



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:26 PM GMT

PDB ID : 4OYO
Title : Human solAC Complexed with 4-(2-Chlorophenyl)-3-methyl-1H-pyrazole
Authors : Vinkovic, M.
Deposited on : 2014-02-12
Resolution : 1.75 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 ⓘ symbol.

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

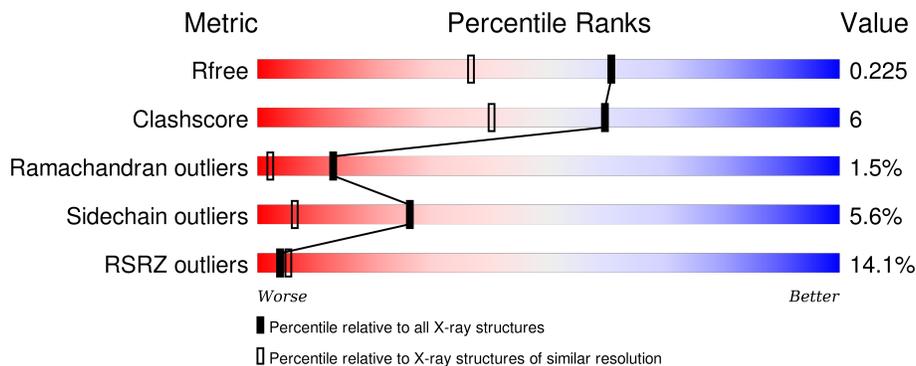
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	1609 (1.76-1.76)
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

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 $\leq 5\%$. 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	470	

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	1WC	A	501	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	1WC	A	502	-	-	X	X
3	GOL	A	504[A]	-	-	-	X
3	GOL	A	504[B]	-	-	-	X
3	GOL	A	505	-	-	-	X

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 4452 atoms, of which 27 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.

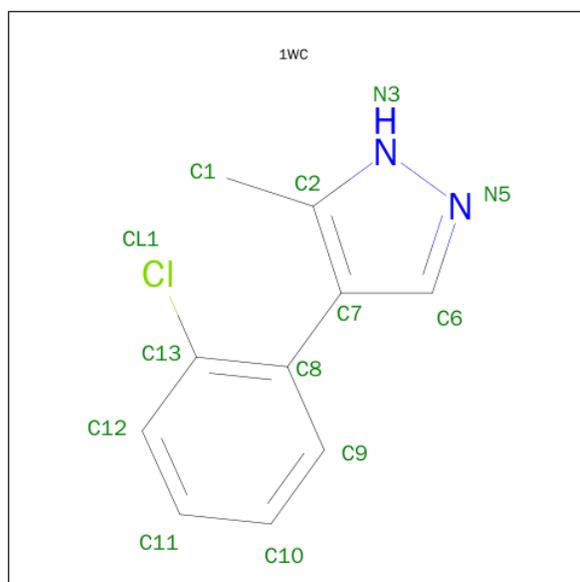
- Molecule 1 is a protein called Adenylate cyclase type 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	469	3826	2477	618	695	36	0	12	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ACE	-	acetylation	UNP Q96PN6

- Molecule 2 is 4-(2-chlorophenyl)-5-methyl-1H-pyrazole (three-letter code: 1WC) (formula: C₁₀H₉ClN₂).



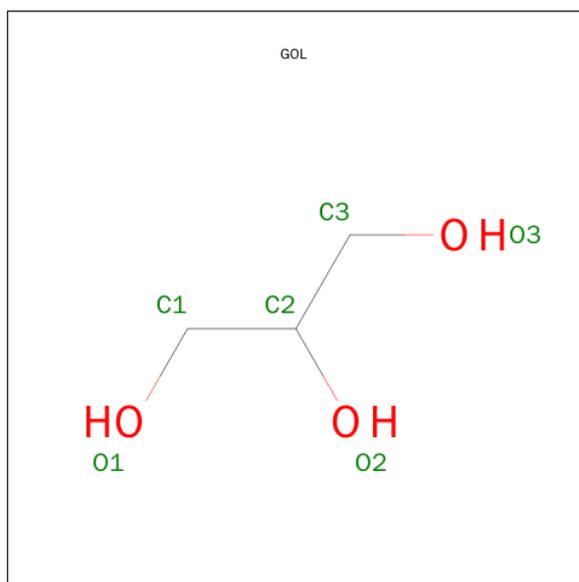
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	H	N		
2	A	1	22	10	1	9	2	0	0
2	A	1	22	10	1	9	2	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	Cl	H			N
2	A	1	22	10	1	9	2	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	12	6	6	0	1
3	A	1	6	3	3	0	0

