



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:50 AM GMT

PDB ID : 2YIB  
Title : Structure of the RNA polymerase VP1 from Infectious Pancreatic Necrosis Virus  
Authors : Graham, S.C.; Sarin, L.P.; Bahar, M.W.; Myers, R.A.; Stuart, D.I.; Bamford, D.H.; Grimes, J.M.  
Deposited on : 2011-05-11  
Resolution : 3.80 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

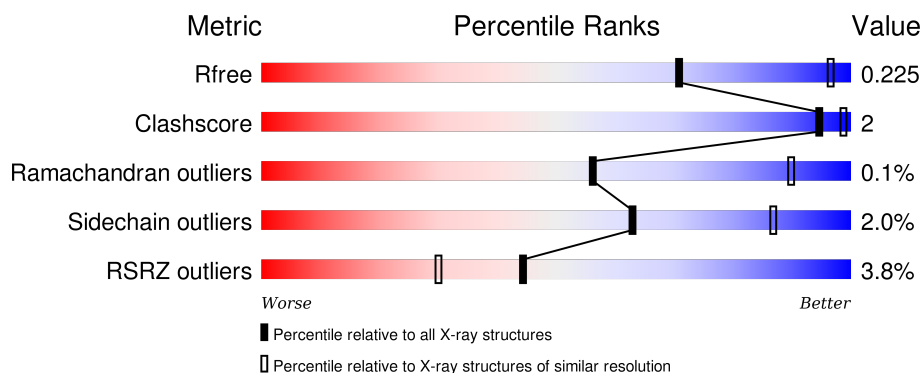
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.80 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	1317 (4.10-3.50)
Clashscore	102246	1458 (4.10-3.50)
Ramachandran outliers	100387	1397 (4.10-3.50)
Sidechain outliers	100360	1392 (4.10-3.50)
RSRZ outliers	91569	1325 (4.10-3.50)

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	853	<div> <div></div> <div>87% 6% 8%</div> </div>
1	B	853	<div> <div>8%</div> <div>87% 6% 8%</div> </div>
1	C	853	<div> <div></div> <div>86% 7% 8%</div> </div>
2	D	770	<div> <div>5%</div> <div>94% 5%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 24183 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 RNA-DIRECTED RNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	789	Total	C	N	O	S	0	0	0
			6159	3908	1038	1187	26			
1	B	789	Total	C	N	O	S	0	0	0
			6155	3906	1038	1185	26			
1	C	789	Total	C	N	O	S	0	0	0
			6159	3908	1038	1187	26			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	846	VAL	-	EXPRESSION TAG	UNP P22173
A	847	GLU	-	EXPRESSION TAG	UNP P22173
A	848	HIS	-	EXPRESSION TAG	UNP P22173
A	849	HIS	-	EXPRESSION TAG	UNP P22173
A	850	HIS	-	EXPRESSION TAG	UNP P22173
A	851	HIS	-	EXPRESSION TAG	UNP P22173
A	852	HIS	-	EXPRESSION TAG	UNP P22173
A	853	HIS	-	EXPRESSION TAG	UNP P22173
B	846	VAL	-	EXPRESSION TAG	UNP P22173
B	847	GLU	-	EXPRESSION TAG	UNP P22173
B	848	HIS	-	EXPRESSION TAG	UNP P22173
B	849	HIS	-	EXPRESSION TAG	UNP P22173
B	850	HIS	-	EXPRESSION TAG	UNP P22173
B	851	HIS	-	EXPRESSION TAG	UNP P22173
B	852	HIS	-	EXPRESSION TAG	UNP P22173
B	853	HIS	-	EXPRESSION TAG	UNP P22173
C	846	VAL	-	EXPRESSION TAG	UNP P22173
C	847	GLU	-	EXPRESSION TAG	UNP P22173
C	848	HIS	-	EXPRESSION TAG	UNP P22173
C	849	HIS	-	EXPRESSION TAG	UNP P22173
C	850	HIS	-	EXPRESSION TAG	UNP P22173
C	851	HIS	-	EXPRESSION TAG	UNP P22173
C	852	HIS	-	EXPRESSION TAG	UNP P22173

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Chain	Residue	Modelled	Actual	Comment	Reference
C	853	HIS	-	EXPRESSION TAG	UNP P22173

