



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 10, 2017 – 09:19 AM EST

PDB ID : 4R5W  
Title : Human artd1 (parp1) - catalytic domain in complex with inhibitor xav939  
Authors : Karlberg, T.; Thorsell, A.G.; Schuler, H.  
Deposited on : 2014-08-22  
Resolution : 2.84 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-20028442  
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-20028442

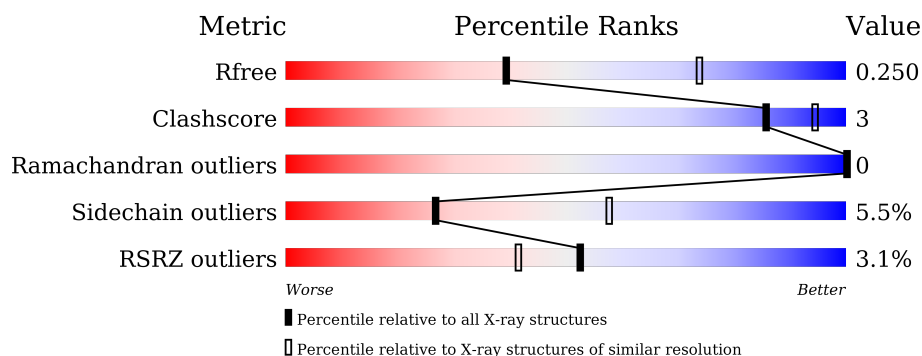
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.84 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	3170 (2.88-2.80)
Clashscore	102246	3658 (2.88-2.80)
Ramachandran outliers	100387	3591 (2.88-2.80)
Sidechain outliers	100360	3594 (2.88-2.80)
RSRZ outliers	91569	3184 (2.88-2.80)

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	358	<div> <div>2%</div> <div>85%</div> <div>12%</div> <div>.</div> </div>
1	B	358	<div> <div>4%</div> <div>86%</div> <div>13%</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
2	SO4	A	1105	-	-	-	X
3	XAV	B	1103	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5644 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 Poly [ADP-ribose] polymerase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	0	0
			2758	1756	468	522	12			
1	B	355	Total	C	N	O	S	0	0	0
			2798	1780	480	526	12			

There are 18 discrepancies between the modelled and reference sequences:

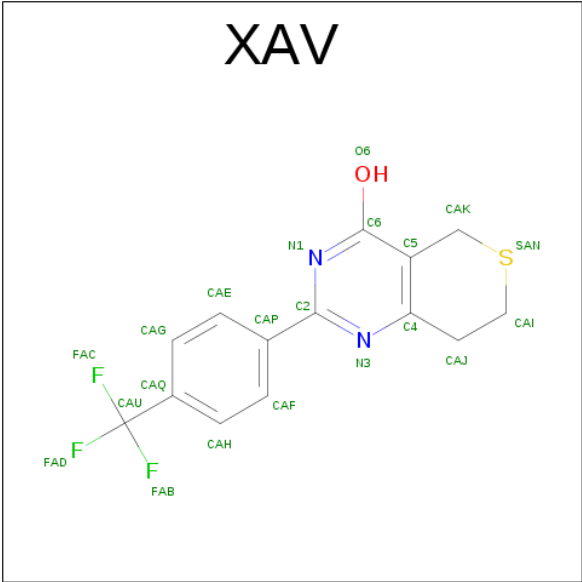
Chain	Residue	Modelled	Actual	Comment	Reference
A	661	MET	-	INITIATING METHIONINE	UNP P09874
A	762	ALA	VAL	VARIANT	UNP P09874
A	1012	ALA	-	EXPRESSION TAG	UNP P09874
A	1013	HIS	-	EXPRESSION TAG	UNP P09874
A	1014	HIS	-	EXPRESSION TAG	UNP P09874
A	1015	HIS	-	EXPRESSION TAG	UNP P09874
A	1016	HIS	-	EXPRESSION TAG	UNP P09874
A	1017	HIS	-	EXPRESSION TAG	UNP P09874
A	1018	HIS	-	EXPRESSION TAG	UNP P09874
B	661	MET	-	INITIATING METHIONINE	UNP P09874
B	762	ALA	VAL	VARIANT	UNP P09874
B	1012	ALA	-	EXPRESSION TAG	UNP P09874
B	1013	HIS	-	EXPRESSION TAG	UNP P09874
B	1014	HIS	-	EXPRESSION TAG	UNP P09874
B	1015	HIS	-	EXPRESSION TAG	UNP P09874
B	1016	HIS	-	EXPRESSION TAG	UNP P09874
B	1017	HIS	-	EXPRESSION TAG	UNP P09874
B	1018	HIS	-	EXPRESSION TAG	UNP P09874

