



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 10:08 am BST

PDB ID : 6HMF  
Title : D-family DNA polymerase - DP1 subunit (3'-5' proof-reading exonuclease)  
H451 proof-reading deficient variant  
Authors : Raia, P.; Delarue, M.; Sauguet, L.  
Deposited on : 2018-09-12  
Resolution : 2.60 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

<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)  
Xtriage (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

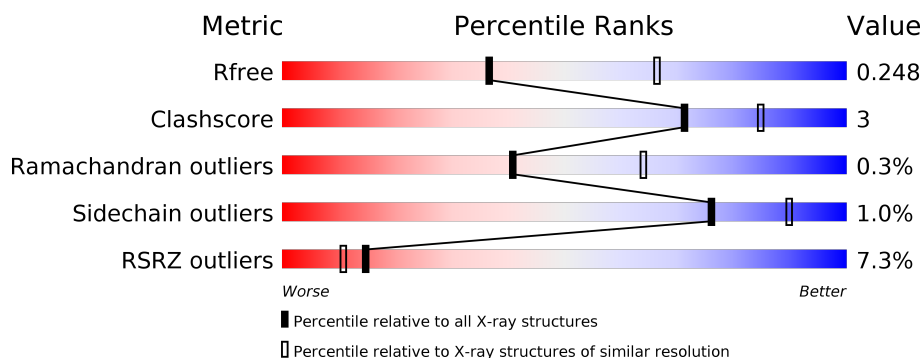
# 1 Overall quality at a glance

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	475	<div> <div>8%</div> <div>82%</div> <div>10%</div> <div>7%</div> </div>
1	B	475	<div> <div>5%</div> <div>84%</div> <div>8%</div> <div>7%</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
6	CA	B	703	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7128 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 DNA polymerase II small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	440	Total	C	N	O	S	0	0	0
			3512	2291	575	639	7			
1	B	442	Total	C	N	O	S	0	1	0
			3530	2304	577	642	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	451	ALA	HIS	engineered mutation	UNP Q9V2F3
B	451	ALA	HIS	engineered mutation	UNP Q9V2F3

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Fe	0	0
			1	1		
2	A	1	Total	Fe	0	0
			1	1		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

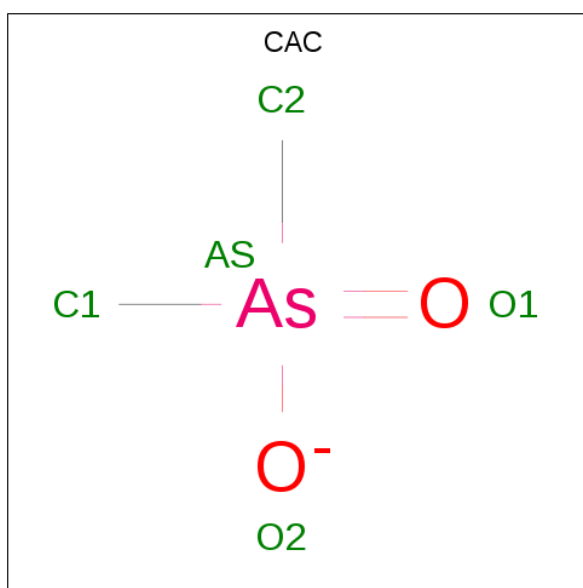
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is CACODYLATE ION (three-letter code: CAC) (formula:  $C_2H_6AsO_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	As	C	O	0	0
			5	1	2	2		
5	B	1	Total	As	C	O	0	0
			5	1	2	2		

