



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:07 AM GMT

PDB ID : 2FOR  
Title : Crystal Structure of the Shigella flexneri Farnesyl Pyrophosphate Synthase Complex with an Isopentenyl Pyrophosphate  
Authors : Minasov, G.; Brunzelle, J.S.; Shuvalova, L.; Collart, F.R.; Joachimiak, A.; Anderson, W.F.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2006-01-13  
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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

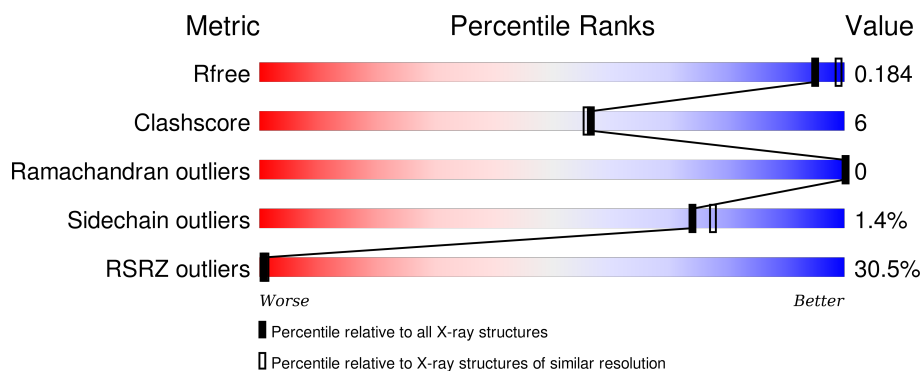
# 1 Overall quality at a glance

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))
$R_{free}$	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (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. 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	323	<div> <div>28%</div> <div>73%</div> <div>14%</div> <div>•</div> <div>12%</div> </div>
1	B	323	<div> <div>26%</div> <div>76%</div> <div>10%</div> <div>•</div> <div>13%</div> </div>

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	A	302[A]	-	-	-	X
2	PO4	B	301[A]	-	-	-	X
3	IPR	A	305[B]	-	-	-	X
3	IPR	B	302[B]	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4743 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 Geranyltranstransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	283	Total	C	N	O	S	0	3	0
			2156	1346	385	414	11			
1	B	281	Total	C	N	O	S	0	6	0
			2170	1355	386	416	13			

There are 48 discrepancies between the modelled and reference sequences:

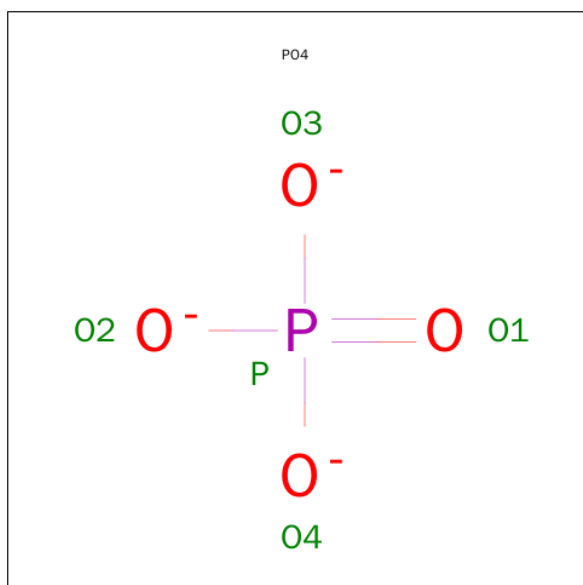
Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	EXPRESSION TAG	GB 24050587
A	-22	HIS	-	EXPRESSION TAG	GB 24050587
A	-21	HIS	-	EXPRESSION TAG	GB 24050587
A	-20	HIS	-	EXPRESSION TAG	GB 24050587
A	-19	HIS	-	EXPRESSION TAG	GB 24050587
A	-18	HIS	-	EXPRESSION TAG	GB 24050587
A	-17	HIS	-	EXPRESSION TAG	GB 24050587
A	-16	SER	-	EXPRESSION TAG	GB 24050587
A	-15	SER	-	EXPRESSION TAG	GB 24050587
A	-14	GLY	-	EXPRESSION TAG	GB 24050587
A	-13	VAL	-	EXPRESSION TAG	GB 24050587
A	-12	ASP	-	EXPRESSION TAG	GB 24050587
A	-11	LEU	-	EXPRESSION TAG	GB 24050587
A	-10	GLY	-	EXPRESSION TAG	GB 24050587
A	-9	THR	-	EXPRESSION TAG	GB 24050587
A	-8	GLU	-	EXPRESSION TAG	GB 24050587
A	-7	ASN	-	EXPRESSION TAG	GB 24050587
A	-6	LEU	-	EXPRESSION TAG	GB 24050587
A	-5	TYR	-	EXPRESSION TAG	GB 24050587
A	-4	PHE	-	EXPRESSION TAG	GB 24050587
A	-3	GLN	-	EXPRESSION TAG	GB 24050587
A	-2	SER	-	EXPRESSION TAG	GB 24050587
A	-1	ASN	-	EXPRESSION TAG	GB 24050587
A	0	ALA	-	EXPRESSION TAG	GB 24050587
B	-23	MET	-	EXPRESSION TAG	GB 24050587