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 2-[4-(TRIFLUOROMETHYL)PHENYL]-7,8-DIHYDRO-5H-THIOPYRANO[4,3-D]PYRIMIDIN-4-OL (three-letter code: XAV) (formula: C<sub>14</sub>H<sub>11</sub>F<sub>3</sub>N<sub>2</sub>OS).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	S	0	0
			21	14	3	2	1	1		
3	B	1	Total	C	F	N	O	S	0	0
			21	14	3	2	1	1		

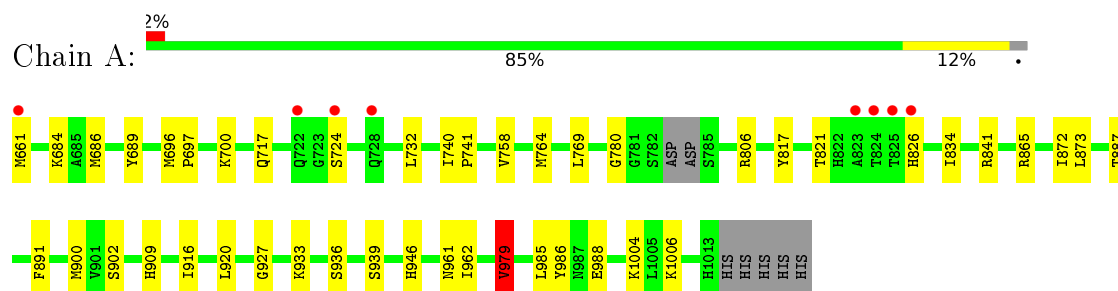
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	5	Total	O	0
			5	5	
4	B	6	Total	O	0
			6	6	

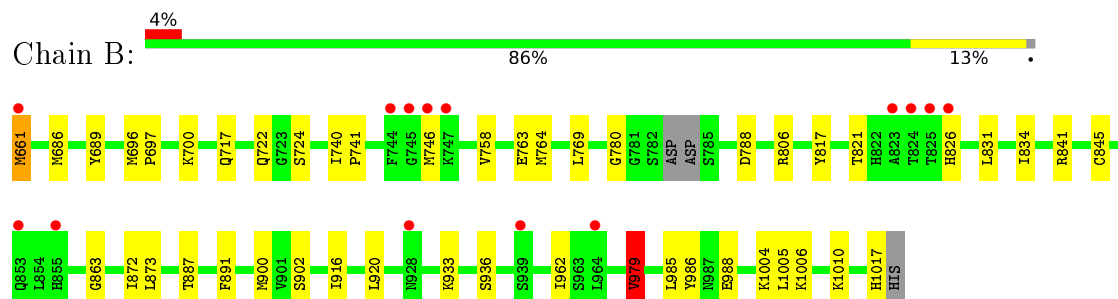
### 3 Residue-property plots [i](#)

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: Poly [ADP-ribose] polymerase 1



- Molecule 1: Poly [ADP-ribose] polymerase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.53 Å 67.66 Å 91.17 Å 90.00° 111.28° 90.00°	Depositor
Resolution (Å)	48.46 – 2.84 48.46 – 2.84	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.46-2.84) 99.8 (48.46-2.84)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.33 (at 2.86 Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, $R_{free}$	0.192 , 0.245 0.200 , 0.250	Depositor DCC
$R_{free}$ test set	1010 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.5	Xtriage
Anisotropy	0.350	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 52.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5644	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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: SO4, XAV

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	0.48	0/2810	0.69	1/3790 (0.0%)
1	B	0.50	0/2854	0.69	1/3850 (0.0%)
All	All	0.49	0/5664	0.69	2/7640 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	979	VAL	C-N-CA	6.42	137.75	121.70
1	B	979	VAL	C-N-CA	6.41	137.73	121.70

