Full wwPDB X-ray Structure Validation Report (i)

Sep 28, 2024 – 06:48 pm BST

PDB ID	:	2W9X
Title	:	The active site of a carbohydrate esterase displays divergent catalytic and non-catalytic binding functions
Authors	:	Montanier, C.; Money, V.A.; Pires, V.; Flint, J.E.; Benedita, P.A.; Goyal, A.; Prates, J.A.; Izumi, A.; Stalbrand, H.; Morland, C.; Cartmell, A.; Kolenova, K.; Topakas, E.; Dobson, E.; Bolam, D.N.; Davies, G.J.; Fontes, C.M.; Gilbert, H.J.
Deposited on	:	2009-01-29
Resolution	:	2.00 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

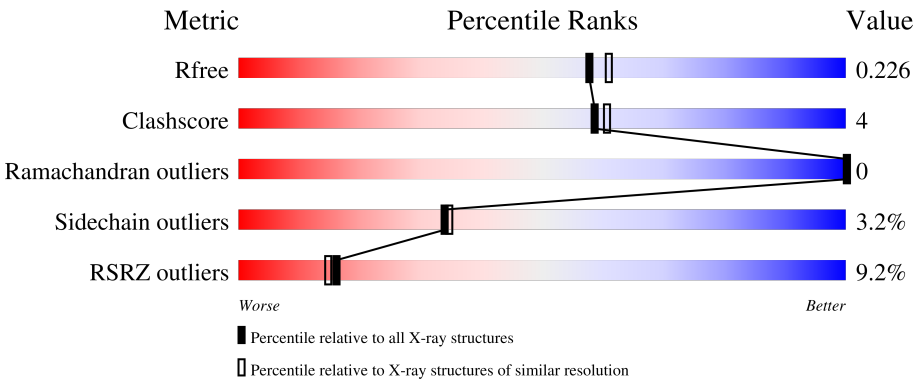
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

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 2.00 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}	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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 >=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 <=5%

Mol	Chain	Length	Quality of chain
1	A	366	8% 75% 9% • 15%
1	B	366	8% 80% 9% • 10%

Validation Pipeline (wwPDB-VP) : 2.39

2 Entry composition (i)

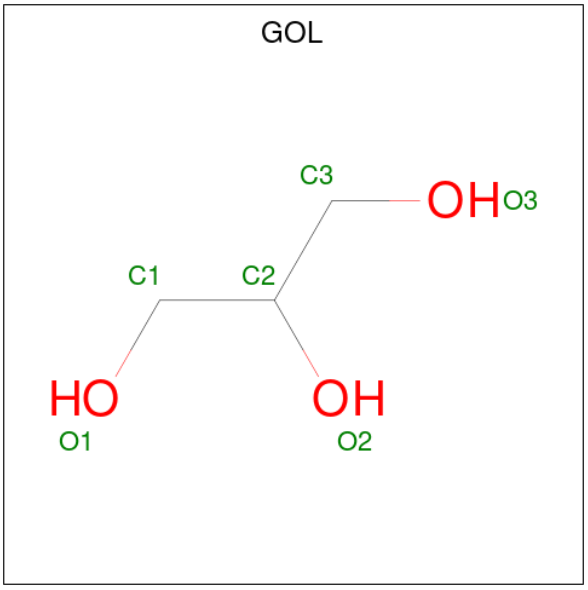
There are 3 unique types of molecules in this entry. The entry contains 5585 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PUTATIVE ACETYL XYLAN ESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	312	2498	1596	433	464	5	11	3	0
1	B	329	2627	1675	455	493	4	41	2	0

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	B	1	6	3	3	0	0
			Total	C	O		
2	B	1	6	3	3	0	0
			Total	C	O		
2	B	1	6	3	3	0	0

- Molecule 3 is water.

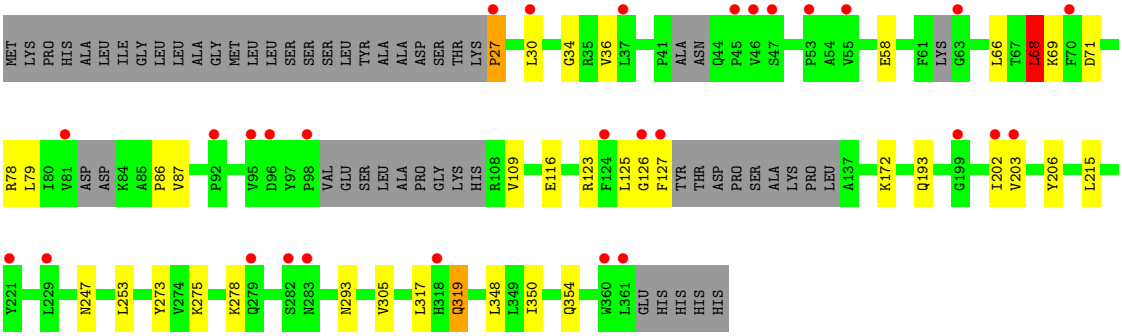
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	187	187	187	0	0
			Total	O		
3	B	231	231	231	0	0

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. 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. 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.

