



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:03 AM UTC

PDB ID : 4PID / pdb\_00004pid  
Title : Crystal structure of human adenovirus 2 protease with a weak pyrimidine nitrile inhibitor  
Authors : Mac Sweeney, A.; Grosche, P.; Ellis, D.; Combrink, K.; Erbel, P.; Hughes, N.; Sirockin, F.; Melkko, S.; Bernardi, A.; Ramage, P.; Jarousse, N.; Altmann, E.  
Deposited on : 2014-05-08  
Resolution : 1.59 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

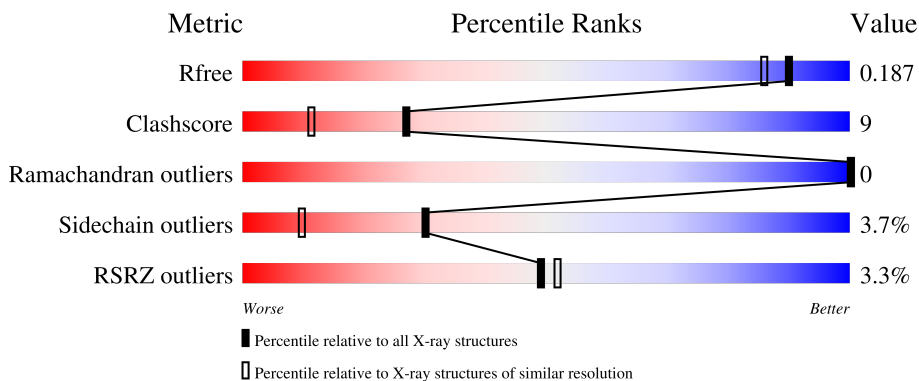
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.59 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))
$R_{free}$	180053	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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 of 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	204	 2% 75% 22% ..
2	B	11	 18% 73% 27%

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
3	ACT	A	301	-	X	-	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 1918 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.

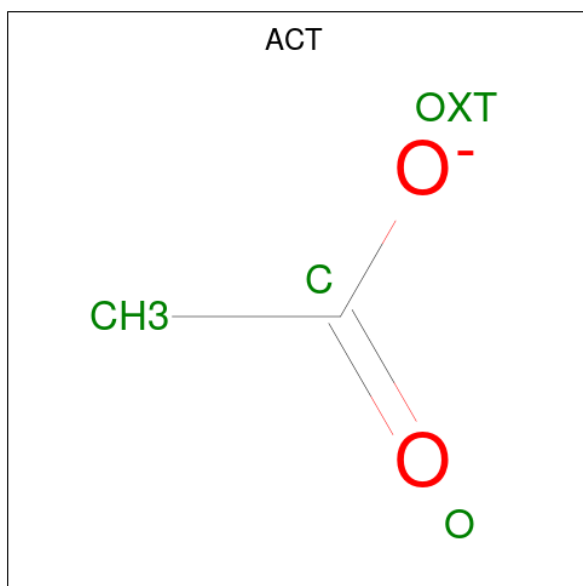
- Molecule 1 is a protein called Protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	204	1642	1039	288	299	16	0	6	0

- Molecule 2 is a protein called Pre-protein VI.

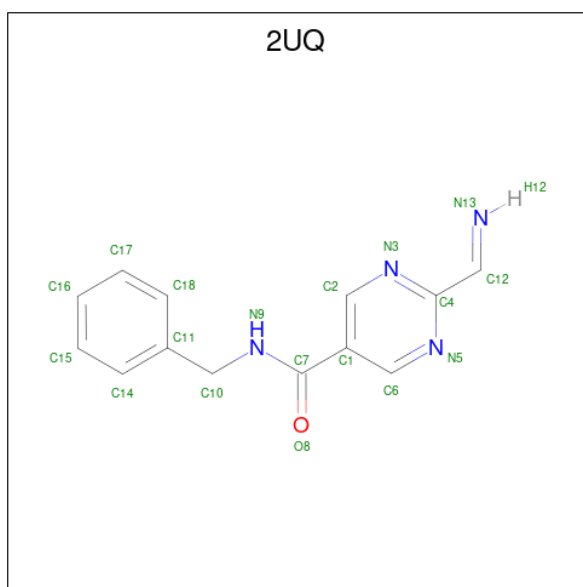
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	11	102	62	25	14	1	0	1	0

