



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 9, 2016 – 04:26 AM EDT

PDB ID : 5FHX  
Title : CRYSTAL STRUCTURE OF CODV IN COMPLEX WITH IL4 AT 2.55 Ang.  
RESOLUTION.  
Authors : Vallee, F.; Dupuy, A.; Rak, A.  
Deposited on : 2015-12-22  
Resolution : 2.55 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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027674  
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) : rb-20027674

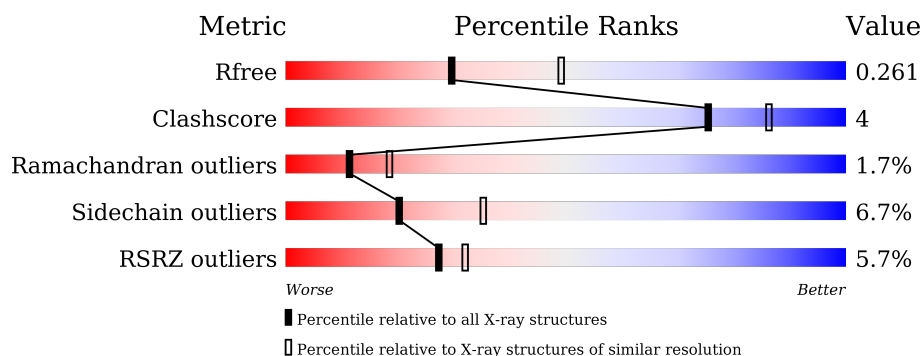
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.55 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	4549 (2.58-2.50)
Clashscore	102246	5292 (2.58-2.50)
Ramachandran outliers	100387	5194 (2.58-2.50)
Sidechain outliers	100360	5196 (2.58-2.50)
RSRZ outliers	91569	4561 (2.58-2.50)

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	124	<div> <div>8%</div> <div> <div></div> <div>81%</div> <div>16%</div> <div>...</div> </div> </div>
2	H	345	<div> <div>5%</div> <div> <div></div> <div>85%</div> <div>12%</div> <div>..</div> </div> </div>
3	L	334	<div> <div>5%</div> <div> <div></div> <div>85%</div> <div>14%</div> <div>.</div> </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
4	PO4	H	401	-	-	-	X
4	PO4	L	401	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6263 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 Interleukin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	122	Total	C	N	O	S	0	0	0
			992	619	181	186	6			

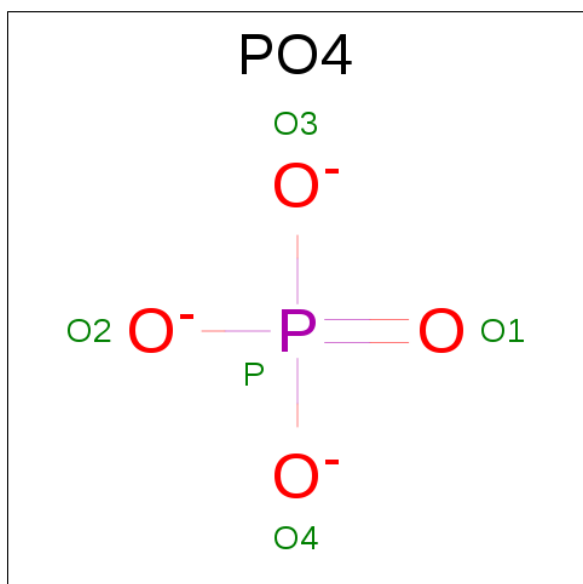
- Molecule 2 is a protein called antibody fragment heavy-chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	340	Total	C	N	O	S	0	0	0
			2590	1637	429	513	11			

- Molecule 3 is a protein called Antibody fragment light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	334	Total	C	N	O	S	0	0	0
			2543	1594	429	511	9			

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	O	P	0	0
			5	4	1		
4	L	1	Total	O	P	0	0
			5	4	1		

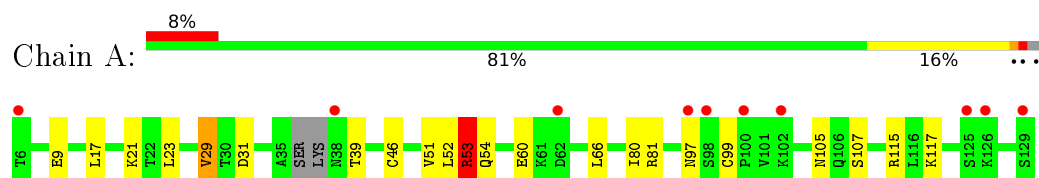
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	15	Total	O	0	0
			15	15		
5	H	55	Total	O	0	0
			55	55		
5	L	58	Total	O	0	0
			58	58		

