å 88.41Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 97.08° 90.00°	Depositor
Resolution (Å)	50.00 - 2.70	Depositor
rtesolution (A)	49.41 - 2.70	EDS
% Data completeness	98.6 (50.00-2.70)	Depositor
(in resolution range)	98.7 (49.41-2.70)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$< I/\sigma(I) > 1$	1.45 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
D D.	0.213 , 0.258	Depositor
$R, R_{free}$	0.214 , $0.253$	DCC
$R_{free}$ test set	4534 reflections $(4.92%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	67.9	Xtriage
Anisotropy	0.333	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.33 , 51.7	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	18457	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.01% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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, ZN, 2RX

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	Bo	nd lengths	Bond angles	
MIOI	Chain	RMSZ   # Z  > 5		RMSZ	# Z  > 5
1	A	0.38	0/5892	0.57	0/7934
2	В	0.37	0/6100	0.60	0/8229
3	С	0.36	0/5851	0.58	0/7897
4	R	0.26	0/273	0.68	0/421
5	V	0.56	1/397~(0.3%)	0.70	0/617
6	X	0.46	0/46	0.41	0/61
6	Y	0.34	0/73	0.47	0/98
All	All	0.37	1/18632 (0.0%)	0.59	0/25257

### All (1) bond length outliers are listed below:

$\mathbf{Mol}$	Chain	$\operatorname{Res}$	$\mathbf{Type}$	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}({ ext{ iny A}})$
5	V	1	A	OP3-P	-10.16	1.49	1.61

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	5770	0	5678	19	0
2	В	5986	0	6006	22	0
3	С	5753	0	5876	14	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	R	247	0	128	0	0
5	V	353	0	175	0	0
6	X	55	0	47	0	0
6	Y	80	0	66	0	0
7	A	15	0	0	0	0
7	В	35	0	0	0	0
7	С	25	0	0	1	0
8	В	1	0	0	0	0
9	A	41	0	0	0	0
9	В	54	0	0	0	0
9	С	35	0	0	0	0
9	R	1	0	0	0	0
9	V	6	0	0	0	0
All	All	18457	0	17976	48	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 1.

The worst 5 of 48 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:719:GLU:OE1	1:A:719:GLU:N	2.20	0.72
1:A:506:LEU:HD11	1:A:513:VAL:HG22	1.73	0.69
1:A:719:GLU:H	1:A:719:GLU:CD	1.99	0.66
1:A:445:VAL:CG1	1:A:580:LEU:HD22	2.26	0.65
1:A:585:GLN:HG2	2:B:505:PHE:CD2	2.37	0.59

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	Perce	ntiles
1	A	705/738~(96%)	652 (92%)	43 (6%)	10 (1%)	11	28
2	В	744/776~(96%)	718 (96%)	24 (3%)	2 (0%)	41	66
3	С	719/809~(89%)	692 (96%)	27 (4%)	0	100	100
6	X	4/22~(18%)	3 (75%)	1 (25%)	0	100	100
6	Y	7/22~(32%)	7 (100%)	0	0	100	100
All	All	$2179/2367\ (92\%)$	2072 (95%)	95 (4%)	12 (1%)	25	50

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	LYS
1	A	68	ASP
1	A	127	VAL
1	A	137	LYS
2	В	651	PRO

### 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	633/657 (96%)	611 (96%)	22 (4%)	36 65		
2	В	659/676 (98%)	647 (98%)	12 (2%)	59 83		
3	С	642/706 (91%)	634 (99%)	8 (1%)	71 88		
6	X	6/19 (32%)	6 (100%)	0	100 100		
6	Y	9/19 (47%)	9 (100%)	0	100 100		
All	All	1949/2077 (94%)	1907 (98%)	42 (2%)	52 79		

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	В	365	ARG
3	С	164	MET
2	В	491	GLU



Mol	Chain	Res	Type
2	В	646	MET
3	С	410	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	ASN
2	В	313	GLN
3	С	379	GLN

#### 5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	R	11/18 (61%)	1 (9%)	0
5	V	15/16 (93%)	3 (20%)	1 (6%)
All	All	26/34 (76%)	4 (15%)	1 (3%)

### All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	R	5	С
5	V	7	A
5	V	8	A
5	V	11	A

#### All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	V	5	G

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

2 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).