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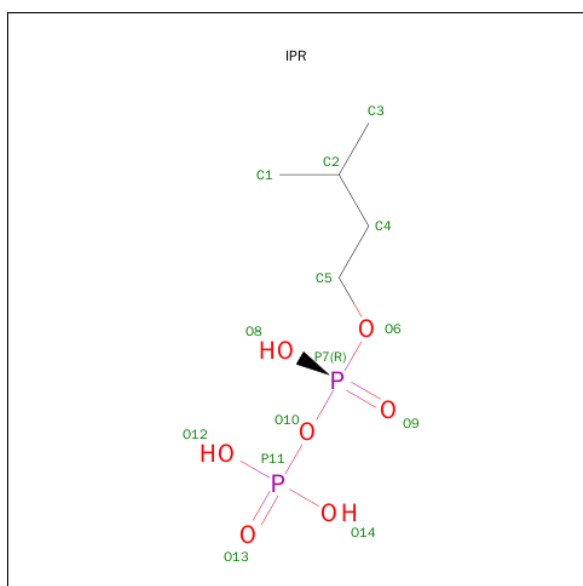
Chain	Residue	Modelled	Actual	Comment	Reference
B	-22	HIS	-	EXPRESSION TAG	GB 24050587
B	-21	HIS	-	EXPRESSION TAG	GB 24050587
B	-20	HIS	-	EXPRESSION TAG	GB 24050587
B	-19	HIS	-	EXPRESSION TAG	GB 24050587
B	-18	HIS	-	EXPRESSION TAG	GB 24050587
B	-17	HIS	-	EXPRESSION TAG	GB 24050587
B	-16	SER	-	EXPRESSION TAG	GB 24050587
B	-15	SER	-	EXPRESSION TAG	GB 24050587
B	-14	GLY	-	EXPRESSION TAG	GB 24050587
B	-13	VAL	-	EXPRESSION TAG	GB 24050587
B	-12	ASP	-	EXPRESSION TAG	GB 24050587
B	-11	LEU	-	EXPRESSION TAG	GB 24050587
B	-10	GLY	-	EXPRESSION TAG	GB 24050587
B	-9	THR	-	EXPRESSION TAG	GB 24050587
B	-8	GLU	-	EXPRESSION TAG	GB 24050587
B	-7	ASN	-	EXPRESSION TAG	GB 24050587
B	-6	LEU	-	EXPRESSION TAG	GB 24050587
B	-5	TYR	-	EXPRESSION TAG	GB 24050587
B	-4	PHE	-	EXPRESSION TAG	GB 24050587
B	-3	GLN	-	EXPRESSION TAG	GB 24050587
B	-2	SER	-	EXPRESSION TAG	GB 24050587
B	-1	ASN	-	EXPRESSION TAG	GB 24050587
B	0	ALA	-	EXPRESSION TAG	GB 24050587

- 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	1
2	A	1	Total O P 5 4 1	0	1
2	A	1	Total O P 5 4 1	0	1
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	1
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0

- Molecule 3 is ISOPENTYL PYROPHOSPHATE (three-letter code: IPR) (formula:  $C_5H_{14}O_7P_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O P 14 5 7 2	0	1
3	B	1	Total C O P 14 5 7 2	0	1

