



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 05:28 pm BST

PDB ID : 2VA0  
Title : Differential regulation of the xylan degrading apparatus of *Cellvibrio japonicus* by a novel two component system  
Authors : Murray, J.W.; Emami, K.; Topakas, E.; Nagy, T.; Henshaw, J.; Jackson, K.A.; Nelson, K.E.; Mongodin, E.F.; Lewis, R.J.; Gilbert, H.J.  
Deposited on : 2007-08-28  
Resolution : 2.60 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (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

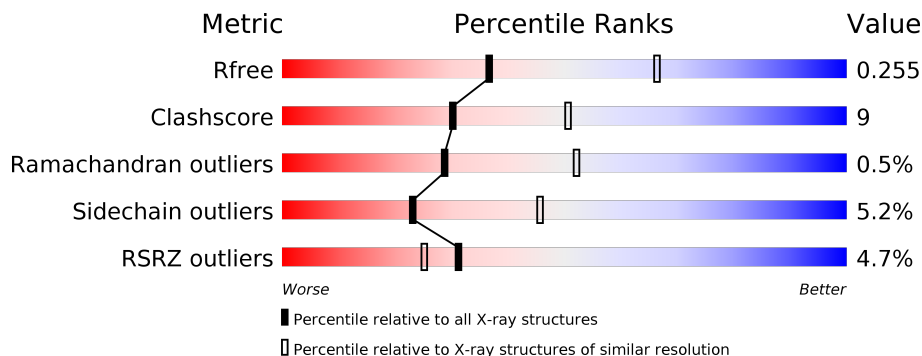
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	131	
1	B	131	
1	C	131	
1	D	131	
1	E	131	
1	F	131	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5290 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 ABFS ARABINOFURANOSIDASE TWO COMPONENT SYSTEM SENSOR PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	99	800	504	155	138	3	0	0	0
1	B	119	973	612	182	175	4	0	0	0
1	C	99	803	505	155	140	3	0	0	0
1	D	98	795	501	154	137	3	0	0	0
1	E	120	980	616	186	174	4	0	0	0
1	F	99	800	504	155	138	3	0	0	0

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	43	MET	-	expression tag	UNP B3PFT7
A	166	LEU	-	expression tag	UNP B3PFT7
A	167	GLU	-	expression tag	UNP B3PFT7
A	168	HIS	-	expression tag	UNP B3PFT7
A	169	HIS	-	expression tag	UNP B3PFT7
A	170	HIS	-	expression tag	UNP B3PFT7
A	171	HIS	-	expression tag	UNP B3PFT7
A	172	HIS	-	expression tag	UNP B3PFT7
A	173	HIS	-	expression tag	UNP B3PFT7
B	43	MET	-	expression tag	UNP B3PFT7
B	166	LEU	-	expression tag	UNP B3PFT7
B	167	GLU	-	expression tag	UNP B3PFT7
B	168	HIS	-	expression tag	UNP B3PFT7
B	169	HIS	-	expression tag	UNP B3PFT7
B	170	HIS	-	expression tag	UNP B3PFT7
B	171	HIS	-	expression tag	UNP B3PFT7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	172	HIS	-	expression tag	UNP B3PFT7
B	173	HIS	-	expression tag	UNP B3PFT7
C	43	MET	-	expression tag	UNP B3PFT7
C	166	LEU	-	expression tag	UNP B3PFT7
C	167	GLU	-	expression tag	UNP B3PFT7
C	168	HIS	-	expression tag	UNP B3PFT7
C	169	HIS	-	expression tag	UNP B3PFT7
C	170	HIS	-	expression tag	UNP B3PFT7
C	171	HIS	-	expression tag	UNP B3PFT7
C	172	HIS	-	expression tag	UNP B3PFT7
C	173	HIS	-	expression tag	UNP B3PFT7
D	43	MET	-	expression tag	UNP B3PFT7
D	166	LEU	-	expression tag	UNP B3PFT7
D	167	GLU	-	expression tag	UNP B3PFT7
D	168	HIS	-	expression tag	UNP B3PFT7
D	169	HIS	-	expression tag	UNP B3PFT7
D	170	HIS	-	expression tag	UNP B3PFT7
D	171	HIS	-	expression tag	UNP B3PFT7
D	172	HIS	-	expression tag	UNP B3PFT7
D	173	HIS	-	expression tag	UNP B3PFT7
E	43	MET	-	expression tag	UNP B3PFT7
E	166	LEU	-	expression tag	UNP B3PFT7
E	167	GLU	-	expression tag	UNP B3PFT7
E	168	HIS	-	expression tag	UNP B3PFT7
E	169	HIS	-	expression tag	UNP B3PFT7
E	170	HIS	-	expression tag	UNP B3PFT7
E	171	HIS	-	expression tag	UNP B3PFT7
E	172	HIS	-	expression tag	UNP B3PFT7
E	173	HIS	-	expression tag	UNP B3PFT7
F	43	MET	-	expression tag	UNP B3PFT7
F	166	LEU	-	expression tag	UNP B3PFT7
F	167	GLU	-	expression tag	UNP B3PFT7
F	168	HIS	-	expression tag	UNP B3PFT7
F	169	HIS	-	expression tag	UNP B3PFT7
F	170	HIS	-	expression tag	UNP B3PFT7
F	171	HIS	-	expression tag	UNP B3PFT7
F	172	HIS	-	expression tag	UNP B3PFT7
F	173	HIS	-	expression tag	UNP B3PFT7