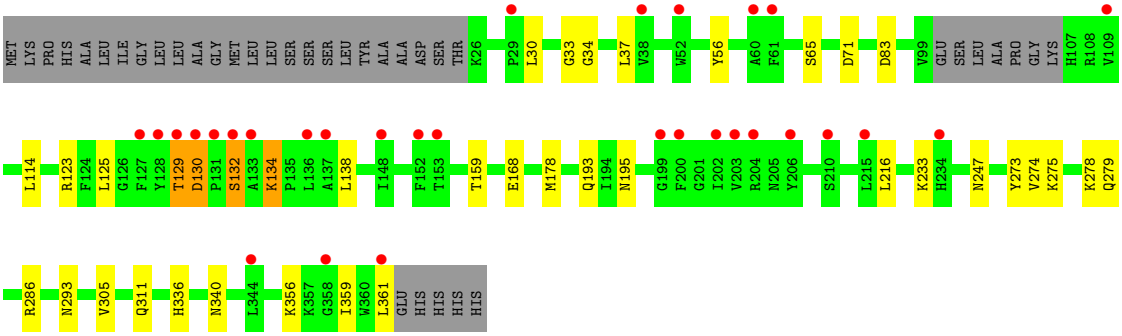
- Molecule 1: PUTATIVE ACETYL XYLAN ESTERASE

Chain A:



- Molecule 1: PUTATIVE ACETYL XYLAN ESTERASE

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	75.27Å 75.27Å 141.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 50.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (50.00-2.00) 100.0 (50.00-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.58 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.191 , 0.231 0.188 , 0.226	Depositor DCC
R_{free} test set	2699 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	32.3	Xtriage
Anisotropy	0.462	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.041 for h,-k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5585	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.17% 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, 0.333 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: GOL

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	0.62	2/2565 (0.1%)	0.65	2/3472 (0.1%)
1	B	0.85	4/2696 (0.1%)	0.68	2/3660 (0.1%)
All	All	0.75	6/5261 (0.1%)	0.66	4/7132 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	132	SER	CA-CB	-24.70	1.15	1.52
1	B	130	ASP	CB-CG	-15.40	1.19	1.51
1	B	134	LYS	CB-CG	-11.13	1.22	1.52
1	B	168	GLU	CG-CD	-11.11	1.35	1.51
1	A	27	PRO	N-CD	6.73	1.57	1.47
1	A	126	GLY	CA-C	6.61	1.62	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	132	SER	N-CA-CB	-7.41	99.38	110.50
1	A	68	LEU	CA-CB-CG	5.93	128.93	115.30
1	B	134	LYS	CA-CB-CG	5.34	125.16	113.40
1	A	348	LEU	CA-CB-CG	5.32	127.54	115.30

