Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 07:52 AM GMT

PDB ID	:	3CHS
Title	:	Crystal structure of leukotriene A4 hydrolase in complex with (2S)-2-amino-5-[[4-[(2S)-2-hydroxy-2-phenyl-ethoxy]phenyl]amino]-5-oxo-pentanoic acid
Authors	:	Thunnissen, M.M.G.M.; Adler, M.; Whitlow, M.
Deposited on	:	2008-03-10
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
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

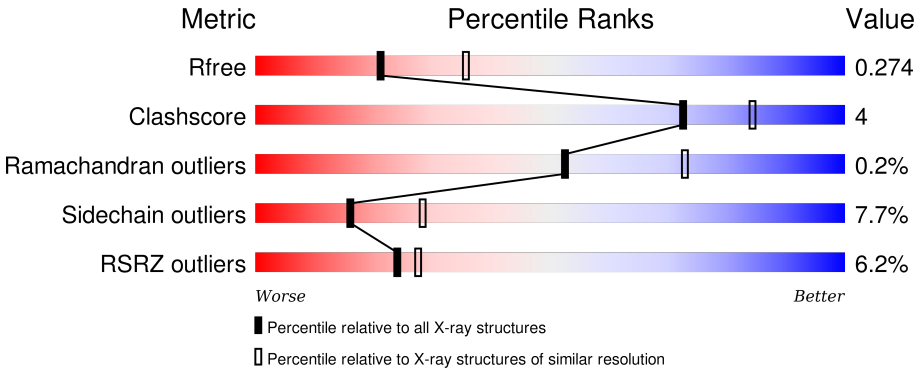
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 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 >=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 <=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	610	6% 82% 16%

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	IMD	A	1001	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	4BU	A	901	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4978 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 Leukotriene A-4 hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	610	Total	C	N	O	S	0	0	0
			4876	3130	811	914	21			

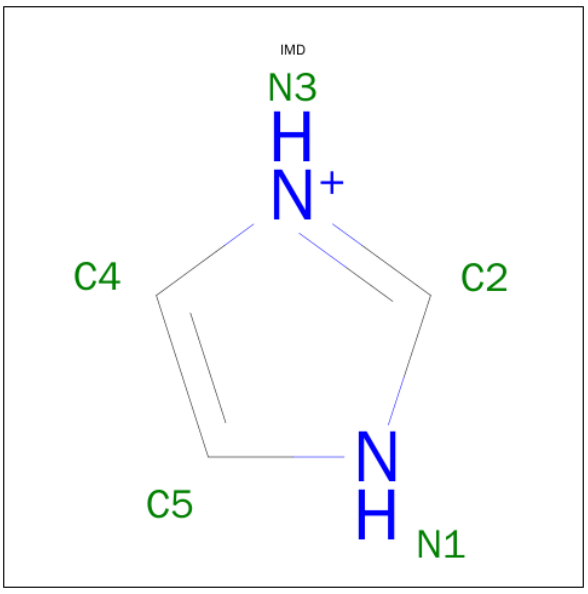
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is YTTERBIUM (III) ION (three-letter code: YB) (formula: Yb).

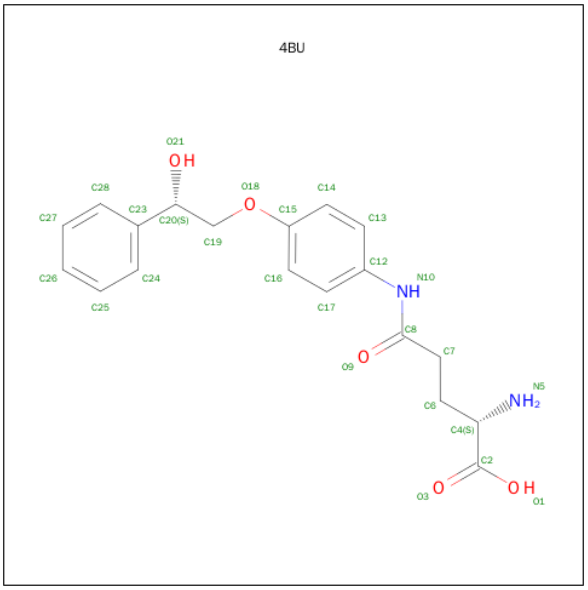
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Yb	0	0
			3	3		

