



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 04:48 am GMT

PDB ID : 3MRV
Title : Glycogen phosphorylase complexed with 3-hydroxybenzaldehyde-4-(beta-D-glucopyranosyl) thiosemicarbazone
Authors : Alexacou, K.-M.
Deposited on : 2010-04-29
Resolution : 1.94 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

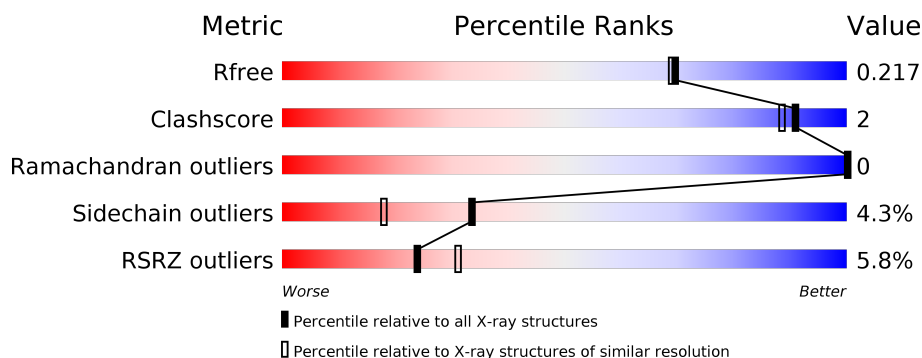
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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}	100719	3233 (1.96-1.92)
Clashscore	112137	3430 (1.96-1.92)
Ramachandran outliers	110173	3395 (1.96-1.92)
Sidechain outliers	110143	3395 (1.96-1.92)
RSRZ outliers	101464	3250 (1.96-1.92)

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	842	<div> <div>6%</div> <div>89%</div> <div>6%</div> <div>.</div> </div>

2 Entry composition [i](#)

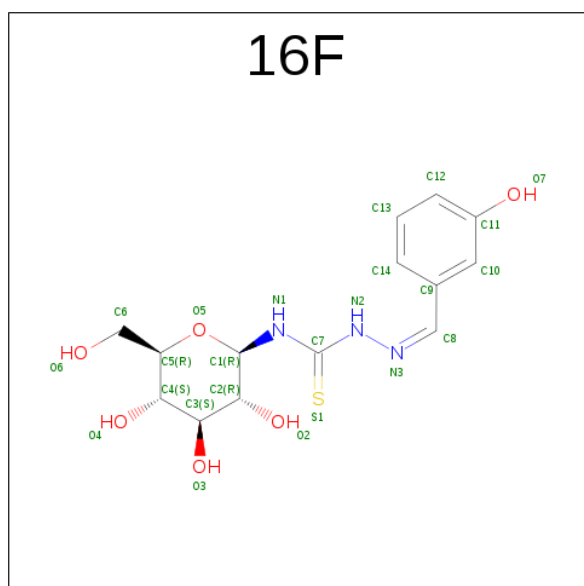
There are 4 unique types of molecules in this entry. The entry contains 6919 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glycogen phosphorylase, muscle form.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	810	Total	C	N	O	P	S	0	3	0
			6622	4221	1165	1206	1	29			

- Molecule 2 is N-((2Z)-2-[(3-HYDROXYPHENYL)METHYLIDENE]HYDRAZINO}CARBONOTHIOYL)-BETA-D-GLUCOPYRANOSYLAMINE (three-letter code: 16F) (formula: C₁₄H₁₉N₃O₆S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			24	14	3	6	1		
2	A	1	Total	C	N	O	S	0	0
			24	14	3	6	1		