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	2498	0	2458	23	0
1	B	2627	0	2575	20	0
2	A	18	0	24	1	0
2	B	24	0	32	1	0
3	A	187	0	0	3	0
3	B	231	0	0	2	0
All	All	5585	0	5089	43	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 (43) 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:123:ARG:HH12	1:B:125:LEU:HD21	1.22	1.00
1:A:30:LEU:HD21	1:A:127:PHE:HE2	1.39	0.84
1:A:293:ASN:ND2	1:A:305:VAL:HG21	2.04	0.72
1:B:123:ARG:NH1	1:B:125:LEU:HD21	2.02	0.67
1:A:30:LEU:HD21	1:A:127:PHE:CE2	2.30	0.63
1:B:311[A]:GLN:HG3	3:B:2182:HOH:O	1.98	0.62
1:A:78[A]:ARG:HG3	1:A:86:PRO:HB3	1.87	0.57
1:B:129:THR:HG22	1:B:130:ASP:H	1.71	0.55
1:A:68:LEU:HD22	1:A:127:PHE:CD1	2.42	0.55
1:A:350:ILE:O	1:A:354:GLN:HG3	2.05	0.55
1:B:65:SER:O	1:B:129:THR:HG23	2.07	0.55
1:A:116:GLU:HB3	2:A:1364:GOL:H32	1.88	0.54
1:A:27:PRO:HA	1:A:127:PHE:O	2.07	0.54
1:A:293:ASN:HB2	3:A:2127:HOH:O	2.08	0.53
1:B:275:LYS:O	1:B:279:GLN:HG3	2.09	0.53
1:B:293:ASN:ND2	1:B:305:VAL:HG21	2.24	0.52
1:B:274:VAL:CG1	1:B:278:LYS:HE3	2.41	0.51
1:A:202:ILE:HG22	1:A:203:VAL:HG13	1.92	0.50
1:A:34:GLY:HA2	1:A:193:GLN:HG2	1.93	0.50
1:A:79:LEU:HB3	1:A:87:VAL:HG13	1.92	0.50
1:A:71:ASP:HB3	1:A:123:ARG:HB2	1.95	0.49
1:A:215:LEU:HD13	1:A:215:LEU:O	2.13	0.49
1:B:33:GLY:HA3	1:B:56:TYR:CZ	2.49	0.48
1:A:78[A]:ARG:CG	1:A:86:PRO:HB3	2.44	0.47
1:B:274:VAL:HG12	1:B:278:LYS:HE3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:LEU:HD22	1:A:127:PHE:HD1	1.79	0.47
1:A:69:LYS:HG2	1:A:125:LEU:HD12	1.96	0.47
1:B:356:LYS:HD3	1:B:359:ILE:HD12	1.97	0.46
1:B:34:GLY:HA2	1:B:193:GLN:HG2	1.96	0.46
1:B:71:ASP:HB3	1:B:123:ARG:HB2	1.98	0.45
1:A:317:LEU:HD23	1:A:319:GLN:HE21	1.82	0.45
1:B:159:THR:CG2	1:B:178:MET:HE3	2.48	0.44
1:B:286:ARG:HB2	1:B:361:LEU:CD1	2.48	0.44
1:A:206:TYR:HB2	1:A:247:ASN:ND2	2.35	0.42
1:B:247:ASN:ND2	3:B:2132:HOH:O	2.52	0.42
1:A:275:LYS:HG3	3:A:2119:HOH:O	2.19	0.41
1:A:278:LYS:HE2	3:A:2147:HOH:O	2.19	0.41
1:B:193:GLN:HE21	1:B:195:ASN:HD21	1.69	0.41
1:A:30:LEU:HD23	1:A:58:GLU:O	2.20	0.41
1:B:286:ARG:HB2	1:B:361:LEU:HD11	2.03	0.41
1:A:66:LEU:HD22	1:A:109:VAL:HG21	2.03	0.41
1:B:356:LYS:HD3	1:B:359:ILE:CD1	2.52	0.40
1:B:336:HIS:CE1	2:B:1362:GOL:H31	2.56	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	303/366 (83%)	292 (96%)	11 (4%)	0	100	100
1	B	327/366 (89%)	315 (96%)	12 (4%)	0	100	100
All	All	630/732 (86%)	607 (96%)	23 (4%)	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	273/314 (87%)	267 (98%)	6 (2%)	47	51
1	B	287/314 (91%)	275 (96%)	12 (4%)	25	24
All	All	560/628 (89%)	542 (97%)	18 (3%)	34	35

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	VAL
1	A	68	LEU
1	A	172	LYS
1	A	253	LEU
1	A	273	TYR
1	A	319	GLN
1	B	30	LEU
1	B	37	LEU
1	B	83	ASP
1	B	114	LEU
1	B	129	THR
1	B	132	SER
1	B	134	LYS
1	B	138	LEU
1	B	216	LEU
1	B	233	LYS
1	B	273	TYR
1	B	340	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	GLN
1	A	75	ASN
1	A	247	ASN
1	A	288	GLN

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Mol	Chain	Res	Type
1	A	293	ASN
1	A	319	GLN
1	A	340	ASN
1	A	343	GLN
1	B	75	ASN
1	B	177	GLN
1	B	193	GLN
1	B	224	ASN
1	B	247	ASN
1	B	293	ASN
1	B	343	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)

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)