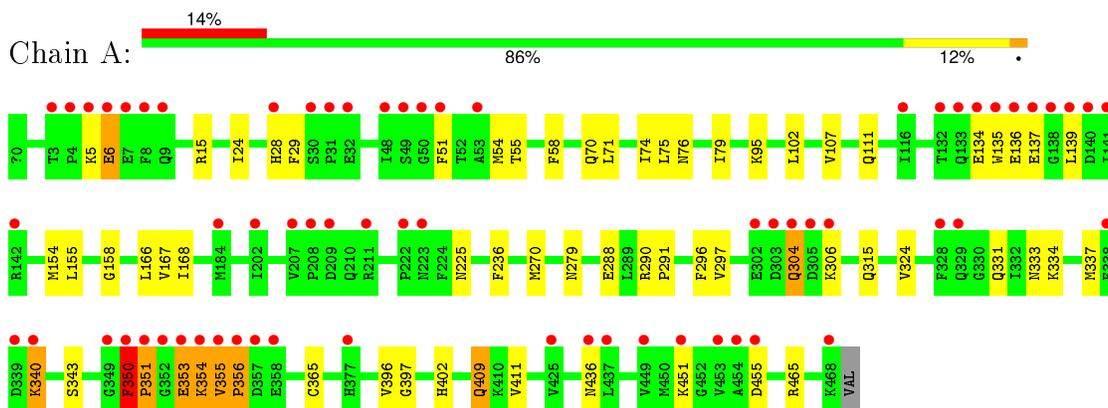
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	542	542	542	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: Adenylate cyclase type 10



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	100.03 Å 100.03 Å 98.01 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.88 – 1.75 28.88 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.7 (28.88-1.75) 99.7 (28.88-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 1.75 Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.176 , 0.212 0.187 , 0.225	Depositor DCC
R_{free} test set	2776 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	20.0	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 62.5	EDS
Estimated twinning fraction	0.043 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 55854 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4452	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CME, 1WC, ACE

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	0.67	0/3916	0.71	2/5297 (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	354[A]	LYS	C-N-CA	5.57	135.62	121.70
1	A	354[B]	LYS	C-N-CA	5.57	135.62	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	3826	0	3803	42	0
2	A	39	27	27	7	0
3	A	18	0	24	3	0
4	A	542	0	0	0	0
All	All	4425	27	3854	44	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 6.