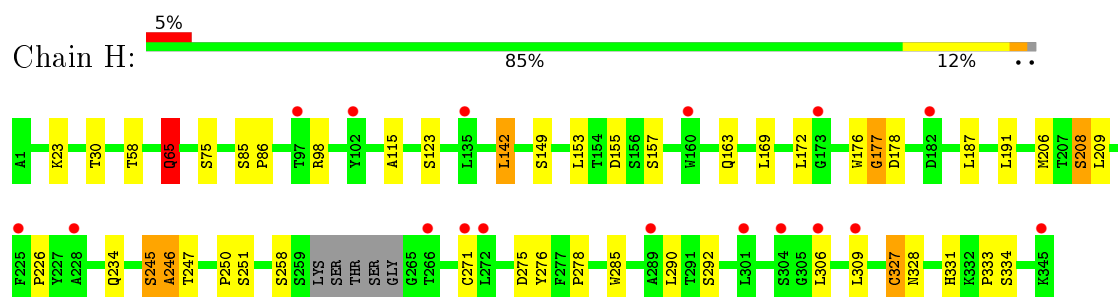
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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.

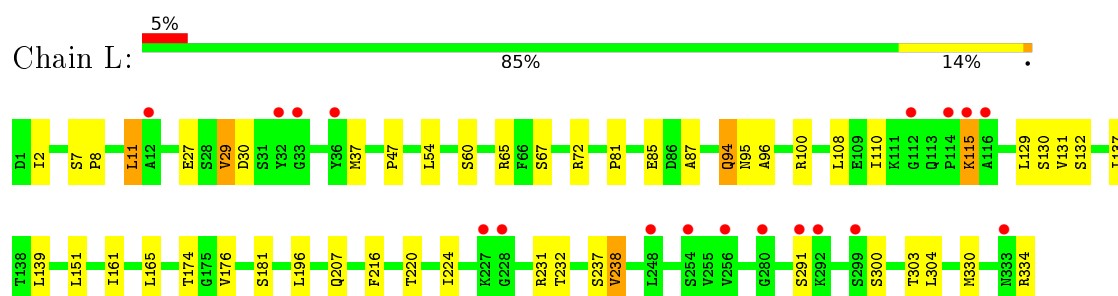
- Molecule 1: Interleukin-4



- Molecule 2: antibody fragment heavy-chain



- Molecule 3: Antibody fragment light chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.21Å 73.33Å 91.40Å 90.00° 112.72° 90.00°	Depositor
Resolution (Å)	23.15 – 2.55 23.15 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.9 (23.15-2.55) 99.9 (23.15-2.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.44 (at 2.57Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, $R_{free}$	0.184 , 0.249 0.197 , 0.261	Depositor DCC
$R_{free}$ test set	1545 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.8	Xtriage
Anisotropy	0.612	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 65.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6263	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% 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: 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	1.30	4/1005 (0.4%)	1.22	3/1348 (0.2%)
2	H	0.50	0/2655	0.78	2/3614 (0.1%)
3	L	0.51	0/2601	0.73	0/3537
All	All	0.70	4/6261 (0.1%)	0.84	5/8499 (0.1%)

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	A	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	53	ARG	C-N	-30.92	0.62	1.34
1	A	39	THR	C-O	-11.97	1.00	1.23
1	A	52	LEU	C-N	-11.96	1.06	1.34
1	A	39	THR	CB-CG2	-7.42	1.27	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	53	ARG	O-C-N	-29.75	75.10	122.70
1	A	53	ARG	CA-C-N	18.89	158.75	117.20
1	A	53	ARG	C-N-CA	9.72	145.99	121.70
2	H	245	SER	C-N-CA	6.19	137.19	121.70
2	H	177	GLY	C-N-CA	6.02	136.74	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	53	ARG	Mainchain

## 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	992	0	1003	5	0
2	H	2590	0	2516	24	0
3	L	2543	0	2476	19	0
4	H	5	0	0	0	0
4	L	5	0	0	0	0
5	A	15	0	0	0	0
5	H	55	0	0	0	0
5	L	58	0	0	0	0
All	All	6263	0	5995	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 4.

