



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 14, 2019 – 07:56 PM EDT

PDB ID : 1V0E  
Title : Endosialidase of Bacteriophage K1F  
Authors : Stummeyer, K.; Dickmanns, A.; Muehlenhoff, M.; Gerady-Schahn, R.; Ficner, R.  
Deposited on : 2004-03-28  
Resolution : 1.90 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

<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 : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : 2.3.2  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.3.2

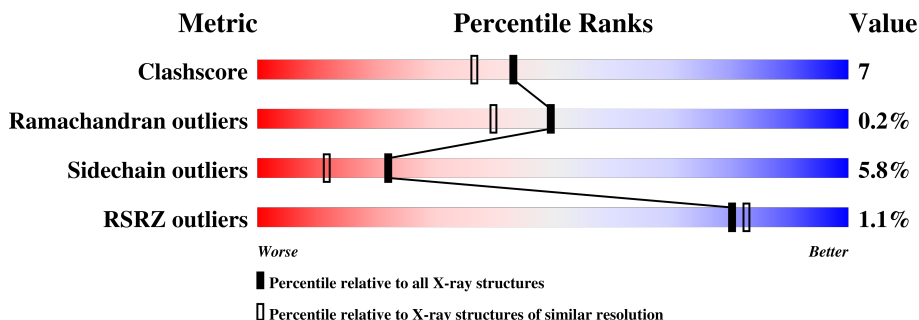
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
Clashscore	122126	6115 (1.90-1.90)
Ramachandran outliers	120053	6048 (1.90-1.90)
Sidechain outliers	120020	6048 (1.90-1.90)
RSRZ outliers	108989	5379 (1.90-1.90)

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	666	 3% 82% 15% •
1	B	666	 82% 14% • •
1	C	666	 84% 13% •
1	D	666	 80% 17% • •
1	E	666	 2% 81% 16% •
1	F	666	 81% 16% • •

## 2 Entry composition [i](#)

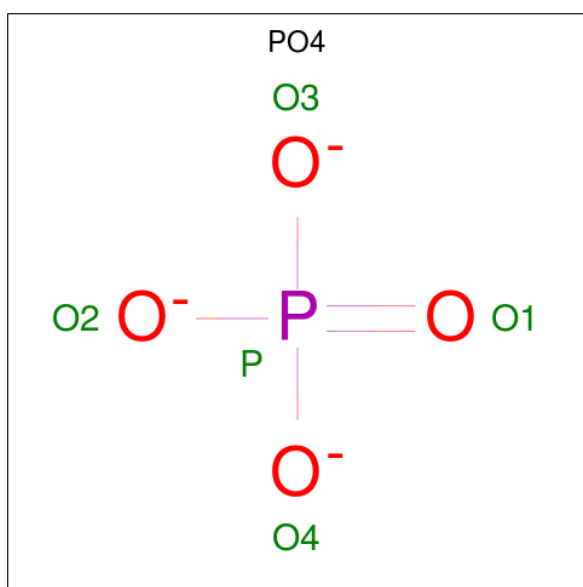
There are 3 unique types of molecules in this entry. The entry contains 34485 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ENDO-ALPHA-SIALIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	666	Total	C	N	O	S	0	0	0
			5230	3293	908	1010	19			
1	B	666	Total	C	N	O	S	0	0	0
			5230	3293	908	1010	19			
1	C	666	Total	C	N	O	S	0	0	0
			5230	3293	908	1010	19			
1	D	666	Total	C	N	O	S	0	0	0
			5230	3293	908	1010	19			
1	E	666	Total	C	N	O	S	0	0	0
			5230	3293	908	1010	19			
1	F	666	Total	C	N	O	S	0	0	0
			5230	3293	908	1010	19			

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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	D	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		