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total 1	Ca 1	0	0

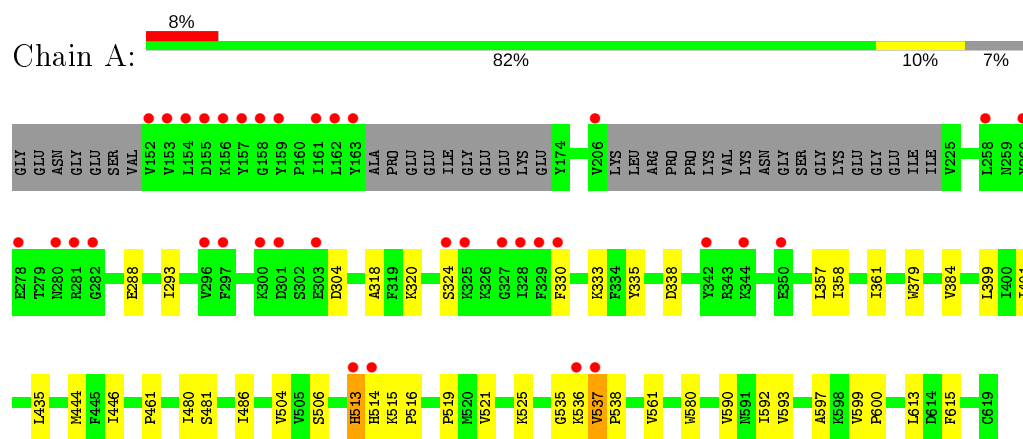
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	33	Total 33	O 33	0	0
7	B	30	Total 30	O 30	0	0

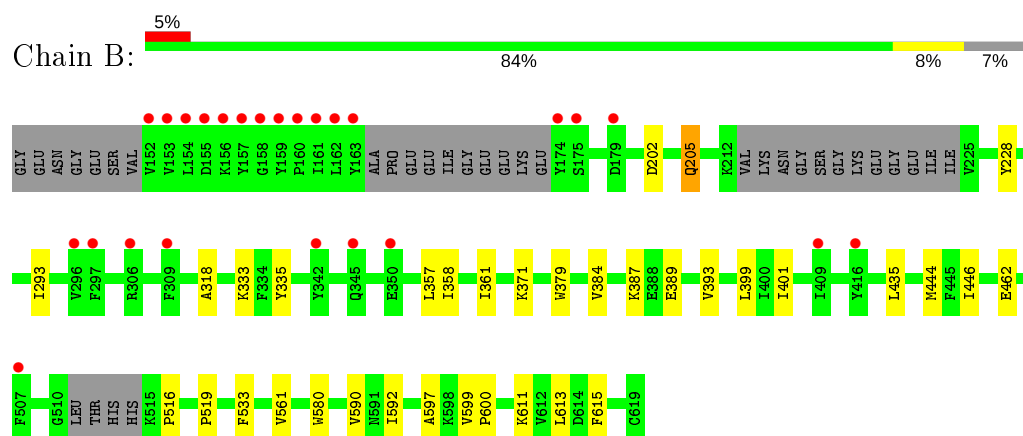
### 3 Residue-property plots [i](#)

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: DNA polymerase II small subunit



- Molecule 1: DNA polymerase II small subunit



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.75Å 91.24Å 143.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.19 – 2.60 47.19 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.19-2.60) 100.0 (47.19-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.41 (at 2.61Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, $R_{free}$	0.227 , 0.255 0.226 , 0.248	Depositor DCC
$R_{free}$ test set	1653 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	73.2	Xtriage
Anisotropy	0.458	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 56.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7128	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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: CAC, ZN, ACT, CA, FE

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	0.45	0/3599	0.68	0/4890
1	B	0.43	0/3619	0.66	0/4915
All	All	0.44	0/7218	0.67	0/9805

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

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	3512	0	3546	29	0
1	B	3530	0	3572	20	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
6	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	33	0	0	0	0
7	B	30	0	0	0	0
All	All	7128	0	7124	49	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 3.