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



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

- Molecule 4 is N-benzyl-2-[(Z)-iminomethyl]pyrimidine-5-carboxamide (CCD ID: 2UQ) (formula: C<sub>13</sub>H<sub>12</sub>N<sub>4</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	18	13	4	1	0	0

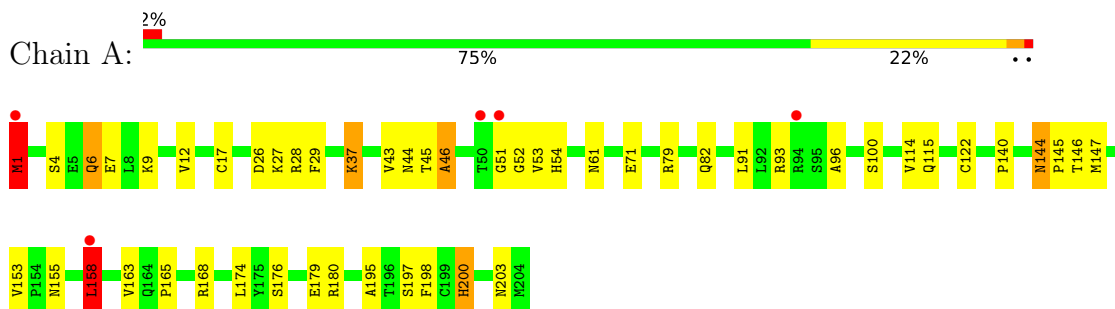
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	136	137	137	0	1
5	B	15	15	15	0	0

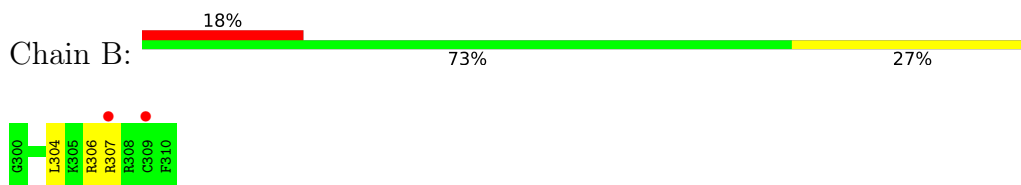
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Protease



- Molecule 2: Pre-protein VI



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	112.78Å 112.78Å 50.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.84 – 1.59 48.84 – 1.59	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.84-1.59) 100.0 (48.84-1.59)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.97 (at 1.59Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.165 , 0.189 0.163 , 0.187	Depositor DCC
$R_{free}$ test set	2466 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.0	Xtrriage
Anisotropy	0.060	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 33.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.034 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	1918	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.35% 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: 2UQ, ACT

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	1.88	14/1709 (0.8%)	1.68	18/2312 (0.8%)
2	B	1.60	1/105 (1.0%)	1.25	0/134
All	All	1.86	15/1814 (0.8%)	1.65	18/2446 (0.7%)

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	GLU	N-CA	7.68	1.55	1.46
1	A	96	ALA	CA-CB	-7.60	1.41	1.53
1	A	54	HIS	N-CA	7.01	1.54	1.46
1	A	37	LYS	CA-C	6.64	1.60	1.52
1	A	52	GLY	N-CA	6.41	1.54	1.45
2	B	306	ARG	N-CA	6.13	1.53	1.46
1	A	96	ALA	N-CA	6.10	1.53	1.46
1	A	153	VAL	N-CA	6.02	1.51	1.46
1	A	203	ASN	N-CA	5.73	1.53	1.46
1	A	200	HIS	C-O	5.72	1.31	1.24
1	A	43	VAL	CA-CB	-5.53	1.47	1.54
1	A	163	VAL	N-CA	5.37	1.53	1.46
1	A	158	LEU	C-O	5.18	1.30	1.24
1	A	46	ALA	N-CA	5.12	1.52	1.45
1	A	26	ASP	CA-CB	5.01	1.60	1.53