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	161	Total O 163 163	0	7

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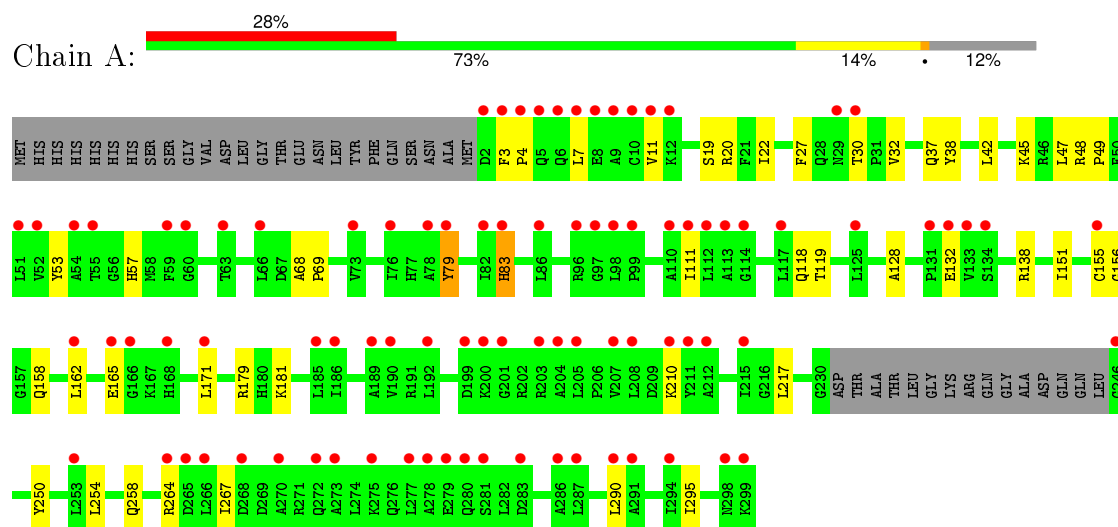
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	187	Total	O	0	12
			191	191		

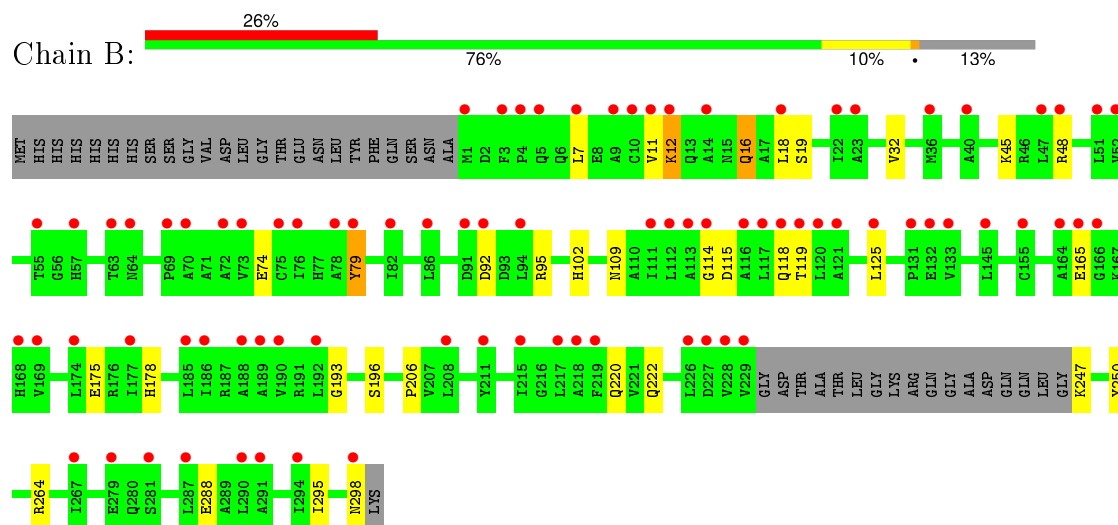
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Geranyltranstransferase