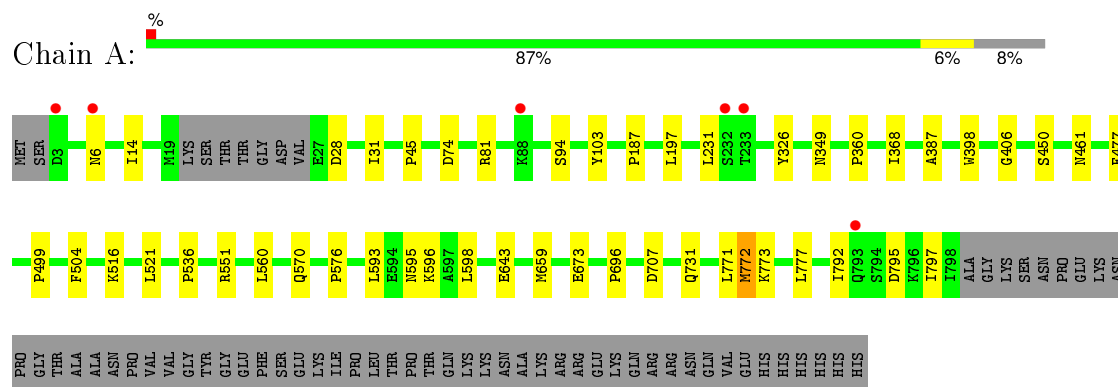
- Molecule 2 is a protein called RNA-DIRECTED RNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	761	Total	C	N	O	S	415	0	0
			5710	3622	966	1097	25			

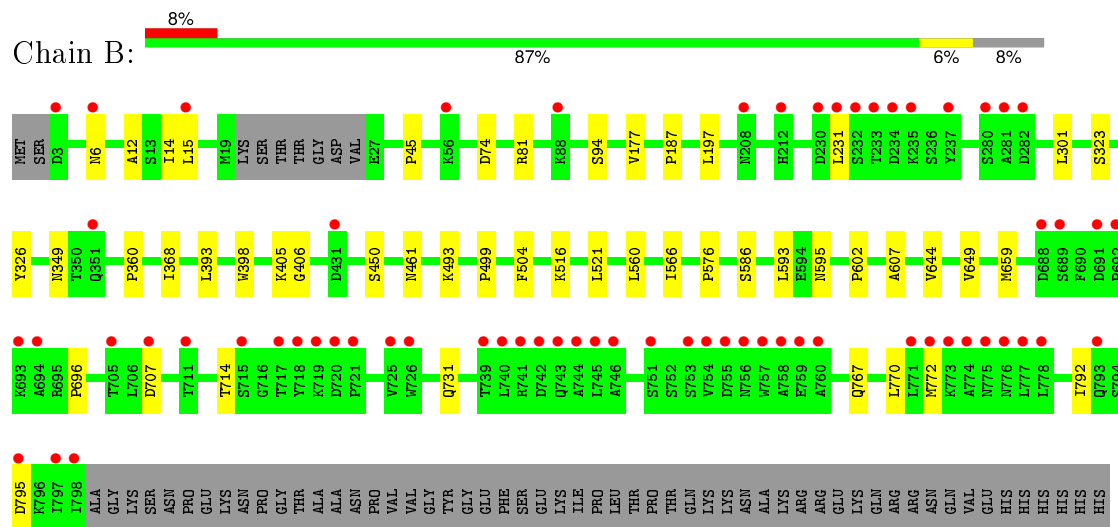
### 3 Residue-property plots

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

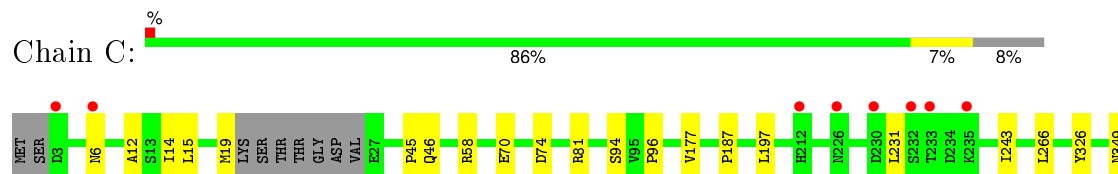
#### • Molecule 1: RNA-DIRECTED RNA POLYMERASE