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)
2:H:271:CYS:HG	2:H:327:CYS:HG	1.07	0.88
1:A:46:CYS:HG	1:A:99:CYS:HG	0.91	0.86
2:H:142:LEU:HD12	2:H:209:LEU:HD11	1.58	0.84
2:H:250:PRO:HB3	2:H:276:TYR:HB3	1.65	0.79
2:H:245:SER:HA	2:H:246:ALA:HB3	1.78	0.64
2:H:187:LEU:HB3	2:H:191:LEU:HD13	1.83	0.61
2:H:247:THR:HG22	2:H:278:PRO:HD3	1.83	0.60
2:H:65:GLN:HB2	3:L:85:GLU:HB3	1.83	0.60
2:H:245:SER:HA	2:H:246:ALA:CB	2.33	0.59
3:L:2:ILE:HG12	3:L:27:GLU:HB2	1.87	0.57
2:H:142:LEU:CD1	2:H:206:MET:HB3	2.38	0.54
3:L:129:LEU:HD21	3:L:137:ILE:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:157:SER:HB3	2:H:176:TRP:HA	1.91	0.53
2:H:275:ASP:HB3	2:H:306:LEU:HD13	1.90	0.52
2:H:271:CYS:HG	2:H:327:CYS:CB	2.22	0.52
2:H:226:PRO:HG3	3:L:54:LEU:HG	1.92	0.51
2:H:142:LEU:HD13	2:H:206:MET:HB3	1.93	0.50
2:H:85:SER:N	2:H:86:PRO:HD3	2.27	0.49
3:L:139:LEU:HD22	3:L:220:THR:HG21	1.93	0.49
3:L:11:LEU:HD23	3:L:108:LEU:HD13	1.95	0.48
2:H:163:GLN:HB2	2:H:169:LEU:HD23	1.95	0.48
3:L:207:GLN:HB2	3:L:216:PHE:CD2	2.49	0.48
1:A:60:GLU:HG3	1:A:80:ILE:HG21	1.96	0.47
3:L:94:GLN:HG2	3:L:96:ALA:H	1.77	0.47
3:L:87:ALA:HB2	3:L:110:ILE:HD12	1.96	0.46
3:L:238:VAL:HG22	3:L:330:MET:HG3	1.97	0.46
2:H:65:GLN:H	2:H:65:GLN:HG2	1.50	0.46
3:L:95:ASN:HA	3:L:100:ARG:HG2	1.98	0.46
2:H:172:LEU:HB3	2:H:191:LEU:HD21	1.98	0.45
3:L:8:PRO:HG2	3:L:11:LEU:HD12	1.99	0.44
3:L:29:VAL:HG11	3:L:37:MET:HB2	1.99	0.43
2:H:234:GLN:HA	3:L:47:PRO:HG3	1.99	0.43
3:L:65:ARG:HD2	3:L:81:PRO:O	2.19	0.43
1:A:29:VAL:HG22	1:A:51:VAL:CG1	2.49	0.42
3:L:165:LEU:HA	3:L:176:VAL:HG21	2.02	0.42
2:H:271:CYS:CB	2:H:327:CYS:HG	2.32	0.42
1:A:17:LEU:HD23	1:A:117:LYS:HD2	2.01	0.41
2:H:285:TRP:HB3	2:H:290:LEU:HD23	2.02	0.41
3:L:115:LYS:HA	3:L:115:LYS:HD3	1.91	0.41
3:L:196:LEU:HD13	3:L:196:LEU:C	2.41	0.41
2:H:331:HIS:CD2	2:H:333:PRO:HD2	2.56	0.41
1:A:31:ASP:HB2	1:A:107:SER:HB2	2.03	0.40
2:H:153:LEU:HD12	2:H:153:LEU:HA	1.93	0.40
2:H:115:ALA:HA	3:L:161:ILE:HG21	2.04	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	118/124 (95%)	111 (94%)	4 (3%)	3 (2%)	7	10
2	H	336/345 (97%)	309 (92%)	21 (6%)	6 (2%)	11	17
3	L	332/334 (99%)	315 (95%)	13 (4%)	4 (1%)	16	27
All	All	786/803 (98%)	735 (94%)	38 (5%)	13 (2%)	11	18

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	ARG
2	H	178	ASP
3	L	115	LYS
1	A	105	ASN
2	H	177	GLY
2	H	246	ALA
3	L	60	SER
3	L	232	THR
1	A	54	GLN
2	H	334	SER
3	L	72	ARG
2	H	65	GLN
2	H	208	SER