#### • Molecule 1: Geranyltranstransferase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.66 Å 75.66 Å 216.66 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	65.51 – 2.00 24.77 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.7 (65.51-2.00) 97.7 (24.77-2.00)	Depositor EDS
$R_{merge}$	0.02	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.60 (at 1.99 Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, $R_{free}$	0.181 , 0.233 0.186 , 0.184	Depositor DCC
$R_{free}$ test set	2301 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.5	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 50.1	EDS
Estimated twinning fraction	0.079 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 46107 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4743	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.81% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: IPR, 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	0.52	1/2187 (0.0%)	0.67	0/2958
1	B	0.69	9/2201 (0.4%)	0.72	2/2978 (0.1%)
All	All	0.61	10/4388 (0.2%)	0.69	2/5936 (0.0%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	12	LYS	C-O	8.56	1.39	1.23
1	B	16[A]	GLN	C-O	7.91	1.38	1.23
1	B	16[B]	GLN	C-O	7.91	1.38	1.23
1	A	155	CYS	CB-SG	-7.03	1.70	1.82
1	B	16[A]	GLN	CD-OE1	6.06	1.37	1.24
1	B	16[B]	GLN	CD-OE1	6.06	1.37	1.24
1	B	16[A]	GLN	CD-NE2	5.61	1.46	1.32
1	B	16[B]	GLN	CD-NE2	5.61	1.46	1.32
1	B	19	SER	C-O	5.38	1.33	1.23
1	B	12	LYS	C-N	5.03	1.45	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	16[A]	GLN	O-C-N	5.41	131.35	122.70
1	B	16[B]	GLN	O-C-N	5.41	131.35	122.70

There are no chirality outliers.

There are no planarity outliers.

## 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	2156	0	2162	31	0
1	B	2170	0	2176	25	0
2	A	25	0	0	1	0
2	B	10	0	0	0	0
3	A	14	0	10	1	0
3	B	14	0	10	4	0
4	A	163	0	0	4	0
4	B	191	0	0	2	0
All	All	4743	0	4358	53	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 6.