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	2758	0	2803	16	0
1	B	2798	0	2831	17	0
2	A	25	0	0	0	0
2	B	10	0	0	0	0
3	A	21	0	10	0	0
3	B	21	0	10	1	0
4	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	6	0	0	0	0
All	All	5644	0	5654	32	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 (32) 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:834:ILE:HD11	1:A:1006:LYS:HB2	1.76	0.68
1:B:834:ILE:HD11	1:B:1006:LYS:HB2	1.76	0.67
1:A:717:GLN:HG2	1:A:887:THR:OG1	1.99	0.61
1:B:717:GLN:HG2	1:B:887:THR:OG1	2.10	0.51
1:A:927:GLY:HA3	1:A:946:HIS:ND1	2.26	0.51
1:A:696:MET:HB2	1:A:741:PRO:HG2	1.93	0.50
1:A:933:LYS:HE2	1:A:979:VAL:HG13	1.93	0.50
1:B:841:ARG:HD2	1:B:873:LEU:O	2.10	0.50
1:B:933:LYS:HE2	1:B:979:VAL:HG13	1.93	0.50
1:A:841:ARG:HD2	1:A:873:LEU:O	2.12	0.49
1:B:697:PRO:HD2	1:B:700:LYS:HD3	1.96	0.48
1:B:696:MET:HB2	1:B:741:PRO:HG2	1.96	0.48
1:A:865:ARG:HG2	1:A:909:HIS:HB3	1.96	0.48
1:A:780:GLY:HA2	1:B:780:GLY:HA2	1.96	0.47
1:B:916:ILE:HG21	1:B:1004:LYS:HE3	1.97	0.47
1:A:697:PRO:HD2	1:A:700:LYS:HD3	1.97	0.47
1:A:821:THR:HB	1:A:900:MET:HA	1.98	0.46
1:B:821:THR:HB	1:B:900:MET:HA	1.99	0.45
1:A:891:PHE:HA	1:A:936:SER:O	2.16	0.44
1:B:891:PHE:HA	1:B:936:SER:O	2.17	0.44
1:A:916:ILE:HG21	1:A:1004:LYS:HE3	1.98	0.44
1:A:689:TYR:CG	1:A:764:MET:HG3	2.54	0.42
1:A:826:HIS:CE1	1:A:986:TYR:CE2	3.07	0.42
1:B:872:ILE:HG21	1:B:920:LEU:HD11	2.00	0.42
1:B:863:GLY:O	3:B:1103:XAV:HAE	2.19	0.42
1:A:826:HIS:ND1	1:A:902:SER:HB2	2.34	0.42
1:B:826:HIS:ND1	1:B:902:SER:HB2	2.34	0.42
1:A:872:ILE:HG21	1:A:920:LEU:HD11	2.02	0.42
1:B:831:LEU:HD22	1:B:1005:LEU:HD13	2.03	0.41
1:B:689:TYR:CG	1:B:764:MET:HG3	2.56	0.41
1:B:661:MET:O	1:B:788:ASP:HB2	2.21	0.40
1:B:826:HIS:CE1	1:B:986:TYR:CE2	3.09	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	347/358 (97%)	340 (98%)	7 (2%)	0	100	100
1	B	351/358 (98%)	343 (98%)	8 (2%)	0	100	100
All	All	698/716 (98%)	683 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	307/314 (98%)	291 (95%)	16 (5%)	29	61
1	B	311/314 (99%)	293 (94%)	18 (6%)	25	55
All	All	618/628 (98%)	584 (94%)	34 (6%)	27	58

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	661	MET
1	A	684	LYS
1	A	686	MET
1	A	724	SER
1	A	732	LEU

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Mol	Chain	Res	Type
1	A	740	ILE
1	A	758	VAL
1	A	769	LEU
1	A	806	ARG
1	A	817	TYR
1	A	939	SER
1	A	961	ASN
1	A	962	ILE
1	A	979	VAL
1	A	985	LEU
1	A	988	GLU
1	B	661	MET
1	B	686	MET
1	B	722	GLN
1	B	724	SER
1	B	740	ILE
1	B	746	MET
1	B	758	VAL
1	B	763	GLU
1	B	769	LEU
1	B	806	ARG
1	B	817	TYR
1	B	845	CYS
1	B	962	ILE
1	B	979	VAL
1	B	985	LEU
1	B	988	GLU
1	B	1010	LYS
1	B	1017	HIS

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

Mol	Chain	Res	Type
1	A	820	ASN
1	A	961	ASN
1	B	1014	HIS
1	B	1016	HIS

### 5.3.3 RNA ⓘ

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	SO4	A	1101	-	4,4,4	0.42	0	6,6,6	0.30	0
2	SO4	A	1102	-	4,4,4	0.20	0	6,6,6	0.25	0
2	SO4	A	1103	-	4,4,4	0.15	0	6,6,6	0.15	0
2	SO4	A	1104	-	4,4,4	0.24	0	6,6,6	0.51	0
2	SO4	A	1105	-	4,4,4	0.30	0	6,6,6	0.41	0
3	XAV	A	1106	-	22,23,23	1.68	5 (22%)	25,34,34	2.93	14 (56%)
2	SO4	B	1101	-	4,4,4	0.40	0	6,6,6	0.16	0
2	SO4	B	1102	-	4,4,4	0.35	0	6,6,6	0.22	0
3	XAV	B	1103	-	22,23,23	1.29	3 (13%)	25,34,34	2.20	8 (32%)