### 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	111/113 (98%)	103 (93%)	8 (7%)	18	31
2	H	290/294 (99%)	273 (94%)	17 (6%)	24	42
3	L	285/285 (100%)	264 (93%)	21 (7%)	17	30
All	All	686/692 (99%)	640 (93%)	46 (7%)	20	35

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	GLU
1	A	21	LYS
1	A	23	LEU
1	A	29	VAL
1	A	66	LEU
1	A	81	ARG
1	A	97	ASN
1	A	115	ARG
2	H	23	LYS
2	H	30	THR
2	H	58	THR
2	H	65	GLN
2	H	75	SER
2	H	98	ARG
2	H	123	SER
2	H	142	LEU
2	H	149	SER
2	H	155	ASP
2	H	208	SER
2	H	251	SER
2	H	258	SER
2	H	292	SER
2	H	309	LEU
2	H	327	CYS
2	H	328	ASN
3	L	7	SER
3	L	11	LEU
3	L	29	VAL
3	L	30	ASP
3	L	67	SER
3	L	94	GLN
3	L	130	SER
3	L	131	VAL
3	L	132	SER
3	L	151	LEU
3	L	174	THR
3	L	181	SER
3	L	224	ILE
3	L	231	ARG
3	L	237	SER
3	L	238	VAL
3	L	291	SER

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Mol	Chain	Res	Type
3	L	300	SER
3	L	303	THR
3	L	304	LEU
3	L	334	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
3	L	57	ASN
3	L	94	GLN
3	L	260	ASN
3	L	261	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](#)

2 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	$\# Z  > 2$
4	PO4	H	401	-	4,4,4	1.91	2 (50%)	6,6,6	0.24	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	PO4	L	401	-	4,4,4	1.87	2 (50%)	6,6,6	0.26	0

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
4	PO4	H	401	-	-	0/0/0/0	0/0/0/0
4	PO4	L	401	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	401	PO4	P-O4	2.17	1.60	1.53
4	H	401	PO4	P-O3	2.19	1.60	1.53
4	L	401	PO4	P-O2	2.20	1.60	1.53
4	L	401	PO4	P-O4	2.21	1.60	1.53

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	52:LEU	C	53:ARG	N	1.06
1	A	53:ARG	C	54:GLN	N	0.62

## 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	122/124 (98%)	0.27	10 (8%)	14 16	25, 61, 98, 123	0
2	H	340/345 (98%)	0.26	17 (5%)	32 38	25, 63, 89, 115	0
3	L	334/334 (100%)	0.29	18 (5%)	29 34	28, 62, 95, 106	0
All	All	796/803 (99%)	0.27	45 (5%)	27 32	25, 62, 94, 123	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	32	TYR	7.1
3	L	292	LYS	5.0
1	A	38	ASN	4.8
1	A	97	ASN	4.6
1	A	102	LYS	4.5
3	L	112	GLY	4.1
3	L	291	SER	4.0
2	H	301	LEU	3.7
2	H	289	ALA	3.6
3	L	116	ALA	3.6
2	H	271	CYS	3.5
2	H	272	LEU	3.5
1	A	129	SER	3.5
3	L	254	SER	3.4
2	H	135	LEU	3.4
3	L	33	GLY	3.3
1	A	126	LYS	3.1
2	H	304	SER	3.0
2	H	345	LYS	2.9
1	A	100	PRO	2.9
3	L	227	LYS	2.8
3	L	333	ASN	2.8
2	H	160	TRP	2.7

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Mol	Chain	Res	Type	RSRZ
2	H	266	THR	2.6
2	H	182	ASP	2.5
3	L	36	TYR	2.5
1	A	6	THR	2.5
3	L	114	PRO	2.4
2	H	306	LEU	2.4
3	L	12	ALA	2.4
3	L	256	VAL	2.4
1	A	125	SER	2.3
3	L	280	GLY	2.3
2	H	102	TYR	2.2
3	L	248	LEU	2.2
1	A	62	ASP	2.2
2	H	225	PHE	2.1
1	A	98	SER	2.1
3	L	115	LYS	2.1
3	L	228	GLY	2.1
2	H	309	LEU	2.0
2	H	173	GLY	2.0
2	H	228	ALA	2.0
3	L	299	SER	2.0
2	H	97	THR	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
4	PO4	H	401	5/5	0.89	0.22	3.58	118,120,120,121	0
4	PO4	L	401	5/5	0.88	0.22	2.31	93,94,97,97	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.