All (49) 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:228:TYR:CE2	1:B:533:PHE:HE1	2.19	0.60
1:B:318:ALA:HB3	1:B:335:TYR:HB2	1.88	0.56
1:A:318:ALA:HB3	1:A:335:TYR:HB2	1.88	0.56
1:A:597:ALA:HB1	1:A:615:PHE:HB2	1.88	0.56
1:A:357:LEU:O	1:A:600:PRO:HD2	2.06	0.55
1:B:357:LEU:O	1:B:600:PRO:HD2	2.06	0.55
1:B:597:ALA:HB1	1:B:615:PHE:HB2	1.87	0.55
1:A:401:ILE:HD12	1:A:446:ILE:HG12	1.90	0.55
1:A:304:ASP:OD2	1:A:333:LYS:HG3	2.08	0.54
1:B:435:LEU:HD22	1:B:444:MET:HE3	1.90	0.54
1:B:288:GLU:HG3	1:B:293:ILE:HG12	1.90	0.53
1:B:401:ILE:HD12	1:B:446:ILE:HG12	1.90	0.52
1:A:513:HIS:HE1	1:A:593:VAL:H	1.58	0.51
1:A:513:HIS:C	1:A:515:LYS:H	2.14	0.51
1:A:461:PRO:O	1:A:481:SER:HB3	2.11	0.51
1:A:262:SER:HB2	1:A:264:ASP:OD1	2.12	0.50
1:A:513:HIS:O	1:A:514:HIS:HB2	2.12	0.49
1:A:288:GLU:HG3	1:A:293:ILE:HG12	1.94	0.49
1:A:537:VAL:O	1:A:537:VAL:HG13	2.14	0.48
1:B:361:ILE:HA	1:B:580:TRP:HB2	1.96	0.48
1:B:379:TRP:CD1	1:B:384:VAL:HG12	2.49	0.47
1:B:599:VAL:HB	1:B:613:LEU:HB2	1.96	0.47
1:A:361:ILE:HA	1:A:580:TRP:HB2	1.96	0.47
1:A:516:PRO:HB3	1:A:561:VAL:HG21	1.98	0.46
1:A:324:SER:HB2	1:A:330:PHE:CE1	2.50	0.46
1:A:599:VAL:HB	1:A:613:LEU:HB2	1.97	0.46
1:A:590:VAL:HG23	1:A:592:ILE:HD13	1.99	0.45
1:A:521:VAL:HG12	1:A:525:LYS:HE2	1.98	0.45
1:A:514:HIS:O	1:A:515:LYS:HG2	2.16	0.45
1:A:480:ILE:HD13	1:A:486:ILE:HD11	1.98	0.45
1:B:358:ILE:HG12	1:B:399:LEU:HD11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:LEU:HD22	1:A:444:MET:HE3	1.98	0.44
1:A:379:TRP:CD1	1:A:384:VAL:HG12	2.52	0.44
1:A:399:LEU:HD23	1:A:444:MET:HG2	1.99	0.44
1:B:399:LEU:HD23	1:B:444:MET:HG2	1.99	0.44
1:B:480:ILE:HD13	1:B:486:ILE:HD11	1.97	0.44
1:B:516:PRO:HB3	1:B:561:VAL:HG21	2.00	0.43
1:A:320:LYS:HB3	1:A:333:LYS:HB3	2.00	0.43
1:A:358:ILE:HG12	1:A:399:LEU:HD11	1.99	0.43
1:A:536:LYS:O	1:A:538:PRO:HD3	2.19	0.42
1:B:590:VAL:HG23	1:B:592:ILE:HD13	2.01	0.42
1:B:249:ILE:HG23	1:B:268:THR:HG21	2.02	0.42
1:A:324:SER:HB2	1:A:330:PHE:HE1	1.85	0.41
1:B:444:MET:HE2	1:B:444:MET:HB3	1.95	0.41
1:A:504:VAL:HG11	1:A:519:PRO:HA	2.03	0.40
1:B:516:PRO:C	1:B:519:PRO:HD2	2.41	0.40
1:B:202:ASP:O	1:B:205:GLN:HB2	2.21	0.40
1:B:389:GLU:O	1:B:393:VAL:HG23	2.21	0.40
1:A:535:GLY:C	1:A:537:VAL:N	2.75	0.40

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	434/475 (91%)	415 (96%)	18 (4%)	1 (0%)	47	71
1	B	435/475 (92%)	421 (97%)	12 (3%)	2 (0%)	29	52
All	All	869/950 (92%)	836 (96%)	30 (4%)	3 (0%)	41	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	537	VAL
1	B	205	GLN
1	B	462	GLU

### 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	385/415 (93%)	382 (99%)	3 (1%)	81	92
1	B	387/415 (93%)	382 (99%)	5 (1%)	69	86
All	All	772/830 (93%)	764 (99%)	8 (1%)	76	90