- 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
2	C	1	Total O P 5 4 1	0	0
2	D	1	Total O P 5 4 1	0	0
2	E	1	Total O P 5 4 1	0	0
2	F	1	Total O P 5 4 1	0	0

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

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

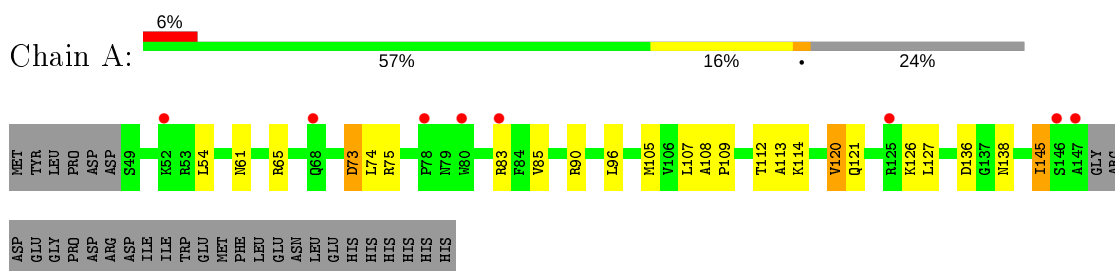
- Molecule 4 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	10	Total 10	O 10	0	0
4	A	1	Total 1	O 1	0	0
4	B	28	Total 28	O 28	0	0
4	B	1	Total 1	O 1	0	0
4	C	23	Total 23	O 23	0	0
4	D	23	Total 23	O 23	0	0
4	D	1	Total 1	O 1	0	0
4	E	11	Total 11	O 11	0	0
4	F	7	Total 7	O 7	0	0
4	F	1	Total 1	O 1	0	0

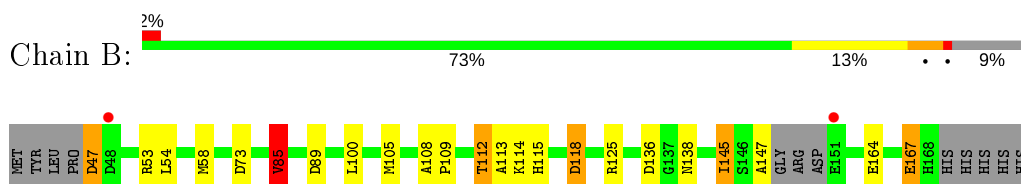
### 3 Residue-property plots [i](#)

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.

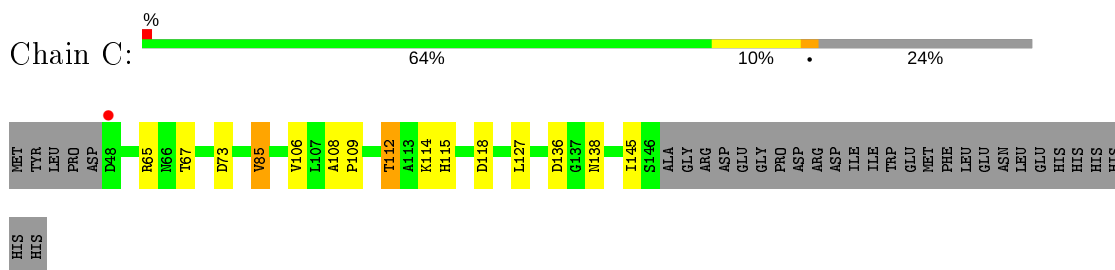
- Molecule 1: ABFS ARABINOFURANOSIDASE TWO COMPONENT SYSTEM SENSOR PROTEIN