7 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	GOL	A	1363	-	5,5,5	0.37	0	5,5,5	0.21	0
2	GOL	B	1365	-	5,5,5	0.54	0	5,5,5	0.92	0
2	GOL	B	1363	-	5,5,5	0.42	0	5,5,5	0.89	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	GOL	A	1362	-	5,5,5	0.41	0	5,5,5	0.33	0
2	GOL	A	1364	-	5,5,5	0.38	0	5,5,5	0.54	0
2	GOL	B	1362	-	5,5,5	0.35	0	5,5,5	0.39	0
2	GOL	B	1364	-	5,5,5	0.40	0	5,5,5	0.41	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	GOL	A	1363	-	-	0/4/4/4	-
2	GOL	B	1365	-	-	0/4/4/4	-
2	GOL	B	1363	-	-	2/4/4/4	-
2	GOL	A	1362	-	-	2/4/4/4	-
2	GOL	A	1364	-	-	2/4/4/4	-
2	GOL	B	1362	-	-	4/4/4/4	-
2	GOL	B	1364	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1362	GOL	C1-C2-C3-O3
2	A	1364	GOL	C1-C2-C3-O3
2	B	1362	GOL	C1-C2-C3-O3
2	B	1362	GOL	O2-C2-C3-O3
2	B	1363	GOL	C1-C2-C3-O3
2	B	1362	GOL	O1-C1-C2-C3
2	A	1364	GOL	O2-C2-C3-O3
2	B	1363	GOL	O2-C2-C3-O3
2	A	1362	GOL	O2-C2-C3-O3
2	B	1362	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1364	GOL	1	0
2	B	1362	GOL	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 (i)

6.1 Protein, DNA and RNA chains (i)

Warning: The R factor obtained from EDS is 0.2653,which does not match the depositor's R factor of 0.191. Please interpret the results in this section carefully.

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	312/366 (85%)	1.01	29 (9%)	16	14	20, 40, 48, 58	6 (1%)
1	B	329/366 (89%)	0.93	30 (9%)	16	15	18, 39, 47, 54	13 (3%)
All	All	641/732 (87%)	0.97	59 (9%)	16	15	18, 39, 47, 58	19 (2%)

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	361	LEU	4.5
1	A	81	VAL	3.9
1	A	63	GLY	3.2
1	A	127	PHE	3.2
1	A	98	PRO	3.1
1	B	206	TYR	3.1
1	A	30	LEU	2.9
1	B	202	ILE	2.9
1	B	129	THR	2.8
1	B	60	ALA	2.8
1	B	109	VAL	2.7
1	A	199	GLY	2.7
1	A	27	PRO	2.7
1	B	148	ILE	2.7
1	B	130	ASP	2.6
1	B	215	LEU	2.6
1	A	360	TRP	2.6
1	B	344	LEU	2.6
1	A	47	SER	2.5
1	B	137	ALA	2.5
1	A	124	PHE	2.5
1	B	132	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	133	ALA	2.5
1	B	361	LEU	2.5
1	A	96	ASP	2.5
1	A	45	PRO	2.4
1	B	38	VAL	2.4
1	A	229	LEU	2.4
1	A	203	VAL	2.4
1	B	131	PRO	2.4
1	B	127	PHE	2.3
1	B	234	HIS	2.3
1	B	153	THR	2.3
1	A	70	PHE	2.3
1	A	283	ASN	2.3
1	A	221	TYR	2.3
1	A	37	LEU	2.3
1	B	136	LEU	2.3
1	B	152	PHE	2.2
1	B	200	PHE	2.2
1	B	204	ARG	2.2
1	B	128	TYR	2.2
1	A	282	SER	2.2
1	A	202	ILE	2.2
1	B	199	GLY	2.2
1	A	95	VAL	2.2
1	B	203	VAL	2.2
1	B	52	TRP	2.1
1	A	92	PRO	2.1
1	A	279	GLN	2.1
1	B	61	PHE	2.1
1	B	210	SER	2.1
1	A	53	PRO	2.1
1	A	126	GLY	2.1
1	B	29	PRO	2.1
1	A	46	VAL	2.1
1	B	358	GLY	2.0
1	A	55	VAL	2.0
1	A	318	HIS	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 monosaccharides 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, 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	B-factors(Å^2)	Q<0.9
2	GOL	B	1364	6/6	0.78	0.19	68,69,69,71	0
2	GOL	A	1363	6/6	0.79	0.14	47,51,52,53	0
2	GOL	A	1362	6/6	0.80	0.17	59,62,62,63	0
2	GOL	A	1364	6/6	0.81	0.17	61,62,63,63	0
2	GOL	B	1362	6/6	0.82	0.14	54,55,56,58	0
2	GOL	B	1363	6/6	0.83	0.14	42,43,45,46	0
2	GOL	B	1365	6/6	0.90	0.13	34,37,39,39	0

6.5 Other polymers (i)

There are no such residues in this entry.