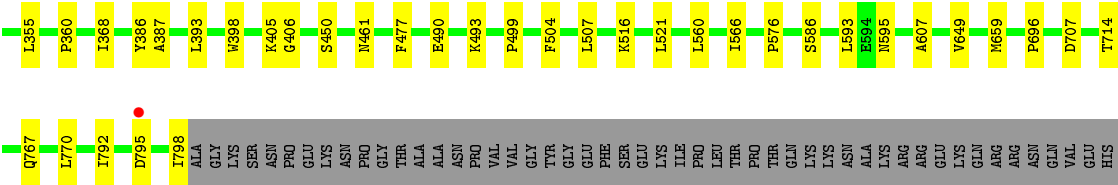


#### • Molecule 1: RNA-DIRECTED RNA POLYMERASE



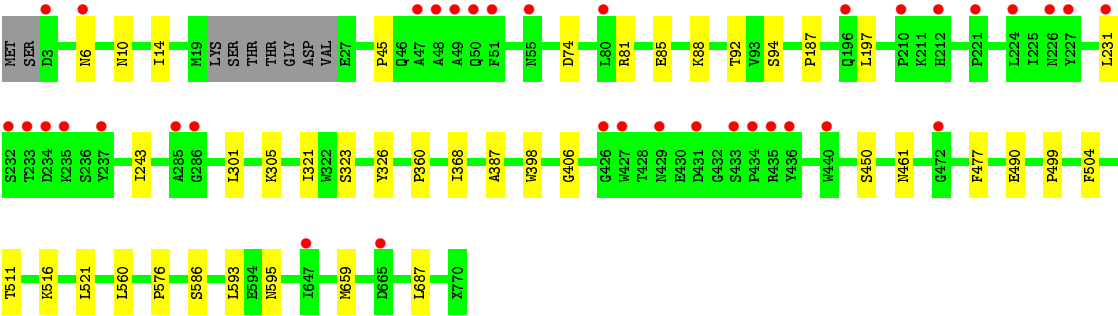
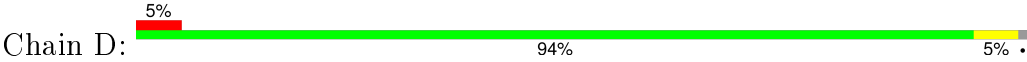
#### • Molecule 1: RNA-DIRECTED RNA POLYMERASE





HIS  
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● Molecule 2: RNA-DIRECTED RNA POLYMERASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	119.74Å 195.45Å 197.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.43 – 3.80 44.43 – 3.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (44.43-3.80) 98.1 (44.43-3.80)	Depositor EDS
$R_{merge}$	0.30	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.91 (at 3.77Å)	Xtriage
Refinement program	BUSTER 2.9.2	Depositor
R, $R_{free}$	0.184 , 0.213 0.199 , 0.225	Depositor DCC
$R_{free}$ test set	2305 reflections (5.07%)	DCC
Wilson B-factor (Å <sup>2</sup> )	88.6	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 94.4	EDS
Estimated twinning fraction	0.056 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	0 of 45473 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	24183	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.98% 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](#)

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	0.47	0/6296	0.64	0/8573
1	B	0.44	0/6292	0.65	0/8568
1	C	0.48	0/6296	0.66	0/8573
2	D	0.46	0/5420	0.65	0/7383
All	All	0.46	0/24304	0.65	0/33097

There are no bond length outliers.

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	6159	0	6090	23	0
1	B	6155	0	6086	24	0
1	C	6159	0	6090	26	0
2	D	5710	0	5296	21	0
All	All	24183	0	23562	79	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 2.