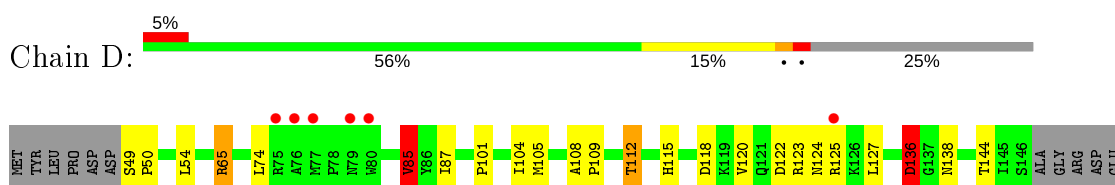
- Molecule 1: ABFS ARABINOFURANOSIDASE TWO COMPONENT SYSTEM SENSOR PROTEIN



- Molecule 1: ABFS ARABINOFURANOSIDASE TWO COMPONENT SYSTEM SENSOR PROTEIN

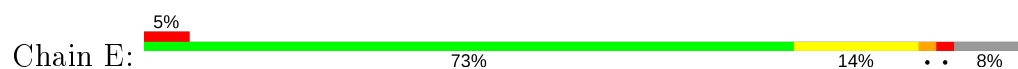


- Molecule 1: ABFS ARABINOFURANOSIDASE TWO COMPONENT SYSTEM SENSOR PROTEIN



GLY  
PRO  
ASP  
ARG  
ASP  
ASP  
ILE  
ILE  
TRP  
GLU  
MET  
PHE  
LEU  
LEU  
GLU  
ASN  
LEU  
LEU  
HIS  
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HIS  
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HIS

- Molecule 1: ABFS ARABINOFURANOSIDASE TWO COMPONENT SYSTEM SENSOR PROTEIN



MET TYR LEU PRO ASP ASP ILE ILE TRP GLU MET PHE LEU LEU GLU ASN LEU LEU HIS HIS HIS HIS HIS HIS  
S49 R65 L70 T71 Q72 D73 V85 R90 D94 L100 T112 H115 D118 Q121 K126 D136 G137 M138 T144 G148 R149 D150 E151 G152 F153 D154 E160 M161 F162 L163 E164 M165 H168 HIS HIS HIS HIS HIS HIS

- Molecule 1: ABFS ARABINOFURANOSIDASE TWO COMPONENT SYSTEM SENSOR PROTEIN



MET TYR LEU PRO ASP ASP ILE ILE TRP GLU MET PHE LEU LEU GLU ASN LEU LEU HIS HIS HIS HIS HIS HIS  
S49 F50 R53 L54 M61 R65 D72 D73 V80 R83 F84 V85 D89 R90 N91 M105 V106 L107 A108 P109 T112 A113 K114 H115 V120 R123 N124 R125 K126 L127 D136 G137 M138 T144 I145 S146 A147 GLY ARG ASP GLU

GLY  
PRO  
ASP  
ARG  
ASP  
ASP  
ILE  
ILE  
TRP  
GLU  
MET  
PHE  
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ASN  
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.77Å 80.01Å 101.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.04 – 2.60 37.04 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (37.04-2.60) 99.8 (37.04-2.60)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.13 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.199 , 0.259 0.200 , 0.255	Depositor DCC
$R_{free}$ test set	1430 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.9	Xtrriage
Anisotropy	0.160	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 43.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5290	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	11.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.68% 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, 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	0.84	2/815 (0.2%)	0.96	2/1104 (0.2%)
1	B	0.91	1/992 (0.1%)	1.06	7/1343 (0.5%)
1	C	0.89	1/818 (0.1%)	1.07	5/1108 (0.5%)
1	D	0.89	1/810 (0.1%)	1.01	6/1097 (0.5%)
1	E	0.85	0/1000	1.01	4/1354 (0.3%)
1	F	0.78	0/815	0.94	3/1104 (0.3%)
All	All	0.86	5/5250 (0.1%)	1.01	27/7110 (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
1	E	0	2
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	136	ASP	CB-CG	-6.55	1.38	1.51
1	B	85	VAL	CB-CG2	-6.32	1.39	1.52
1	C	73	ASP	CB-CG	-6.22	1.38	1.51
1	A	136	ASP	CB-CG	-5.49	1.40	1.51
1	A	73	ASP	CB-CG	-5.43	1.40	1.51

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	73	ASP	CB-CG-OD1	-8.75	110.42	118.30
1	D	136	ASP	CB-CG-OD1	-8.59	110.57	118.30
1	C	65	ARG	NE-CZ-NH2	-7.88	116.36	120.30
1	C	65	ARG	NE-CZ-NH1	7.50	124.05	120.30
1	B	58	MET	CG-SD-CE	-7.31	88.51	100.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	47	ASP	Peptide
1	E	149	ARG	Peptide
1	E	150	ASP	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	800	0	834	18	0
1	B	973	0	981	23	0
1	C	803	0	833	12	0
1	D	795	0	829	18	0
1	E	980	0	994	13	0
1	F	800	0	834	18	0
2	A	5	0	0	1	0
2	B	5	0	0	1	0
2	C	5	0	0	1	0
2	D	5	0	0	1	0
2	E	5	0	0	1	0
2	F	5	0	0	1	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	F	1	0	0	0	0
4	A	11	0	0	1	0
4	B	29	0	0	5	0
4	C	23	0	0	0	0
4	D	24	0	0	1	0
4	E	11	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	8	0	0	1	0
All	All	5290	0	5305	98	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 9.