- Molecule 3 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



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

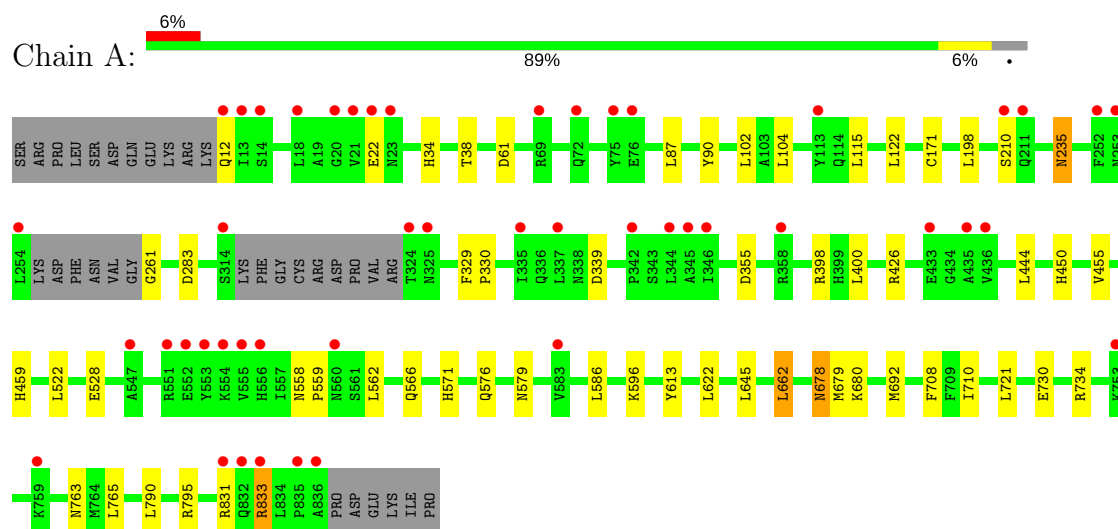
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	245	Total	O	0	0
			245	245		

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 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: Glycogen phosphorylase, muscle form



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	128.87Å 128.87Å 116.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.09 – 1.94 28.78 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.2 (29.09-1.94) 99.2 (28.78-1.94)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.98 (at 1.93Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.192 , 0.216 0.193 , 0.217	Depositor DCC
R_{free} test set	3643 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 49.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6919	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: 16F, DMS, LLP

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	0/6756	0.59	1/9143 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	87	LEU	CA-CB-CG	-5.60	102.42	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	6622	0	6553	24	0
2	A	48	0	37	1	0
3	A	4	0	6	1	0
4	A	245	0	0	5	0
All	All	6919	0	6596	26	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 2.

All (26) 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:283[B]:ASP:OD2	1:A:571[B]:HIS:CE1	1.68	1.45
1:A:283[B]:ASP:OD2	1:A:571[B]:HIS:HE1	0.76	1.11
1:A:283[B]:ASP:CG	1:A:571[B]:HIS:CE1	2.50	0.84
1:A:283[B]:ASP:CG	1:A:571[B]:HIS:HE1	1.80	0.84
1:A:455:VAL:H	1:A:459:HIS:HD2	1.38	0.71
1:A:678:ASN:HD22	1:A:679:MET:H	1.39	0.70
1:A:730:GLU:O	1:A:734:ARG:HG3	1.98	0.63
3:A:843:DMS:H21	4:A:901:HOH:O	1.98	0.63
1:A:34:HIS:HE1	1:A:61:ASP:OD1	1.81	0.63
1:A:450:HIS:HE1	4:A:952:HOH:O	1.83	0.61
1:A:34:HIS:HD2	1:A:38:THR:OG1	1.85	0.59
1:A:355:ASP:OD1	1:A:398:ARG:HD3	2.02	0.59
1:A:235:ASN:H	1:A:235:ASN:HD22	1.52	0.56
1:A:171:CYS:SG	4:A:1087:HOH:O	2.58	0.54
1:A:450:HIS:HD2	4:A:948:HOH:O	1.91	0.54
1:A:261:GLY:N	4:A:965:HOH:O	2.43	0.52
1:A:678:ASN:HD22	1:A:679:MET:N	2.06	0.51
1:A:680:LLP:NZ	1:A:680:LLP:O3	2.43	0.51
1:A:562:LEU:HD21	1:A:662:LEU:HB2	1.97	0.46
1:A:235:ASN:HA	1:A:833:ARG:HG3	1.97	0.46
2:A:998:16F:HN2	2:A:998:16F:H14	1.81	0.45
1:A:329:PHE:HB3	1:A:330:PRO:HD3	1.99	0.44
1:A:528:GLU:OE1	1:A:795:ARG:NH2	2.52	0.43
1:A:692:MET:CE	1:A:710:ILE:HD13	2.49	0.42
1:A:558:ASN:HA	1:A:559:PRO:HD3	1.89	0.41
1:A:566:GLN:HE22	1:A:576:GLN:HA	1.86	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	806/842 (96%)	782 (97%)	24 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	703/730 (96%)	673 (96%)	30 (4%)	33	18

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	22	GLU
1	A	90	TYR
1	A	102	LEU
1	A	104	LEU
1	A	115	LEU
1	A	122	LEU
1	A	198	LEU
1	A	210	SER
1	A	235	ASN
1	A	339	ASP
1	A	400	LEU
1	A	426	ARG
1	A	444	LEU
1	A	522	LEU
1	A	579	ASN
1	A	586	LEU
1	A	596	LYS
1	A	613	TYR
1	A	622	LEU
1	A	645	LEU
1	A	662	LEU
1	A	678	ASN