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	338	ASP
1	A	506	SER
1	A	513	HIS
1	B	333	LYS
1	B	371	LYS
1	B	387	LYS
1	B	506	SER
1	B	611	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	513	HIS

### 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 ⓘ

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 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	$\# Z  > 2$
4	ACT	A	703	-	1,3,3	5.53	1 (100%)	0,3,3	0.00	-
5	CAC	B	705	3,2	0,4,4	0.00	-	0,6,6	0.00	-
5	CAC	A	704	2	0,4,4	0.00	-	0,6,6	0.00	-
4	ACT	B	704	-	1,3,3	5.35	1 (100%)	0,3,3	0.00	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	703	ACT	CH3-C	5.53	1.55	1.48
4	B	704	ACT	CH3-C	5.35	1.55	1.48

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

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	440/475 (92%)	0.44	39 (8%) 9 6	58, 78, 124, 159	0
1	B	442/475 (93%)	0.47	25 (5%) 23 18	55, 79, 127, 162	0
All	All	882/950 (92%)	0.46	64 (7%) 15 11	55, 78, 126, 162	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	152	VAL	8.5
1	B	154	LEU	8.1
1	A	156	LYS	8.1
1	B	157	TYR	7.3
1	A	155	ASP	7.0
1	B	158	GLY	6.8
1	B	162	LEU	6.4
1	B	160	PRO	6.2
1	A	154	LEU	6.0
1	B	161	ILE	6.0
1	B	163	TYR	5.9
1	B	155	ASP	5.7
1	B	159	TYR	5.7
1	A	162	LEU	5.4
1	A	159	TYR	5.1
1	B	156	LYS	4.9
1	A	157	TYR	4.6
1	A	325	LYS	4.5
1	A	281	ARG	4.4
1	B	306	ARG	4.4
1	A	328	ILE	4.3
1	B	416	TYR	4.3
1	A	301	ASP	4.2
1	A	324	SER	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	174	TYR	4.0
1	A	297	PHE	3.9
1	A	350	GLU	3.9
1	B	153	VAL	3.8
1	A	163	TYR	3.8
1	A	282	GLY	3.5
1	A	514	HIS	3.4
1	A	161	ILE	3.3
1	A	280	ASN	3.2
1	B	175	SER	3.1
1	A	158	GLY	2.9
1	A	300	LYS	2.9
1	A	329	PHE	2.8
1	A	330	PHE	2.8
1	A	537	VAL	2.8
1	B	179	ASP	2.8
1	A	413	PRO	2.8
1	A	327	GLY	2.7
1	A	303	GLU	2.7
1	A	342	TYR	2.6
1	A	416	TYR	2.5
1	A	513	HIS	2.5
1	A	260	TYR	2.4
1	A	152	VAL	2.4
1	B	342	TYR	2.4
1	B	297	PHE	2.4
1	B	350	GLU	2.4
1	A	258	LEU	2.4
1	B	309	PHE	2.3
1	A	153	VAL	2.2
1	B	345	GLN	2.2
1	A	296	VAL	2.1
1	A	412	TYR	2.1
1	A	278	GLU	2.1
1	A	536	LYS	2.1
1	A	206	VAL	2.1
1	A	344	LYS	2.1
1	B	409	ILE	2.0
1	B	507	PHE	2.0
1	B	296	VAL	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. 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
6	CA	B	703	1/1	0.58	0.41	137,137,137,137	0
5	CAC	B	705	5/5	0.96	0.20	135,135,136,136	0
4	ACT	A	703	4/4	0.96	0.21	69,69,70,71	0
5	CAC	A	704	5/5	0.96	0.17	137,137,138,140	0
2	FE	B	701	1/1	0.98	0.21	72,72,72,72	0
4	ACT	B	704	4/4	0.98	0.25	61,62,62,63	0
2	FE	A	701	1/1	0.98	0.19	65,65,65,65	0
3	ZN	A	702	1/1	0.99	0.18	74,74,74,74	0
3	ZN	B	702	1/1	0.99	0.17	79,79,79,79	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.