- Molecule 4 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N 5 3 2	0	0

- Molecule 5 is (2S)-2-AMINO-5-[[4-[(2S)-2-HYDROXY-2-PHENYL-ETHOXY]PHENYL]AMINO]-5-OXO-PENTANOIC ACID (three-letter code: 4BU) (formula: $C_{19}H_{22}N_2O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O 26 19 2 5	0	0

- Molecule 6 is water.

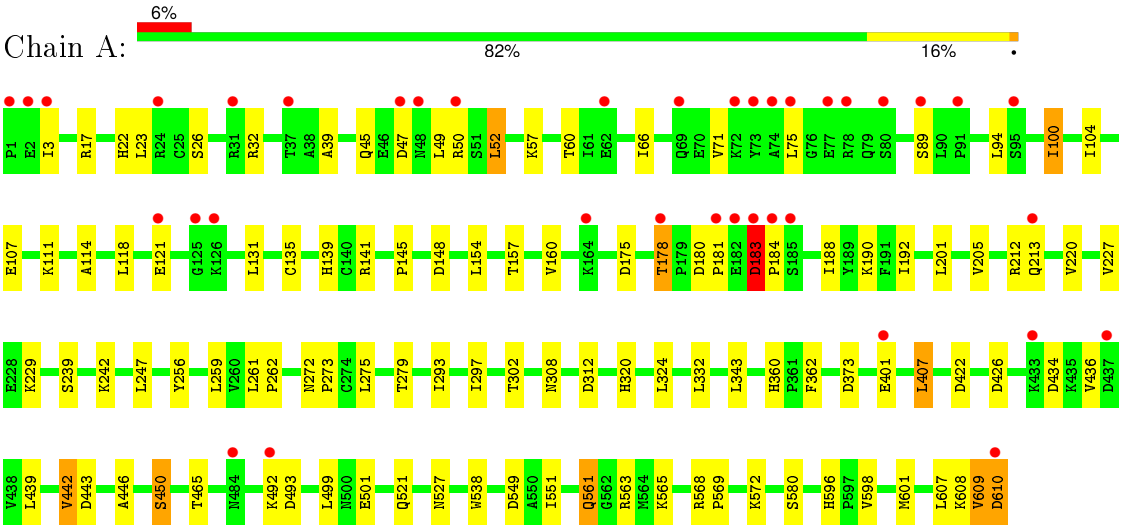
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	67	Total O 67 67	0	0

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 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: Leukotriene A-4 hydrolase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	67.62Å 133.27Å 83.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.55 19.98 – 2.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.96-2.55) 100.0 (19.98-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.41 (at 2.56Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.211 , 0.248 0.247 , 0.274	Depositor DCC
R_{free} test set	1291 reflections (5.38%)	DCC
Wilson B-factor (Å^2)	38.1	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 26.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 25283 reflections	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	4978	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, YB, 4BU, IMD

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	0.38	0/5001	0.70	11/6798 (0.2%)

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

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	426	ASP	CB-CG-OD2	7.15	124.73	118.30
1	A	422	ASP	CB-CG-OD2	5.71	123.44	118.30
1	A	549	ASP	CB-CG-OD2	5.50	123.25	118.30
1	A	312	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	443	ASP	CB-CG-OD2	5.18	122.97	118.30
1	A	183	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	610	ASP	CB-CG-OD2	5.12	122.91	118.30
1	A	493	ASP	CB-CG-OD2	5.12	122.91	118.30
1	A	47	ASP	CB-CG-OD2	5.09	122.89	118.30
1	A	373	ASP	CB-CG-OD2	5.03	122.83	118.30
1	A	52	LEU	CA-CB-CG	5.02	126.86	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	183	ASP	Peptide