All (79) 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:644:VAL:HG22	2:D:92:THR:CG2	1.90	1.01
1:B:644:VAL:HG22	2:D:92:THR:HG21	1.54	0.88
1:B:644:VAL:HG22	2:D:92:THR:HG23	1.61	0.81
1:C:187:PRO:HB3	1:C:197:LEU:HD11	1.73	0.70
1:A:187:PRO:HB3	1:A:197:LEU:HD11	1.74	0.69
1:C:12:ALA:HB3	2:D:243:ILE:HD11	1.76	0.67
1:C:493:LYS:HE2	1:C:714:THR:HG22	1.77	0.66
1:B:644:VAL:CG2	2:D:92:THR:HG21	2.28	0.63
1:A:673:GLU:HG3	1:C:798:ILE:HG12	1.80	0.63
1:B:187:PRO:HB3	1:B:197:LEU:HD11	1.81	0.63
2:D:187:PRO:HB3	2:D:197:LEU:HD11	1.80	0.62
1:C:74:ASP:HB2	1:C:81:ARG:HG2	1.86	0.57
1:B:398:TRP:HB3	1:B:521:LEU:HB3	1.87	0.57
1:A:74:ASP:HB2	1:A:81:ARG:HG2	1.87	0.57
1:B:74:ASP:HB2	1:B:81:ARG:HG2	1.87	0.56
2:D:398:TRP:HB3	2:D:521:LEU:HB3	1.87	0.56
1:A:593:LEU:CD1	1:A:659:MET:HB2	2.36	0.56
1:B:593:LEU:CD1	1:B:659:MET:HB2	2.35	0.56
2:D:74:ASP:HB2	2:D:81:ARG:HG2	1.88	0.55
1:C:19:MET:HB3	2:D:88:LYS:O	2.08	0.54
1:C:593:LEU:CD1	1:C:659:MET:HB2	2.38	0.53
2:D:593:LEU:CD1	2:D:659:MET:HB2	2.39	0.52
1:A:31:ILE:HD13	1:B:602:PRO:HG2	1.90	0.52
1:C:398:TRP:HB3	1:C:521:LEU:HB3	1.90	0.52
1:A:398:TRP:HB3	1:A:521:LEU:HB3	1.91	0.51
2:D:45:PRO:HB3	2:D:461:ASN:OD1	2.10	0.51
1:A:731:GLN:HG2	1:A:772:MET:CE	2.41	0.51
1:A:570:GLN:HG3	1:C:46:GLN:NE2	2.26	0.51
1:C:45:PRO:HB3	1:C:461:ASN:OD1	2.12	0.50
1:C:360:PRO:HB2	1:C:576:PRO:HB3	1.94	0.49
1:C:349:ASN:O	1:C:696:PRO:HD2	2.13	0.48
1:A:551:ARG:NH2	2:D:85:GLU:HA	2.29	0.48
2:D:368:ILE:HG21	2:D:560:LEU:HD22	1.95	0.47
2:D:360:PRO:HB2	2:D:576:PRO:HB3	1.96	0.47
1:C:177:VAL:HG21	1:C:405:LYS:HB2	1.96	0.47
1:C:368:ILE:HG21	1:C:560:LEU:HD22	1.96	0.47
1:B:368:ILE:HG21	1:B:560:LEU:HD22	1.97	0.46
1:A:31:ILE:CD1	1:B:602:PRO:HG2	2.46	0.46
1:B:45:PRO:HB3	1:B:461:ASN:OD1	2.15	0.46
1:A:349:ASN:O	1:A:696:PRO:HD2	2.16	0.46
1:B:767:GLN:HA	1:B:770:LEU:HD12	1.98	0.46
1:A:387:ALA:HB2	1:A:477:PHE:CD2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:595:ASN:CB	1:C:659:MET:HA	2.47	0.45
1:B:177:VAL:HG21	1:B:405:LYS:HB2	1.98	0.45
1:A:771:LEU:HD22	1:A:777:LEU:CD1	2.47	0.45
1:B:595:ASN:CB	1:B:659:MET:HA	2.47	0.45
1:A:368:ILE:HG21	1:A:560:LEU:HD22	1.97	0.45
1:A:360:PRO:HB2	1:A:576:PRO:HB3	1.99	0.45
1:A:643:GLU:OE2	1:C:70:GLU:HG3	2.17	0.45
1:B:731:GLN:HG2	1:B:772:MET:SD	2.57	0.45
1:A:103:TYR:CE2	1:A:797:ILE:HG21	2.52	0.44
1:B:360:PRO:HB2	1:B:576:PRO:HB3	1.97	0.44
1:B:301:LEU:HB2	1:B:323:SER:HB2	1.99	0.44
2:D:387:ALA:HB2	2:D:477:PHE:CD2	2.53	0.44
2:D:499:PRO:HA	2:D:504:PHE:CG	2.53	0.44
1:C:767:GLN:HA	1:C:770:LEU:HD12	1.99	0.44
1:A:187:PRO:CB	1:A:197:LEU:HD11	2.46	0.43
1:B:493:LYS:HE2	1:B:714:THR:HG22	2.00	0.43
1:C:499:PRO:HA	1:C:504:PHE:CG	2.52	0.43
1:A:499:PRO:HA	1:A:504:PHE:CG	2.54	0.43
1:A:45:PRO:HB3	1:A:461:ASN:OD1	2.18	0.43
1:C:387:ALA:HB2	1:C:477:PHE:CD2	2.53	0.43
2:D:305:LYS:HG3	2:D:321:ILE:HD11	2.01	0.42
2:D:301:LEU:HB2	2:D:323:SER:HB2	2.01	0.42
1:C:12:ALA:CB	2:D:243:ILE:HD11	2.47	0.42
1:C:607:ALA:HB2	1:C:649:VAL:HB	2.02	0.41
1:B:349:ASN:O	1:B:696:PRO:HD2	2.20	0.41
1:B:12:ALA:HB3	1:C:243:ILE:HD11	2.01	0.41
1:B:607:ALA:HB2	1:B:649:VAL:HB	2.01	0.41
1:A:28:ASP:OD2	1:B:602:PRO:HD2	2.20	0.41
1:C:187:PRO:CB	1:C:197:LEU:HD11	2.47	0.41
1:B:499:PRO:HA	1:B:504:PHE:CG	2.56	0.41
2:D:490:GLU:HG3	2:D:511:THR:HG22	2.03	0.41
1:C:96:PRO:HD2	1:C:266:LEU:HD21	2.03	0.40
1:C:355:LEU:HB2	1:C:386:TYR:HB2	2.03	0.40
1:A:595:ASN:CB	1:A:659:MET:HA	2.51	0.40
1:A:596:LYS:CB	1:A:598:LEU:HG	2.51	0.40
2:D:595:ASN:CB	2:D:659:MET:HA	2.51	0.40
1:C:490:GLU:HB3	1:C:507:LEU:HD22	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	785/853 (92%)	761 (97%)	23 (3%)	1 (0%)	56	90
1	B	785/853 (92%)	761 (97%)	23 (3%)	1 (0%)	56	90
1	C	785/853 (92%)	758 (97%)	26 (3%)	1 (0%)	56	90
2	D	674/770 (88%)	651 (97%)	22 (3%)	1 (0%)	56	90
All	All	3029/3329 (91%)	2931 (97%)	94 (3%)	4 (0%)	56	90