The worst 5 of 98 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:100:LEU:CD1	1:B:105:MET:CE	2.28	1.10
1:F:112:THR:HG22	1:F:115:HIS:H	1.03	1.08
1:B:100:LEU:HD13	1:B:105:MET:CE	1.85	1.07
1:D:112:THR:HG22	1:D:115:HIS:H	1.26	1.00
1:D:112:THR:HG21	2:D:1147:PO4:O1	1.61	1.00

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	97/131 (74%)	95 (98%)	2 (2%)	0	100	100
1	B	115/131 (88%)	111 (96%)	4 (4%)	0	100	100
1	C	97/131 (74%)	95 (98%)	2 (2%)	0	100	100
1	D	96/131 (73%)	95 (99%)	1 (1%)	0	100	100
1	E	118/131 (90%)	114 (97%)	2 (2%)	2 (2%)	9	18
1	F	97/131 (74%)	95 (98%)	1 (1%)	1 (1%)	15	32
All	All	620/786 (79%)	605 (98%)	12 (2%)	3 (0%)	29	52

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	150	ASP
1	E	154	ASP
1	F	83	ARG

### 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	89/119 (75%)	85 (96%)	4 (4%)	27	52
1	B	108/119 (91%)	101 (94%)	7 (6%)	17	34
1	C	90/119 (76%)	88 (98%)	2 (2%)	52	76
1	D	89/119 (75%)	86 (97%)	3 (3%)	37	63
1	E	108/119 (91%)	100 (93%)	8 (7%)	13	28
1	F	89/119 (75%)	83 (93%)	6 (7%)	16	33
All	All	573/714 (80%)	543 (95%)	30 (5%)	23	46

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	85	VAL
1	E	72	GLN
1	F	112	THR
1	D	136	ASP
1	E	73	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	ASN
1	A	121	GLN
1	B	124	ASN
1	E	72	GLN
1	E	121	GLN

### 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](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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
2	PO4	D	1147	-	4,4,4	0.72	0	6,6,6	1.22	0
2	PO4	A	1148	-	4,4,4	1.02	0	6,6,6	0.57	0
2	PO4	F	1148	-	4,4,4	0.98	0	6,6,6	0.47	0
2	PO4	E	1169	-	4,4,4	0.97	0	6,6,6	0.82	0
2	PO4	B	1169	-	4,4,4	0.84	0	6,6,6	0.88	0
2	PO4	C	1147	-	4,4,4	0.93	0	6,6,6	0.80	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.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1147	PO4	1	0
2	A	1148	PO4	1	0
2	F	1148	PO4	1	0
2	E	1169	PO4	1	0
2	B	1169	PO4	1	0
2	C	1147	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<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	99/131 (75%)	0.46	8 (8%) 12 8	3, 9, 17, 22	0
1	B	119/131 (90%)	0.15	2 (1%) 70 66	3, 9, 24, 35	0
1	C	99/131 (75%)	-0.03	1 (1%) 82 80	3, 9, 19, 22	0
1	D	98/131 (74%)	0.30	6 (6%) 21 16	3, 9, 17, 22	0
1	E	120/131 (91%)	0.25	7 (5%) 23 17	3, 11, 36, 49	0
1	F	99/131 (75%)	0.27	6 (6%) 21 16	3, 9, 18, 21	0
All	All	634/786 (80%)	0.23	30 (4%) 31 25	3, 9, 22, 49	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	80	TRP	6.4
1	E	150	ASP	4.8
1	A	80	TRP	4.7
1	F	80	TRP	4.5
1	E	149	ARG	4.3

### 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	F	1148	5/5	0.96	0.17	24,27,28,28	0
2	PO4	C	1147	5/5	0.96	0.15	12,12,17,17	0
2	PO4	D	1147	5/5	0.97	0.17	7,9,13,15	0
2	PO4	A	1148	5/5	0.98	0.17	29,29,30,32	0
3	CL	A	1149	1/1	0.98	0.21	7,7,7,7	0
2	PO4	E	1169	5/5	0.98	0.19	16,17,20,20	0
2	PO4	B	1169	5/5	0.98	0.11	14,18,21,23	0
3	CL	C	1148	1/1	0.98	0.16	3,3,3,3	0
3	CL	F	1149	1/1	0.99	0.13	8,8,8,8	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.