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	4876	0	4837	41	0
2	A	1	0	0	0	0
3	A	3	0	0	0	0
4	A	5	0	5	1	0
5	A	26	0	21	0	0
6	A	67	0	0	1	0
All	All	4978	0	4863	41	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 (41) 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:180:ASP:HB3	1:A:183:ASP:HB3	1.40	1.04
1:A:360:HIS:HD2	1:A:362:PHE:H	1.33	0.77
1:A:180:ASP:HB3	1:A:183:ASP:CB	2.14	0.76
1:A:527:ASN:ND2	1:A:538:TRP:HE1	1.92	0.67
1:A:521:GLN:HE22	1:A:527:ASN:H	1.43	0.65
1:A:439:LEU:O	1:A:442:VAL:HG13	1.99	0.62
1:A:175:ASP:HB3	1:A:190:LYS:HB2	1.87	0.57
1:A:22:HIS:HB3	1:A:39:ALA:HB3	1.86	0.57
1:A:201:LEU:HD22	1:A:273:PRO:HD3	1.88	0.55
1:A:561:GLN:HE22	1:A:563:ARG:HB3	1.73	0.53
1:A:94:LEU:HD11	1:A:100:ILE:HG12	1.91	0.52
1:A:343:LEU:HD23	1:A:465:THR:HG21	1.92	0.51
1:A:205:VAL:HG11	1:A:259:LEU:HD22	1.93	0.50
1:A:501:GLU:OE1	4:A:1001:IMD:H2	2.11	0.50
1:A:434:ASP:HB3	6:A:1027:HOH:O	2.11	0.50
1:A:66:ILE:HD12	1:A:71:VAL:HG21	1.93	0.50
1:A:94:LEU:HD11	1:A:100:ILE:CG1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:609:VAL:O	1:A:610:ASP:HB2	2.14	0.48
1:A:446:ALA:O	1:A:450:SER:HB2	2.14	0.48
1:A:17:ARG:HD2	1:A:45:GLN:CD	2.34	0.48
1:A:324:LEU:HD21	1:A:407:LEU:HD22	1.96	0.47
1:A:568:ARG:HB2	1:A:569:PRO:HD3	1.95	0.47
1:A:261:LEU:HB3	1:A:262:PRO:HD2	1.97	0.47
1:A:141:ARG:HH21	1:A:148:ASP:HB3	1.80	0.47
1:A:49:LEU:HD23	1:A:94:LEU:HD12	1.96	0.46
1:A:157:THR:HG22	1:A:192:ILE:HG22	1.96	0.46
1:A:272:ASN:HB2	1:A:275:LEU:O	2.17	0.45
1:A:135:CYS:HA	1:A:139:HIS:HB2	1.99	0.44
1:A:261:LEU:HB3	1:A:262:PRO:CD	2.48	0.44
1:A:446:ALA:HA	1:A:450:SER:HB2	1.99	0.44
1:A:596:HIS:CD2	1:A:598:VAL:H	2.35	0.44
1:A:60:THR:HB	1:A:107:GLU:HB2	1.99	0.43
1:A:302:THR:HG21	1:A:320:HIS:HB3	1.99	0.43
1:A:256:TYR:CZ	1:A:297:ILE:HG13	2.53	0.43
1:A:17:ARG:HH11	1:A:45:GLN:HG3	1.84	0.42
1:A:551:ILE:HG12	1:A:580:SER:HB3	2.00	0.42
1:A:104:ILE:HG21	1:A:145:PRO:HG2	2.00	0.41
1:A:178:THR:O	1:A:188:ILE:HG22	2.20	0.41
1:A:293:ILE:HG22	1:A:297:ILE:HD12	2.03	0.40
1:A:114:ALA:HB2	1:A:139:HIS:O	2.22	0.40
1:A:180:ASP:OD1	1:A:181:PRO:HD2	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	608/610 (100%)	588 (97%)	19 (3%)	1 (0%)	52 73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	PRO

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	542/542 (100%)	500 (92%)	42 (8%)	16 28

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ILE
1	A	23	LEU
1	A	26	SER
1	A	32	ARG
1	A	50	ARG
1	A	52	LEU
1	A	57	LYS
1	A	75	LEU
1	A	89	SER
1	A	100	ILE
1	A	111	LYS
1	A	118	LEU
1	A	121	GLU
1	A	131	LEU
1	A	154	LEU
1	A	160	VAL
1	A	178	THR
1	A	212	ARG
1	A	213	GLN
1	A	220	VAL
1	A	227	VAL
1	A	229	LYS
1	A	239	SER
1	A	242	LYS