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	406	GLY
1	B	406	GLY
1	C	406	GLY
1	A	406	GLY

### 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	669/739 (90%)	656 (98%)	13 (2%)	65	87
1	B	668/739 (90%)	654 (98%)	14 (2%)	61	86
1	C	669/739 (90%)	654 (98%)	15 (2%)	60	85
2	D	573/593 (97%)	563 (98%)	10 (2%)	68	89
All	All	2579/2810 (92%)	2527 (98%)	52 (2%)	63	87

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	14	ILE
1	A	94	SER
1	A	231	LEU
1	A	326	TYR
1	A	450	SER
1	A	516	LYS
1	A	536	PRO
1	A	707	ASP
1	A	772	MET
1	A	773	LYS
1	A	792	ILE
1	A	795	ASP
1	B	6	ASN
1	B	14	ILE
1	B	15	LEU
1	B	94	SER
1	B	231	LEU
1	B	326	TYR
1	B	393	LEU
1	B	450	SER
1	B	516	LYS
1	B	566	ILE
1	B	586	SER
1	B	707	ASP
1	B	792	ILE
1	B	795	ASP
1	C	6	ASN
1	C	14	ILE
1	C	15	LEU
1	C	58	ARG
1	C	94	SER
1	C	231	LEU
1	C	326	TYR
1	C	393	LEU
1	C	450	SER
1	C	516	LYS
1	C	566	ILE
1	C	586	SER
1	C	707	ASP
1	C	792	ILE
1	C	795	ASP

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Mol	Chain	Res	Type
2	D	6	ASN
2	D	10	ASN
2	D	14	ILE
2	D	94	SER
2	D	231	LEU
2	D	326	TYR
2	D	450	SER
2	D	516	LYS
2	D	586	SER
2	D	687	LEU