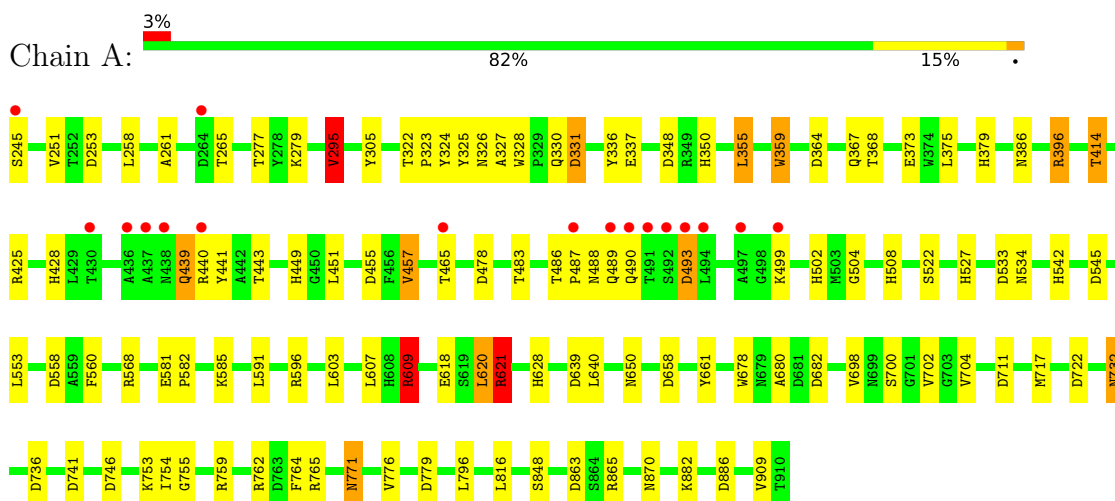
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	528	Total	O	0	0
			528	528		
3	B	534	Total	O	0	0
			534	534		
3	C	516	Total	O	0	0
			516	516		
3	D	529	Total	O	0	0
			529	529		
3	E	459	Total	O	0	0
			459	459		
3	F	509	Total	O	0	0
			509	509		

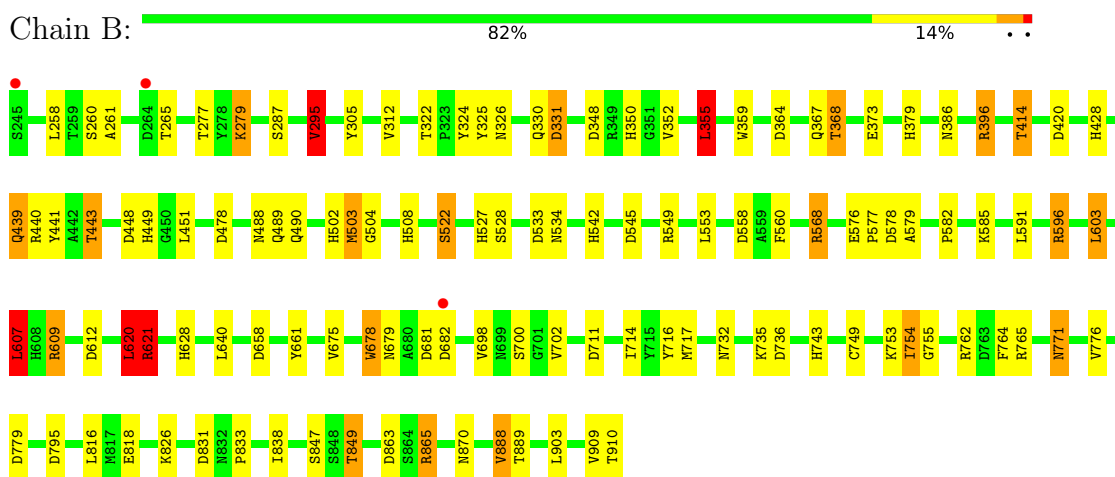
### 3 Residue-property plots

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.