All (53) 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:162:LEU:O	1:A:165:GLU:HG2	1.85	0.77
1:A:27:PHE:O	1:A:30:THR:HG22	1.88	0.73
1:A:132:GLU:HB2	4:A:413:HOH:O	1.91	0.70
1:A:83:HIS:HD2	1:B:115:ASP:OD2	1.75	0.70
1:B:165:GLU:HG2	1:B:247:LYS:HE2	1.77	0.67
1:B:175:GLU:HG2	1:B:250:TYR:OH	1.95	0.66
1:A:264:ARG:HA	1:A:295:ILE:CD1	2.28	0.64
1:A:128:ALA:O	1:A:138:ARG:NH2	2.22	0.64
1:B:45:LYS:HE2	3:B:302[B]:IPR:O13	2.02	0.60
1:A:267:ILE:HG13	1:A:295:ILE:HB	1.85	0.59
1:B:222:GLN:HE21	1:B:222:GLN:HA	1.69	0.57
1:A:32:VAL:HG23	4:A:336:HOH:O	2.03	0.57
1:A:7:LEU:O	1:A:11:VAL:HG23	2.03	0.57
1:B:95:ARG:HH22	3:B:302[B]:IPR:HC41	1.70	0.57
1:A:258[A]:GLN:HG3	4:A:390[A]:HOH:O	2.05	0.56
1:A:264:ARG:HA	1:A:295:ILE:HD12	1.88	0.55
1:B:12:LYS:O	1:B:16[A]:GLN:HG3	2.06	0.55
1:B:264:ARG:HG3	1:B:295:ILE:HD11	1.88	0.55
1:A:53:TYR:O	1:A:57:HIS:ND1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:ARG:NH2	3:B:302[B]:IPR:O14	2.39	0.54
1:A:118:GLN:NE2	1:B:119:THR:OG1	2.39	0.54
1:B:165:GLU:HG2	1:B:247:LYS:CE	2.39	0.52
1:A:3:PHE:N	1:A:4:PRO:HD2	2.25	0.52
1:A:38:TYR:CD1	1:A:42:LEU:HD12	2.45	0.52
1:A:68:ALA:HB3	1:A:69:PRO:CD	2.40	0.51
1:B:95:ARG:NH2	3:B:302[B]:IPR:HC41	2.26	0.50
1:B:7:LEU:O	1:B:11:VAL:HG23	2.12	0.49
1:A:158:GLN:OE1	1:A:181:LYS:HE2	2.13	0.48
1:A:68:ALA:HB3	1:A:69:PRO:HD3	1.96	0.48
1:B:18:LEU:HD11	1:B:74:GLU:HG2	1.94	0.48
1:A:264:ARG:HA	1:A:295:ILE:HD11	1.95	0.48
1:A:22:ILE:HG21	1:A:37:GLN:HG2	1.96	0.47
1:A:83:HIS:HE1	1:A:111:ILE:O	1.97	0.47
1:A:45:LYS:NZ	3:A:305[B]:IPR:HC52	2.29	0.47
1:B:178:HIS:CE1	1:B:220:GLN:HG2	2.49	0.47
1:A:119:THR:OG1	1:B:118:GLN:NE2	2.45	0.46
1:A:179:ARG:NH1	2:A:303:PO4:O2	2.36	0.45
1:B:288:GLU:HG3	4:B:447:HOH:O	2.16	0.45
1:A:47:LEU:HA	1:A:47:LEU:HD23	1.74	0.45
1:A:19:SER:HB2	4:A:332:HOH:O	2.16	0.44
1:A:217:LEU:HD11	1:A:250:TYR:OH	2.17	0.44
1:B:32:VAL:HG22	1:B:109:ASN:HD22	1.82	0.43
1:A:48:ARG:HB2	1:A:49:PRO:HD3	2.00	0.43
1:B:206:PRO:HD2	4:B:477:HOH:O	2.18	0.43
1:B:193:GLY:O	1:B:196:SER:HB3	2.19	0.42
1:B:222:GLN:NE2	1:B:298:ASN:HD22	2.17	0.42
1:B:79:TYR:C	1:B:79:TYR:CD1	2.93	0.42
1:A:79:TYR:C	1:A:79:TYR:CD1	2.93	0.42
1:A:171:LEU:HD22	1:A:254:LEU:HD21	2.01	0.41
1:B:92:ASP:O	1:B:102:HIS:HE1	2.02	0.41
1:B:125:LEU:HA	1:B:125:LEU:HD23	1.94	0.40
1:B:79:TYR:HB2	1:B:114:GLY:O	2.20	0.40
1:A:151:ILE:O	1:A:156:GLY:HA3	2.20	0.40

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	282/323 (87%)	276 (98%)	6 (2%)	0	100	100
1	B	283/323 (88%)	280 (99%)	3 (1%)	0	100	100
All	All	565/646 (88%)	556 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	224/254 (88%)	219 (98%)	5 (2%)	60	62
1	B	227/254 (89%)	226 (100%)	1 (0%)	93	95
All	All	451/508 (89%)	445 (99%)	6 (1%)	74	79

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

Mol	Chain	Res	Type
1	A	20	ARG
1	A	79	TYR
1	A	83	HIS
1	A	210	LYS
1	A	290	LEU
1	B	79	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	28	GLN
1	A	29	ASN
1	A	37	GLN
1	A	83	HIS
1	A	109	ASN
1	A	118	GLN
1	A	178	HIS
1	A	296	GLN
1	A	298	ASN
1	B	6	GLN
1	B	37	GLN
1	B	102	HIS
1	B	109	ASN
1	B	118	GLN
1	B	222	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](#)

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	A	300[A]	-	4,4,4	0.63	0	6,6,6	0.28	0
2	PO4	A	301[A]	-	4,4,4	0.40	0	6,6,6	0.27	0
2	PO4	A	302[A]	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	A	303	-	4,4,4	0.44	0	6,6,6	0.27	0
2	PO4	A	304	-	4,4,4	0.39	0	6,6,6	0.27	0
3	IPR	A	305[B]	-	11,13,13	1.09	1 (9%)	17,19,19	1.17	1 (5%)
2	PO4	B	300	-	4,4,4	0.38	0	6,6,6	0.28	0
2	PO4	B	301[A]	-	4,4,4	0.40	0	6,6,6	0.27	0
3	IPR	B	302[B]	-	11,13,13	1.11	1 (9%)	17,19,19	1.18	1 (5%)