Mal	Trino	Type Chain	Res	Link	Bond lengths			В	ond ang	gles
Mol	туре				Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	2RX	Y	19	6	6,9,10	1.54	2 (33%)	4,12,14	1.22	0
6	2RX	X	5	6	6,9,10	1.27	2 (33%)	4,12,14	2.04	2 (50%)

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
6	2RX	Y	19	6	-	0/4/8/10	-
6	2RX	X	5	6	-	1/4/8/10	-

#### All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(A)	$\operatorname{Ideal}(\text{\AA})$
6	Y	19	2RX	P40-OG	2.69	1.62	1.57
6	Y	19	2RX	P40-O42	-2.34	1.50	1.56
6	X	5	2RX	P40-O42	-2.04	1.51	1.56
6	X	5	2RX	P40-OG	2.02	1.61	1.57

### All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
6	X	5	2RX	OG-CB-CA	3.03	111.09	108.14
6	X	5	2RX	OG-P40-O43	-2.38	105.65	114.42

There are no chirality outliers.

#### All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	X	5	2RX	N-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



# 5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 1 is monoatomic - leaving 15 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	Trino	Chain	Dog	Link	В	ond leng	${ m gths}$	Bond angles		
MIOI	Type	Chain	Res	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
7	PO4	С	904	-	4,4,4	1.01	0	6,6,6	0.40	0
7	PO4	С	902	-	4,4,4	0.96	0	6,6,6	0.46	0
7	PO4	A	803	-	4,4,4	0.89	0	6,6,6	0.39	0
7	PO4	С	905	-	4,4,4	0.95	0	6,6,6	0.41	0
7	PO4	В	806	-	4,4,4	0.97	0	6,6,6	0.55	0
7	PO4	В	802	-	4,4,4	0.83	0	6,6,6	0.51	0
7	PO4	С	903	-	4,4,4	0.86	0	6,6,6	0.42	0
7	PO4	С	901	-	4,4,4	0.94	0	6,6,6	0.36	0
7	PO4	В	805	-	4,4,4	0.82	0	6,6,6	0.52	0
7	PO4	В	804	-	4,4,4	0.82	0	6,6,6	0.48	0
7	PO4	В	808	-	4,4,4	0.89	0	6,6,6	0.43	0
7	PO4	A	802	-	4,4,4	0.91	0	6,6,6	0.56	0
7	PO4	A	801	-	4,4,4	0.89	0	6,6,6	0.50	0
7	PO4	В	803	-	4,4,4	0.85	0	6,6,6	0.50	0
7	PO4	В	807	-	4,4,4	0.93	0	6,6,6	0.52	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
7	С	901	PO4	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,  $95^{th}$  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>	$\# \mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	A	709/738 (96%)	1.40	155 (21%) 0 0	49, 80, 228, 288	0
2	В	750/776 (96%)	0.45	43 (5%) 23 22	45, 77, 136, 177	0
3	С	725/809 (89%)	0.54	65 (8%) 9 7	49, 83, 132, 162	0
4	R	13/18 (72%)	0.18	0 100 100	62, 74, 111, 113	0
5	V	16/16 (100%)	-0.21	1 (6%) 20 19	64, 70, 103, 167	0
6	X	6/22~(27%)	0.15	0 100 100	70, 74, 98, 110	0
6	Y	9/22 (40%)	0.64	0 100 100	61, 66, 108, 125	0
All	All	2228/2401 (92%)	0.77	264 (11%) 4 3	45, 80, 193, 288	0

The worst 5 of 264 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	121	GLY	23.9
1	A	8	ASN	15.1
1	A	132	TYR	14.8
1	A	71	MET	14.7
1	A	177	VAL	12.5

## 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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
6	2RX	X	5	10/11	0.96	0.11	68,78,89,94	0
6	2RX	Y	19	10/11	0.97	0.20	61,64,66,67	0



### 6.3 Carbohydrates (i)

There are no monosaccharides 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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
7	PO4	A	801	5/5	0.74	0.29	140,144,146,148	0
7	PO4	В	805	5/5	0.81	0.21	101,106,113,115	0
7	PO4	С	904	5/5	0.83	0.23	108,110,113,113	0
7	PO4	В	808	5/5	0.87	0.33	110,111,116,119	0
7	PO4	В	802	5/5	0.87	0.16	90,90,101,101	0
7	PO4	С	901	5/5	0.88	0.16	99,99,105,107	0
7	PO4	В	806	5/5	0.88	0.24	95,101,111,114	0
7	PO4	A	802	5/5	0.90	0.22	88,92,98,102	0
7	PO4	A	803	5/5	0.90	0.19	126,129,133,133	0
7	PO4	С	905	5/5	0.90	0.23	123,126,128,132	0
7	PO4	В	804	5/5	0.92	0.18	98,100,105,109	0
7	PO4	В	803	5/5	0.93	0.17	98,100,101,107	0
7	PO4	С	903	5/5	0.93	0.12	98,101,108,109	0
7	PO4	В	807	5/5	0.96	0.14	89,90,93,93	0
7	PO4	С	902	5/5	0.97	0.17	95,97,98,99	0
8	ZN	В	801	1/1	0.99	0.19	82,82,82,82	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