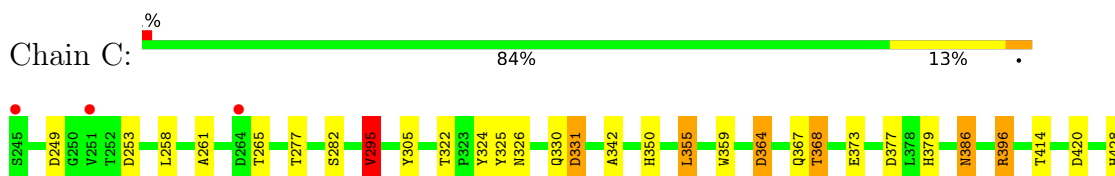
#### • Molecule 1: ENDO-ALPHA-SIALIDASE



#### • Molecule 1: ENDO-ALPHA-SIALIDASE



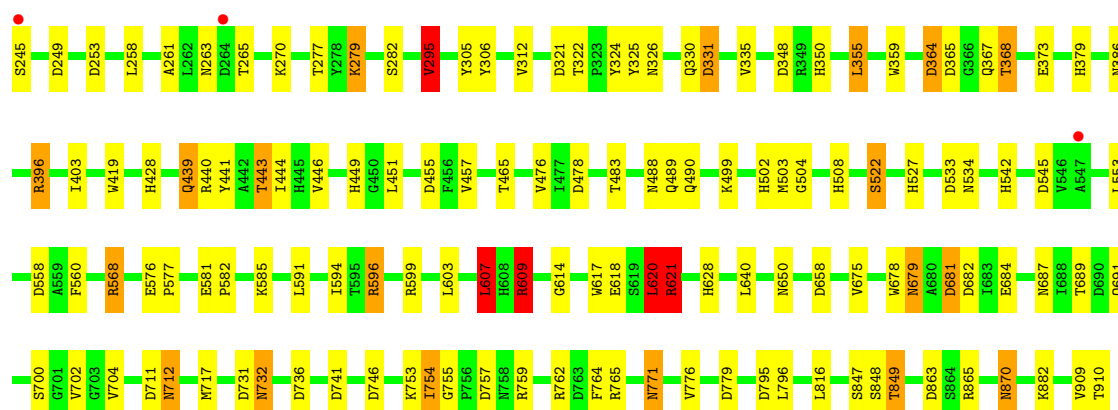
#### • Molecule 1: ENDO-ALPHA-SIALIDASE





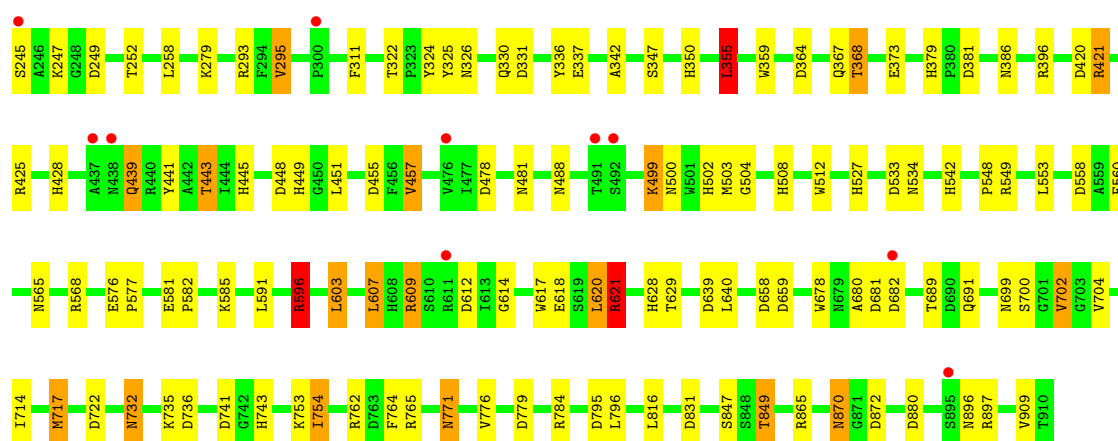
• Molecule 1: ENDO-ALPHA-SIALIDASE

Chain D: 80% 17% . .



• Molecule 1: ENDO-ALPHA-SIALIDASE

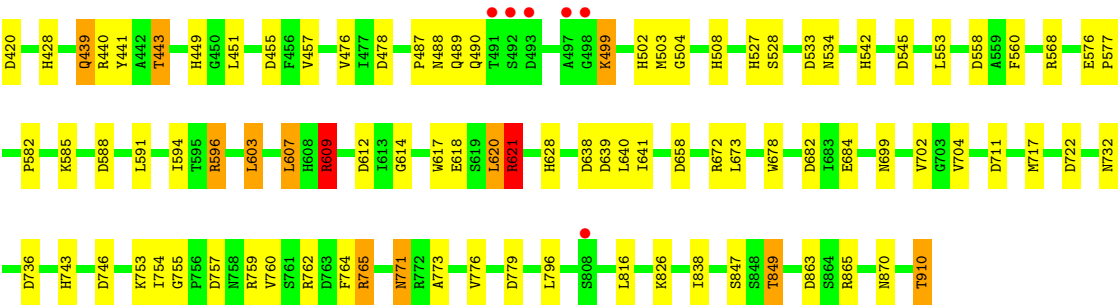
Chain E: 2% 81% 16% .



• Molecule 1: ENDO-ALPHA-SIALIDASE

Chain F: 81% 16% . .





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.65Å 131.25Å 346.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.90 20.04 – 1.90	Depositor EDS
% Data completeness (in resolution range)	93.7 (30.00-1.90) 93.8 (20.04-1.90)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.19 (at 1.90Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.166 , 0.202 0.187 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.6	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 48.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	34485	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.10% 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: 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	0.58	0/5376	0.89	27/7325 (0.4%)
1	B	0.58	0/5376	0.90	26/7325 (0.4%)
1	C	0.55	0/5376	0.88	34/7325 (0.5%)
1	D	0.57	0/5376	0.90	32/7325 (0.4%)
1	E	0.56	0/5376	0.85	29/7325 (0.4%)
1	F	0.55	0/5376	0.89	29/7325 (0.4%)
All	All	0.57	0/32256	0.88	177/43950 (0.4%)

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	B	0	1

There are no bond length outliers.