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
2	PO4	A	300[A]	-	-	0/0/0/0	0/0/0/0
2	PO4	A	301[A]	-	-	0/0/0/0	0/0/0/0
2	PO4	A	302[A]	-	-	0/0/0/0	0/0/0/0
2	PO4	A	303	-	-	0/0/0/0	0/0/0/0
2	PO4	A	304	-	-	0/0/0/0	0/0/0/0
3	IPR	A	305[B]	-	-	0/13/13/13	0/0/0/0
2	PO4	B	300	-	-	0/0/0/0	0/0/0/0
2	PO4	B	301[A]	-	-	0/0/0/0	0/0/0/0
3	IPR	B	302[B]	-	-	0/13/13/13	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	305[B]	IPR	C1-C2	-3.14	1.32	1.51
3	B	302[B]	IPR	C1-C2	-3.13	1.32	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	302[B]	IPR	P7-O10-P11	-3.08	122.36	132.67
3	A	305[B]	IPR	P7-O10-P11	-3.04	122.46	132.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	303	PO4	1	0
3	A	305[B]	IPR	1	0
3	B	302[B]	IPR	4	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

### 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	283/323 (87%)	1.66	89 (31%)	<b>1</b> <b>1</b>	33, 50, 57, 68	0
1	B	281/323 (86%)	1.59	83 (29%)	<b>1</b> <b>1</b>	46, 51, 60, 73	0
All	All	564/646 (87%)	1.62	172 (30%)	<b>1</b> <b>1</b>	33, 50, 59, 73	0