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	SO4	A	1101	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1102	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1103	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1104	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1105	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	XAV	A	1106	-	-	0/10/17/17	0/2/3/3
2	SO4	B	1101	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1102	-	-	0/0/0/0	0/0/0/0
3	XAV	B	1103	-	-	0/10/17/17	0/2/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1106	XAV	CAP-C2	-4.28	1.36	1.48
3	B	1103	XAV	CAP-C2	-3.33	1.39	1.48
3	A	1106	XAV	C4-N3	-2.36	1.30	1.34
3	A	1106	XAV	CAK-C5	-2.29	1.47	1.50
3	B	1103	XAV	CAU-CAQ	2.07	1.54	1.49
3	A	1106	XAV	FAC-CAU	2.12	1.40	1.32
3	B	1103	XAV	C5-C4	2.14	1.43	1.40
3	A	1106	XAV	C5-C4	3.28	1.45	1.40

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1106	XAV	CAJ-CAI-SAN	-5.86	106.46	112.91
3	B	1103	XAV	FAB-CAU-CAQ	-4.28	103.90	112.92
3	B	1103	XAV	C5-C4-N3	-4.12	119.83	123.24
3	A	1106	XAV	FAB-CAU-CAQ	-3.90	104.70	112.92
3	A	1106	XAV	CAI-CAJ-C4	-3.78	108.28	113.50
3	A	1106	XAV	CAJ-C4-N3	-3.66	111.32	115.66
3	B	1103	XAV	N3-C2-N1	-3.64	119.52	125.31
3	A	1106	XAV	FAD-CAU-CAQ	-3.28	106.02	112.92
3	A	1106	XAV	C5-C4-N3	-2.94	120.80	123.24
3	A	1106	XAV	CAP-C2-N3	-2.81	112.38	117.28
3	A	1106	XAV	N3-C2-N1	-2.51	121.31	125.31
3	B	1103	XAV	CAJ-CAI-SAN	-2.27	110.42	112.91
3	B	1103	XAV	CAE-CAG-CAQ	-2.24	118.32	121.26
3	A	1106	XAV	FAC-CAU-CAQ	-2.15	108.40	112.92
3	B	1103	XAV	CAP-C2-N1	2.05	120.87	117.28
3	A	1106	XAV	O6-C6-N1	2.14	122.60	116.91
3	A	1106	XAV	CAH-CAQ-CAG	2.14	121.11	117.95
3	B	1103	XAV	FAC-CAU-FAB	2.39	114.33	105.75
3	A	1106	XAV	FAD-CAU-FAC	3.06	116.74	105.75
3	B	1103	XAV	CAJ-C4-C5	4.86	126.59	121.72
3	A	1106	XAV	CAP-C2-N1	5.17	126.30	117.28
3	A	1106	XAV	CAJ-C4-C5	6.15	127.88	121.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1103	XAV	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 ⓘ

### 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	351/358 (98%)	-0.03	8 (2%) 64 54	25, 43, 82, 117	0
1	B	355/358 (99%)	0.04	14 (3%) 43 32	24, 45, 84, 111	0
All	All	706/716 (98%)	0.00	22 (3%) 52 41	24, 44, 84, 117	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	824	THR	6.8
1	B	824	THR	6.2
1	B	855	HIS	4.4
1	B	746	MET	3.8
1	B	661	MET	3.3
1	A	826	HIS	3.3
1	B	825	THR	3.2
1	A	825	THR	3.2
1	A	728	GLN	3.1
1	A	722	GLN	2.9
1	A	661	MET	2.8
1	B	853	GLN	2.8
1	B	823	ALA	2.8
1	B	744	PHE	2.7
1	A	823	ALA	2.5
1	B	964	LEU	2.4
1	B	747	LYS	2.3
1	B	745	GLY	2.3
1	B	939	SER	2.2
1	A	724	SER	2.1
1	B	826	HIS	2.1
1	B	928	ASN	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
2	SO4	A	1105	5/5	0.88	0.28	5.99	88,90,93,93	0
3	XAV	B	1103	21/21	0.95	0.20	2.13	44,51,72,76	0
3	XAV	A	1106	21/21	0.96	0.19	1.66	42,48,63,65	0
2	SO4	A	1103	5/5	0.96	0.19	1.00	78,79,80,80	0
2	SO4	A	1104	5/5	0.96	0.18	0.52	77,77,77,78	0
2	SO4	A	1101	5/5	0.99	0.17	0.19	31,32,34,39	0
2	SO4	B	1102	5/5	0.95	0.15	-1.28	62,67,68,70	0
2	SO4	A	1102	5/5	0.98	0.11	-1.34	57,57,59,60	0
2	SO4	B	1101	5/5	0.99	0.11	-2.11	35,36,38,39	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.