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	158	LEU	N-CA-C	8.86	123.09	111.75
1	A	45	THR	O-C-N	6.44	131.06	122.43
1	A	168	ARG	NE-CZ-NH2	6.31	124.88	119.20
1	A	61	ASN	O-C-N	6.20	128.19	121.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	PHE	N-CA-C	5.97	118.56	111.33
1	A	71	GLU	N-CA-C	-5.94	99.89	109.40
1	A	9	LYS	CD-CE-NZ	-5.58	94.04	111.90
1	A	163	VAL	CB-CA-C	-5.51	104.36	111.20
1	A	180	ARG	NE-CZ-NH2	-5.45	114.29	119.20
1	A	27	LYS	CG-CD-CE	-5.39	98.90	111.30
1	A	93	ARG	NE-CZ-NH2	5.36	124.03	119.20
1	A	197	SER	CA-CB-OG	-5.36	100.37	111.10
1	A	100	SER	CA-CB-OG	-5.26	100.58	111.10
1	A	43	VAL	CA-C-O	5.25	125.92	120.36
1	A	114	VAL	O-C-N	5.12	127.24	122.23
1	A	1	MET	CG-SD-CE	5.07	112.05	100.90
1	A	174	LEU	CA-C-N	-5.05	113.51	120.28
1	A	174	LEU	C-N-CA	-5.05	113.51	120.28

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	1642	0	1591	30	0
2	B	102	0	113	1	0
3	A	4	0	3	1	0
4	A	18	0	10	0	0
5	A	137	0	0	3	0
5	B	15	0	0	1	0
All	All	1918	0	1717	31	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 9.

All (31) 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:1:MET:HG3	1:A:200:HIS:CE1	1.91	1.06
1:A:1:MET:HG3	1:A:200:HIS:NE2	1.73	1.03
1:A:44:ASN:HD21	1:A:53:VAL:H	1.12	0.97
1:A:1:MET:HB3	1:A:200:HIS:HE1	1.37	0.90
1:A:1:MET:HB3	1:A:200:HIS:CE1	2.07	0.89
1:A:1:MET:CG	1:A:200:HIS:CE1	2.57	0.87
1:A:1:MET:CB	1:A:200:HIS:HE1	1.88	0.86
1:A:44:ASN:HD22	1:A:46:ALA:H	1.27	0.82
1:A:51:GLY:HA2	5:A:402:HOH:O	1.81	0.80
1:A:79:ARG:HH21	1:A:82:GLN:NE2	1.85	0.73
1:A:1:MET:CB	1:A:200:HIS:CE1	2.68	0.69
1:A:176[B]:SER:OG	5:A:401:HOH:O	2.12	0.68
2:B:304:LEU:HD12	5:B:415:HOH:O	1.95	0.66
1:A:1:MET:CG	1:A:200:HIS:HE1	2.06	0.62
1:A:144:ASN:HD21	1:A:147:MET:H	1.49	0.60
1:A:44:ASN:ND2	1:A:53:VAL:H	1.91	0.60
1:A:144:ASN:ND2	1:A:147:MET:H	2.01	0.58
1:A:79:ARG:HH21	1:A:82:GLN:HE22	1.55	0.54
1:A:145:PRO:O	3:A:301:ACT:H3	2.09	0.53
1:A:144:ASN:HD22	1:A:146:THR:H	1.55	0.53
1:A:28:ARG:O	1:A:29:PHE:C	2.53	0.51
1:A:12:VAL:CG1	1:A:17[A]:CYS:HB2	2.40	0.51
1:A:12:VAL:HG13	1:A:17[A]:CYS:HB2	1.98	0.46
1:A:115:GLN:HE22	1:A:122:CYS:HB3	1.80	0.46
1:A:155[B]:ASN:ND2	5:A:482:HOH:O	2.49	0.45
1:A:1:MET:HE3	1:A:195:ALA:HA	1.98	0.45
1:A:155[A]:ASN:ND2	1:A:158:LEU:HD22	2.32	0.44
1:A:4:SER:H	1:A:7[B]:GLU:CD	2.26	0.43
1:A:91:LEU:C	1:A:91:LEU:HD12	2.46	0.41
1:A:140:PRO:O	1:A:147:MET:HG3	2.22	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	208/204 (102%)	205 (99%)	3 (1%)	0	100	100
2	B	10/11 (91%)	10 (100%)	0	0	100	100
All	All	218/215 (101%)	215 (99%)	3 (1%)	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	184/178 (103%)	178 (97%)	6 (3%)	33	12
2	B	11/10 (110%)	9 (82%)	2 (18%)	2	0
All	All	195/188 (104%)	187 (96%)	8 (4%)	30	8