All (44) 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)
2:A:502:1WC:H17	2:A:502:1WC:CL1	2.12	0.86
1:A:55:THR:HG22	1:A:71:LEU:HD21	1.66	0.78
1:A:324:VAL:HG12	1:A:365[B]:CYS:SG	2.27	0.74
1:A:158:GLY:H	1:A:315:GLN:HE22	1.33	0.73
1:A:290:ARG:HH21	1:A:353[B]:GLU:HG3	1.62	0.65
1:A:58:PHE:CD1	1:A:71:LEU:HD13	2.31	0.65
1:A:102:LEU:HD23	2:A:502:1WC:CL1	2.34	0.64
1:A:76:ASN:HD21	1:A:396:VAL:HA	1.62	0.64
1:A:76:ASN:ND2	1:A:397:GLY:H	1.97	0.63
1:A:74:ILE:HD11	1:A:135:TRP:CZ2	2.36	0.60
1:A:291:PRO:HB2	1:A:356[B]:PRO:HB3	1.84	0.59
1:A:168:ILE:HD12	1:A:337:MET:SD	2.44	0.58
1:A:28:HIS:N	3:A:505:GOL:H11	2.19	0.57
2:A:502:1WC:C1	2:A:502:1WC:CL1	2.88	0.56
1:A:350[A]:PHE:CD1	1:A:351[A]:PRO:HD2	2.41	0.56
1:A:290:ARG:HD3	1:A:350[A]:PHE:HA	1.88	0.56
1:A:355[B]:VAL:HG13	1:A:356[B]:PRO:HD2	1.88	0.55
1:A:324:VAL:CG1	1:A:365[B]:CYS:SG	2.95	0.55
1:A:155:LEU:HD23	1:A:166:LEU:HD12	1.90	0.54
1:A:51:PHE:CZ	1:A:71:LEU:HD11	2.43	0.54
1:A:24:ILE:O	3:A:505:GOL:H2	2.09	0.52
1:A:350[A]:PHE:CG	1:A:351[A]:PRO:HD2	2.45	0.52
1:A:28:HIS:H	3:A:505:GOL:H11	1.75	0.51
1:A:15:ARG:HH22	1:A:279:ASN:HD21	1.60	0.49
1:A:95:LYS:HB2	2:A:502:1WC:CL1	2.50	0.48
1:A:107:VAL:HG22	1:A:111:GLN:HB2	1.95	0.48
1:A:167:VAL:H	2:A:502:1WC:H4	1.62	0.48
1:A:304:GLN:HB2	1:A:340:LYS:HG2	1.95	0.47
1:A:331:GLN:HG3	1:A:350[B]:PHE:HE2	1.80	0.47
1:A:411:VAL:CG1	2:A:503:1WC:H18	2.45	0.46
1:A:291:PRO:HG2	1:A:356[B]:PRO:HD3	1.97	0.45
1:A:288:GLU:CD	1:A:290:ARG:HD2	2.38	0.44
1:A:111:GLN:HG3	1:A:236:PHE:CG	2.53	0.44
1:A:355[B]:VAL:HG22	1:A:356[B]:PRO:HD2	2.00	0.43
1:A:350[A]:PHE:HB2	1:A:351[A]:PRO:CD	2.49	0.42
1:A:355[B]:VAL:HG13	1:A:356[B]:PRO:CD	2.49	0.42
1:A:75:LEU:HD11	1:A:79:ILE:HD11	2.01	0.42
1:A:166:LEU:HA	2:A:502:1WC:H16	2.01	0.42
1:A:331:GLN:HG3	1:A:350[A]:PHE:HE1	1.85	0.42
1:A:333:ASN:ND2	1:A:334:LYS:HG2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:VAL:HG12	1:A:365[B]:CYS:HG	1.82	0.41
1:A:290:ARG:HD3	1:A:350[B]:PHE:HA	2.01	0.41
1:A:297:VAL:O	1:A:343:SER:HA	2.21	0.41
1:A:409:GLN:HA	1:A:409:GLN:HE21	1.87	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	478/470 (102%)	449 (94%)	17 (4%)	12 (2%)	7 1

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	351[A]	PRO
1	A	351[B]	PRO
1	A	353[A]	GLU
1	A	353[B]	GLU
1	A	6	GLU
1	A	455	ASP
1	A	355[A]	VAL
1	A	355[B]	VAL
1	A	356[A]	PRO
1	A	356[B]	PRO
1	A	350[A]	PHE
1	A	350[B]	PHE

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	422/412 (102%)	397 (94%)	25 (6%)	24 6

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LYS
1	A	6	GLU
1	A	29	PHE
1	A	54	MET
1	A	70	GLN
1	A	134	GLU
1	A	136	GLU
1	A	137	GLU
1	A	139	LEU
1	A	154	MET
1	A	225	ASN
1	A	270	MET
1	A	296	PHE
1	A	304	GLN
1	A	306	LYS
1	A	340	LYS
1	A	350[A]	PHE
1	A	350[B]	PHE
1	A	354[A]	LYS
1	A	354[B]	LYS
1	A	402	HIS
1	A	409	GLN
1	A	436	ASN
1	A	451	LYS
1	A	465	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	ASN
1	A	78	HIS
1	A	225	ASN
1	A	279	ASN
1	A	298	ASN
1	A	315	GLN
1	A	331	GLN
1	A	333	ASN
1	A	361	HIS
1	A	375	GLN
1	A	409	GLN
1	A	461	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	CME	A	253	1	8,9,10	0.37	0	6,9,11	1.53	2 (33%)