All (172) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	246	GLY	10.3
1	A	2	ASP	7.5
1	A	278	ALA	7.3
1	B	298	ASN	7.2
1	B	73	VAL	6.0
1	A	29	ASN	6.0
1	A	51	LEU	5.2
1	A	98	LEU	5.2
1	A	190	VAL	5.2
1	B	166	GLY	5.2
1	A	166	GLY	5.1
1	A	4	PRO	5.0
1	B	227	ASP	5.0
1	A	8	GLU	4.8
1	A	200	LYS	4.8
1	A	203	ARG	4.8
1	B	215	ILE	4.7
1	B	51	LEU	4.7
1	B	228	VAL	4.6
1	A	165	GLU	4.6
1	B	165	GLU	4.6
1	B	190	VAL	4.6
1	B	192	LEU	4.4
1	A	280	GLN	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	299	LYS	4.4
1	A	290	LEU	4.4
1	B	9	ALA	4.3
1	A	97	GLY	4.3
1	A	134	SER	4.3
1	A	111	ILE	4.3
1	A	82	ILE	4.3
1	B	229	VAL	4.3
1	A	279	GLU	4.2
1	B	22	ILE	4.2
1	A	272	GLN	4.1
1	B	117	LEU	4.1
1	B	287	LEU	4.0
1	B	10[A]	CYS	4.0
1	B	18	LEU	4.0
1	B	64	ASN	4.0
1	A	208	LEU	3.9
1	B	7	LEU	3.9
1	A	205	LEU	3.9
1	B	112	LEU	3.9
1	A	66	LEU	3.9
1	A	277	LEU	3.9
1	A	5	GLN	3.8
1	A	199	ASP	3.8
1	A	52	VAL	3.8
1	A	168	HIS	3.8
1	A	287	LEU	3.8
1	B	132	GLU	3.7
1	A	112	LEU	3.7
1	A	162	LEU	3.7
1	A	201	GLY	3.7
1	A	3	PHE	3.7
1	B	1	MET	3.7
1	B	76	ILE	3.7
1	A	73	VAL	3.6
1	B	226	LEU	3.6
1	B	125	LEU	3.6
1	B	111	ILE	3.6
1	B	208	LEU	3.6
1	A	281	SER	3.6
1	B	281	SER	3.5
1	A	186	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	164	ALA	3.5
1	B	186	ILE	3.4
1	B	116	ALA	3.4
1	B	189	ALA	3.4
1	B	185	LEU	3.4
1	B	131	PRO	3.4
1	A	268	ASP	3.3
1	B	82	ILE	3.2
1	B	23	ALA	3.2
1	B	290	LEU	3.2
1	A	215	ILE	3.2
1	A	275	LYS	3.2
1	A	55	THR	3.1
1	A	185	LEU	3.1
1	B	72	ALA	3.1
1	B	86	LEU	3.1
1	B	75	CYS	3.0
1	B	14	ALA	3.0
1	A	266	LEU	3.0
1	B	211	TYR	3.0
1	A	117	LEU	3.0
1	B	78	ALA	3.0
1	A	86	LEU	3.0
1	B	114	GLY	2.9
1	A	7	LEU	2.9
1	B	92	ASP	2.9
1	A	10[A]	CYS	2.9
1	A	192	LEU	2.9
1	B	120	LEU	2.9
1	A	79	TYR	2.9
1	A	212	ALA	2.9
1	A	132	GLU	2.9
1	B	36	MET	2.9
1	A	99	PRO	2.8
1	B	279	GLU	2.8
1	A	273	ALA	2.8
1	A	211	TYR	2.8
1	A	189	ALA	2.8
1	A	133	VAL	2.8
1	B	218	ALA	2.8
1	A	96	ARG	2.8
1	A	270	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	113	ALA	2.7
1	B	294	ILE	2.7
1	A	78	ALA	2.7
1	B	121	ALA	2.7
1	B	219	PHE	2.7
1	A	12	LYS	2.7
1	B	4	PRO	2.7
1	A	110	ALA	2.6
1	B	11	VAL	2.6
1	B	119	THR	2.6
1	B	70	ALA	2.6
1	A	63	THR	2.6
1	A	59	PHE	2.5
1	A	9	ALA	2.5
1	B	63	THR	2.5
1	A	204	ALA	2.5
1	B	168	HIS	2.5
1	A	76	ILE	2.5
1	A	131	PRO	2.5
1	B	55	THR	2.5
1	B	79	TYR	2.5
1	A	294	ILE	2.5
1	A	125	LEU	2.4
1	B	3	PHE	2.4
1	A	11	VAL	2.4
1	B	94[A]	LEU	2.4
1	A	60	GLY	2.4
1	A	114	GLY	2.4
1	B	40	ALA	2.4
1	B	133	VAL	2.4
1	A	265	ASP	2.3
1	B	118	GLN	2.3
1	A	83	HIS	2.3
1	A	30	THR	2.3
1	B	267	ILE	2.3
1	A	286	ALA	2.3
1	B	217	LEU	2.3
1	B	155[A]	CYS	2.2
1	A	54	ALA	2.2
1	B	47	LEU	2.2
1	B	52	VAL	2.2
1	B	57	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	177	ILE	2.2
1	A	291	ALA	2.2
1	A	155	CYS	2.2
1	B	12	LYS	2.2
1	B	174	LEU	2.1
1	A	298	ASN	2.1
1	B	291	ALA	2.1
1	A	171	LEU	2.1
1	A	253	LEU	2.1
1	B	48	ARG	2.1
1	A	283	ASP	2.1
1	B	145	LEU	2.1
1	B	5	GLN	2.1
1	A	264	ARG	2.1
1	B	91	ASP	2.1
1	A	113	ALA	2.1
1	B	188	ALA	2.1
1	A	207	VAL	2.1
1	A	210	LYS	2.0
1	B	169	VAL	2.0
1	A	6	GLN	2.0
1	B	69	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	IPR	A	305[B]	14/14	0.77	0.47	5.24	71,73,75,75	14
3	IPR	B	302[B]	14/14	0.78	0.37	3.89	46,51,53,54	14
2	PO4	A	302[A]	5/5	0.81	0.27	2.37	56,58,59,59	5
2	PO4	B	301[A]	5/5	0.81	0.28	2.08	143,143,144,144	5
2	PO4	A	301[A]	5/5	0.84	0.24	1.54	51,51,52,52	5
2	PO4	B	300	5/5	0.98	0.19	0.11	45,49,50,51	0
2	PO4	A	300[A]	5/5	0.98	0.13	-0.85	36,38,40,42	5
2	PO4	A	304	5/5	0.73	0.30	-	70,71,73,74	5
2	PO4	A	303	5/5	0.80	0.32	-	55,56,58,58	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.