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

Mol	Chain	Res	Type
1	A	731	GLN
1	C	46	GLN
1	C	768	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	789/853 (92%)	-0.12	6 (0%) 87 77	50, 80, 118, 174	0
1	B	789/853 (92%)	0.32	65 (8%) 14 9	62, 113, 183, 214	0
1	C	789/853 (92%)	-0.03	9 (1%) 82 69	49, 85, 131, 179	0
2	D	678/770 (88%)	0.23	36 (5%) 30 20	58, 103, 162, 190	0
All	All	3045/3329 (91%)	0.10	116 (3%) 44 30	49, 93, 158, 214	0

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	3	ASP	6.4
1	B	3	ASP	6.4
1	B	692	PRO	5.8
1	B	755	ASP	5.6
1	B	721	PRO	5.3
2	D	3	ASP	5.1
1	B	756	ASN	5.1
1	B	754	VAL	4.8
1	B	693	LYS	4.5
1	B	745	LEU	4.4
1	C	233	THR	4.2
1	B	757	TRP	4.2
1	B	281	ALA	4.0
1	B	795	ASP	4.0
1	B	282	ASP	3.8
2	D	286	GLY	3.8
2	D	51	PHE	3.7
2	D	6	ASN	3.7
1	B	741	ARG	3.7
1	B	208	ASN	3.6
2	D	434	PRO	3.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	3	ASP	3.4
1	C	226	ASN	3.3
1	B	771	LEU	3.2
1	B	774	ALA	3.2
1	B	776	ASN	3.2
2	D	233	THR	3.2
2	D	237	TYR	3.1
1	B	720	ASP	3.1
1	B	775	ASN	3.1
2	D	232	SER	3.1
1	B	232	SER	3.0
2	D	80	LEU	3.0
2	D	48	ALA	3.0
2	D	50	GLN	3.0
2	D	433	SER	3.0
1	B	233	THR	2.9
1	B	351	GLN	2.9
1	C	235	LYS	2.9
2	D	212	HIS	2.8
1	B	711	THR	2.8
1	B	798	ILE	2.8
1	A	233	THR	2.8
2	D	429	ASN	2.8
1	B	744	ALA	2.7
1	C	232	SER	2.7
1	C	795	ASP	2.7
1	A	6	ASN	2.7
2	D	436	TYR	2.7
2	D	55	ASN	2.7
1	B	88	LYS	2.7
1	B	717	THR	2.7
2	D	234	ASP	2.6
1	B	691	ASP	2.6
1	C	6	ASN	2.6
1	B	742	ASP	2.6
1	B	759	GLU	2.6
1	B	280	SER	2.6
2	D	49	ALA	2.6
1	B	705	THR	2.6
2	D	226	ASN	2.5
1	B	725	VAL	2.5
1	B	230	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	751	SER	2.5
1	B	15	LEU	2.5
2	D	665	ASP	2.5
1	A	88	LYS	2.5
1	B	235	LYS	2.5
1	B	212	HIS	2.5
2	D	231	LEU	2.4
2	D	427	TRP	2.4
1	A	232	SER	2.4
2	D	435	ARG	2.4
1	B	777	LEU	2.4
2	D	210	PRO	2.4
2	D	285	ALA	2.4
1	B	707	ASP	2.4
2	D	47	ALA	2.4
2	D	224	LEU	2.4
1	B	753	SER	2.4
2	D	440	TRP	2.3
2	D	235	LYS	2.3
1	B	237	TYR	2.3
1	B	689	SER	2.3
2	D	431	ASP	2.3
1	B	772	MET	2.3
1	B	743	GLN	2.3
2	D	472	GLY	2.3
1	B	758	ALA	2.2
1	C	230	ASP	2.2
1	B	778	LEU	2.2
1	B	234	ASP	2.2
1	B	431	ASP	2.2
1	B	694	ALA	2.2
2	D	227	TYR	2.2
1	B	740	LEU	2.2
1	B	726	TRP	2.1
1	B	56	LYS	2.1
1	B	719	LYS	2.1
2	D	221	PRO	2.1
1	C	212	HIS	2.1
1	B	6	ASN	2.1
1	B	718	TYR	2.1
1	A	793	GLN	2.1
2	D	196	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	760	ALA	2.1
1	B	773	LYS	2.1
1	B	797	ILE	2.1
1	B	688	ASP	2.1
2	D	647	ILE	2.1
1	B	231	LEU	2.0
2	D	426	GLY	2.0
1	B	746	ALA	2.0
1	B	793	GLN	2.0
1	B	715	SER	2.0
1	B	739	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.