The worst 5 of 177 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	596	ARG	NE-CZ-NH2	11.90	126.25	120.30
1	B	596	ARG	NE-CZ-NH2	9.23	124.92	120.30
1	A	596	ARG	NE-CZ-NH1	-9.08	115.76	120.30
1	F	621	ARG	NE-CZ-NH2	-8.80	115.90	120.30
1	D	355	LEU	CA-CB-CG	8.68	135.26	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	503	MET	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	5230	0	4942	72	0
1	B	5230	0	4942	78	0
1	C	5230	0	4942	70	0
1	D	5230	0	4942	84	0
1	E	5230	0	4942	91	0
1	F	5230	0	4942	80	0
2	B	5	0	0	1	0
2	C	10	0	0	1	0
2	D	5	0	0	0	0
2	F	10	0	0	0	0
3	A	528	0	0	13	0
3	B	534	0	0	14	0
3	C	516	0	0	11	0
3	D	529	0	0	12	0
3	E	459	0	0	18	0
3	F	509	0	0	19	0
All	All	34485	0	29652	447	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 7.

The worst 5 of 447 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:D:263:ASN:HB3	3:D:2012:HOH:O	1.36	1.19
1:A:449:HIS:HD2	1:A:451:LEU:H	1.03	1.00
1:B:490:GLN:HG3	3:B:2170:HOH:O	1.61	0.99
1:E:499:LYS:HE3	1:E:500:ASN:H	1.27	0.98
3:A:2050:HOH:O	1:B:368:THR:HG21	1.65	0.96

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	664/666 (100%)	642 (97%)	21 (3%)	1 (0%)	49	40
1	B	664/666 (100%)	640 (96%)	23 (4%)	1 (0%)	49	40
1	C	664/666 (100%)	642 (97%)	21 (3%)	1 (0%)	49	40
1	D	664/666 (100%)	639 (96%)	24 (4%)	1 (0%)	49	40
1	E	664/666 (100%)	636 (96%)	27 (4%)	1 (0%)	49	40
1	F	664/666 (100%)	639 (96%)	24 (4%)	1 (0%)	49	40
All	All	3984/3996 (100%)	3838 (96%)	140 (4%)	6 (0%)	49	40

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	678	TRP
1	A	704	VAL
1	C	704	VAL
1	E	704	VAL
1	D	704	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	564/564 (100%)	534 (95%)	30 (5%)	25	14
1	B	564/564 (100%)	532 (94%)	32 (6%)	23	12
1	C	564/564 (100%)	534 (95%)	30 (5%)	25	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	564/564 (100%)	525 (93%)	39 (7%)	17	8
1	E	564/564 (100%)	532 (94%)	32 (6%)	23	12
1	F	564/564 (100%)	531 (94%)	33 (6%)	21	11
All	All	3384/3384 (100%)	3188 (94%)	196 (6%)	22	12

5 of 196 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	771	ASN
1	D	585	LYS
1	F	621	ARG
1	C	910	THR
1	D	355	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 174 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	650	ASN
1	D	481	ASN
1	F	542	HIS
1	C	732	ASN
1	D	338	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](#)

6 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	1685	-	4,4,4	1.18	0	6,6,6	0.67	0
2	PO4	C	1685	-	4,4,4	1.00	0	6,6,6	0.48	0
2	PO4	C	1686	-	4,4,4	1.27	0	6,6,6	0.69	0
2	PO4	D	1685	-	4,4,4	1.19	0	6,6,6	0.43	0
2	PO4	F	1685	-	4,4,4	0.99	0	6,6,6	0.34	0
2	PO4	F	1686	-	4,4,4	1.01	0	6,6,6	0.55	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 [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	666/666 (100%)	-0.11	17 (2%) 56 59	8, 14, 21, 28	0
1	B	666/666 (100%)	-0.23	3 (0%) 90 92	9, 13, 20, 29	0
1	C	666/666 (100%)	-0.23	5 (0%) 86 87	9, 13, 21, 28	0
1	D	666/666 (100%)	-0.28	3 (0%) 90 92	9, 13, 20, 28	0
1	E	666/666 (100%)	-0.17	10 (1%) 73 76	9, 14, 20, 29	0
1	F	666/666 (100%)	-0.23	7 (1%) 80 83	9, 14, 20, 28	0
All	All	3996/3996 (100%)	-0.21	45 (1%) 80 83	8, 13, 21, 29	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	491	THR	4.0
1	A	436	ALA	4.0
1	B	245	SER	3.9
1	D	547	ALA	3.3
1	C	681	ASP	3.2

### 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	F	1686	5/5	0.97	0.13	39,40,40,42	0
2	PO4	F	1685	5/5	0.97	0.14	38,38,39,40	0
2	PO4	D	1685	5/5	0.97	0.10	36,36,39,39	0
2	PO4	C	1686	5/5	0.98	0.10	32,34,35,36	0
2	PO4	C	1685	5/5	0.98	0.10	32,33,36,38	0
2	PO4	B	1685	5/5	0.98	0.13	32,33,34,36	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.