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Mol	Chain	Res	Type
1	A	247	LEU
1	A	279	THR
1	A	308	ASN
1	A	332	LEU
1	A	401	GLU
1	A	407	LEU
1	A	436	VAL
1	A	442	VAL
1	A	450	SER
1	A	492	LYS
1	A	499	LEU
1	A	561	GLN
1	A	565	LYS
1	A	572	LYS
1	A	601	MET
1	A	607	LEU
1	A	608	LYS
1	A	609	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	HIS
1	A	226	GLN
1	A	272	ASN
1	A	341	ASN
1	A	350	GLN
1	A	360	HIS
1	A	440	ASN
1	A	441	GLN
1	A	466	ASN
1	A	521	GLN
1	A	525	ASN
1	A	527	ASN
1	A	561	GLN
1	A	596	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)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	IMD	A	1001	-	3,5,5	0.62	0	4,5,5	0.38	0
5	4BU	A	901	2	24,27,27	1.45	4 (16%)	27,35,35	1.86	4 (14%)

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	IMD	A	1001	-	-	0/0/0/0	0/1/1/1
5	4BU	A	901	2	-	0/18/22/22	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	901	4BU	C12-N10	-2.33	1.37	1.41
5	A	901	4BU	C17-C12	2.13	1.42	1.39
5	A	901	4BU	C24-C23	2.20	1.42	1.39
5	A	901	4BU	C28-C23	2.43	1.43	1.39

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	901	4BU	C6-C7-C8	-4.48	102.62	113.27
5	A	901	4BU	O18-C19-C20	-2.62	100.43	107.89
5	A	901	4BU	C7-C8-N10	2.11	118.09	114.52
5	A	901	4BU	C19-O18-C15	6.96	132.84	117.89

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
4	A	1001	IMD	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^{th} 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^2)	Q<0.9
1	A	610/610 (100%)	0.38	38 (6%) 24 27	17, 26, 45, 62	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	PRO	9.1
1	A	3	ILE	6.7
1	A	181	PRO	6.7
1	A	2	GLU	6.4
1	A	610	ASP	6.1
1	A	178	THR	4.8
1	A	182	GLU	4.0
1	A	183	ASP	3.7
1	A	50	ARG	3.4
1	A	62	GLU	3.4
1	A	95	SER	3.3
1	A	125	GLY	3.2
1	A	48	ASN	3.1
1	A	74	ALA	3.1
1	A	185	SER	3.0
1	A	184	PRO	3.0
1	A	24	ARG	2.9
1	A	31	ARG	2.9
1	A	72	LYS	2.8
1	A	77	GLU	2.7
1	A	126	LYS	2.6
1	A	437	ASP	2.6
1	A	37	THR	2.6
1	A	75	LEU	2.5
1	A	484	ASN	2.5
1	A	492	LYS	2.5
1	A	80	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	73	TYR	2.4
1	A	213	GLN	2.3
1	A	433	LYS	2.3
1	A	89	SER	2.3
1	A	47	ASP	2.3
1	A	164	LYS	2.3
1	A	78	ARG	2.3
1	A	69	GLN	2.2
1	A	121	GLU	2.2
1	A	91	PRO	2.2
1	A	401	GLU	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^{th} 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(Å^2)	Q<0.9
4	IMD	A	1001	5/5	0.95	0.20	3.60	38,38,38,39	0
5	4BU	A	901	26/26	0.93	0.24	2.79	31,34,41,43	0
2	ZN	A	701	1/1	0.99	0.15	1.13	41,41,41,41	0
3	YB	A	802	1/1	0.83	0.11	-	120,120,120,120	1
3	YB	A	803	1/1	0.82	0.09	-	102,102,102,102	1
3	YB	A	801	1/1	0.99	0.22	-	46,46,46,46	0

6.5 Other polymers (i)

There are no such residues in this entry.