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

Mol	Chain	Res	Type
1	A	1	MET
1	A	6	GLN
1	A	37	LYS
1	A	144	ASN
1	A	158	LEU
1	A	165	PRO
2	B	307[A]	ARG
2	B	307[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	ASN
1	A	82	GLN
1	A	115	GLN
1	A	144	ASN
1	A	159	ASN

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Mol	Chain	Res	Type
1	A	181	HIS
1	A	200	HIS
1	A	203	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 oligosaccharides 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
3	ACT	A	301	-	3,3,3	2.79	2 (66%)	3,3,3	4.28	2 (66%)
4	2UQ	A	302	1	18,19,19	2.41	13 (72%)	24,24,24	1.40	3 (12%)

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	2UQ	A	302	1	-	0/9/11/11	0/2/2/2

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	ACT	O-C	4.36	1.41	1.22
4	A	302	2UQ	C4-N5	3.51	1.39	1.34
4	A	302	2UQ	C4-N3	3.49	1.39	1.34
4	A	302	2UQ	C6-C1	2.92	1.43	1.39
4	A	302	2UQ	C18-C11	2.80	1.44	1.38
4	A	302	2UQ	C10-C11	2.80	1.57	1.51
4	A	302	2UQ	C17-C18	2.67	1.43	1.38
4	A	302	2UQ	C7-N9	2.63	1.39	1.33
4	A	302	2UQ	C1-C7	2.45	1.55	1.50
4	A	302	2UQ	C14-C11	2.43	1.43	1.38
4	A	302	2UQ	C17-C16	2.38	1.43	1.38
4	A	302	2UQ	C2-N3	2.37	1.39	1.34
4	A	302	2UQ	C16-C15	2.06	1.42	1.38
4	A	302	2UQ	C15-C14	2.05	1.42	1.38
3	A	301	ACT	OXT-C	2.04	1.40	1.30

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	301	ACT	OXT-C-O	5.61	142.85	122.03
3	A	301	ACT	O-C-CH3	-4.84	102.69	122.53
4	A	302	2UQ	C1-C6-N5	-3.77	118.05	123.59
4	A	302	2UQ	C6-C1-C2	3.65	119.80	115.36
4	A	302	2UQ	C6-N5-C4	2.33	120.66	117.92

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	A	301	ACT	1	0

## 5.7 Other polymers [i](#)

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	204/204 (100%)	-0.15	5 (2%) 58 61	8, 16, 29, 44	6 (2%)
2	B	11/11 (100%)	0.40	2 (18%) 3 3	9, 16, 29, 33	1 (9%)
All	All	215/215 (100%)	-0.12	7 (3%) 49 52	8, 16, 30, 44	7 (3%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	5.9
1	A	50	THR	4.3
1	A	158	LEU	3.4
2	B	309	CYS	3.2
1	A	51	GLY	2.3
2	B	307[A]	ARG	2.1
1	A	94	ARG	2.1

### 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 oligosaccharides 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
4	2UQ	A	302	18/18	0.87	0.19	21,41,57,58	0
3	ACT	A	301	4/4	0.90	0.26	19,22,29,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.