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
1	CME	A	253	1	-	0/5/8/10	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	253	CME	O-C-CA	-2.58	118.78	125.49
1	A	253	CME	CZ-CE-SD	-2.02	108.23	113.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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	1WC	A	501	-	11,14,14	0.27	0	13,19,19	0.76	1 (7%)
2	1WC	A	502	-	12,14,14	0.41	0	11,19,19	0.88	1 (9%)
2	1WC	A	503	-	11,14,14	0.19	0	13,19,19	0.91	1 (7%)
3	GOL	A	504[A]	-	5,5,5	0.15	0	5,5,5	0.22	0
3	GOL	A	504[B]	-	5,5,5	0.17	0	5,5,5	0.72	0
3	GOL	A	505	-	5,5,5	0.36	0	5,5,5	0.98	0

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	1WC	A	501	-	-	0/3/4/4	0/2/2/2
2	1WC	A	502	-	-	0/3/4/4	0/2/2/2
2	1WC	A	503	-	-	0/3/4/4	0/2/2/2
3	GOL	A	504[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	A	504[B]	-	-	0/4/4/4	0/0/0/0
3	GOL	A	505	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	503	1WC	C8-C7-C2	2.50	129.43	127.09
2	A	501	1WC	C8-C7-C2	2.55	129.47	127.09
2	A	502	1WC	C7-C8-C13	2.56	125.71	123.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	502	1WC	6	0
2	A	503	1WC	1	0
3	A	505	GOL	3	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 [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, 95th 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	467/470 (99%)	0.86	66 (14%) 4 5	6, 24, 66, 114	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	135	TRP	13.8
1	A	138	GLY	11.6
1	A	351[A]	PRO	10.9
1	A	356[A]	PRO	10.7
1	A	303	ASP	9.4
1	A	355[A]	VAL	9.3
1	A	353[A]	GLU	7.5
1	A	134	GLU	7.4
1	A	354[A]	LYS	7.4
1	A	140	ASP	7.3
1	A	352[A]	GLY	7.1
1	A	141	ILE	6.7
1	A	8	PHE	6.6
1	A	350[A]	PHE	6.6
1	A	137	GLU	6.5
1	A	31	PRO	6.5
1	A	304	GLN	6.4
1	A	6	GLU	6.4
1	A	5	LYS	6.4
1	A	136	GLU	6.4
1	A	305	ASP	6.0
1	A	139	LEU	5.9
1	A	357[A]	ASP	5.5
1	A	451	LYS	5.2
1	A	132	THR	5.2
1	A	449	VAL	5.0
1	A	302	GLU	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	328	PHE	4.7
1	A	349	GLY	4.5
1	A	208	PRO	4.4
1	A	30	SER	4.2
1	A	223	ASN	4.1
1	A	7	GLU	4.0
1	A	53	ALA	3.9
1	A	209	ASP	3.7
1	A	49	SER	3.7
1	A	377	HIS	3.6
1	A	32	GLU	3.6
1	A	4	PRO	3.4
1	A	339	ASP	3.4
1	A	51	PHE	3.3
1	A	184	MET	3.3
1	A	3	THR	3.2
1	A	50	GLY	3.2
1	A	453	VAL	3.2
1	A	9	GLN	3.2
1	A	207	VAL	3.0
1	A	455	ASP	2.9
1	A	358[A]	GLU	2.9
1	A	28	HIS	2.6
1	A	306	LYS	2.6
1	A	454	ALA	2.6
1	A	436	ASN	2.6
1	A	48	ILE	2.4
1	A	468	LYS	2.4
1	A	202	ILE	2.4
1	A	211	ARG	2.3
1	A	222	PRO	2.3
1	A	133	GLN	2.3
1	A	116	ILE	2.2
1	A	338	PHE	2.2
1	A	437	LEU	2.2
1	A	329	GLN	2.1
1	A	142	ARG	2.1
1	A	340	LYS	2.0
1	A	425	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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, 95th 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
1	CME	A	253	10/11	0.97	0.08	-	8,17,28,28	0

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, 95th 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
2	1WC	A	501	13/13	0.87	0.43	9.32	28,32,40,40	22
3	GOL	A	504[A]	6/6	0.74	0.29	8.13	41,45,46,48	6
3	GOL	A	504[B]	6/6	0.74	0.29	7.62	23,26,32,33	6
2	1WC	A	502	13/13	0.68	0.20	3.69	22,27,31,38	0
3	GOL	A	505	6/6	0.77	0.25	2.91	23,29,33,48	0
2	1WC	A	503	13/13	0.77	0.18	1.74	31,34,35,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.