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Mol	Chain	Res	Type
1	A	708	PHE
1	A	721	LEU
1	A	763	ASN
1	A	765	LEU
1	A	790	LEU
1	A	831	ARG
1	A	833	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	34	HIS
1	A	73	HIS
1	A	235	ASN
1	A	270	ASN
1	A	325	ASN
1	A	412	ASN
1	A	450	HIS
1	A	459	HIS
1	A	481	ASN
1	A	484	ASN
1	A	566	GLN
1	A	579	ASN
1	A	614	HIS
1	A	678	ASN
1	A	727	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	LLP	A	680	1	24,24,25	1.84	5 (20%)	28,32,34	1.29	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
1	LLP	A	680	1	-	0/15/17/19	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	680	LLP	O3-C3	-5.15	1.25	1.37
1	A	680	LLP	C4'-NZ	2.53	1.34	1.27
1	A	680	LLP	CE-NZ	2.91	1.52	1.46
1	A	680	LLP	CA-C	3.36	1.54	1.50
1	A	680	LLP	C4-C4'	3.44	1.52	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	680	LLP	OP4-P-OP1	-2.71	98.88	106.47
1	A	680	LLP	CE-NZ-C4'	-2.60	111.48	119.03
1	A	680	LLP	C4-C4'-NZ	-2.46	112.70	124.66
1	A	680	LLP	C5-C6-N1	-2.05	120.41	123.87

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
1	A	680	LLP	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 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	DMS	A	843	-	3,3,3	2.60	1 (33%)	3,3,3	0.38	0
2	16F	A	920	-	25,25,25	2.46	3 (12%)	34,34,34	1.36	4 (11%)
2	16F	A	998	-	25,25,25	2.48	2 (8%)	34,34,34	1.99	4 (11%)

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
3	DMS	A	843	-	-	0/0/0/0	0/0/0/0
2	16F	A	920	-	-	0/12/32/32	0/2/2/2
2	16F	A	998	-	-	0/12/32/32	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	998	16F	N2-N3	-11.21	1.25	1.38
2	A	920	16F	N2-N3	-11.19	1.25	1.38
2	A	920	16F	C2-C1	2.03	1.55	1.52
2	A	920	16F	C1-N1	2.90	1.46	1.43
2	A	998	16F	C1-N1	3.83	1.47	1.43
3	A	843	DMS	O-S	4.39	1.80	1.50

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	920	16F	O5-C1-N1	-4.35	100.80	107.98
2	A	998	16F	O5-C1-C2	-3.12	106.65	109.84
2	A	920	16F	N2-C7-N1	2.01	118.82	115.88
2	A	920	16F	C9-C8-N3	2.05	124.19	121.33
2	A	920	16F	C7-N2-N3	2.39	122.92	120.23
2	A	998	16F	N2-C7-N1	3.01	120.29	115.88
2	A	998	16F	C9-C8-N3	6.57	130.50	121.33
2	A	998	16F	C8-N3-N2	7.31	127.97	115.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	843	DMS	1	0
2	A	998	16F	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, 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	809/842 (96%)	0.32	47 (5%) 24 31	21, 33, 51, 72	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	324	THR	8.9
1	A	556	HIS	5.9
1	A	252	PHE	5.8
1	A	435	ALA	5.4
1	A	555	VAL	5.3
1	A	253	ASN	5.1
1	A	835	PRO	4.7
1	A	551	ARG	4.6
1	A	211	GLN	4.5
1	A	75	TYR	4.4
1	A	836	ALA	4.3
1	A	436	VAL	4.1
1	A	831	ARG	4.0
1	A	13	ILE	4.0
1	A	21	VAL	3.9
1	A	69	ARG	3.8
1	A	18	LEU	3.8
1	A	832	GLN	3.7
1	A	547	ALA	3.5
1	A	753	LYS	3.3
1	A	210	SER	3.3
1	A	314	SER	3.2
1	A	554	LYS	3.1
1	A	553	TYR	3.1
1	A	337	LEU	2.9
1	A	254	LEU	2.9
1	A	344	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	113	TYR	2.7
1	A	22	GLU	2.6
1	A	325	ASN	2.5
1	A	12	GLN	2.4
1	A	14	SER	2.4
1	A	345	ALA	2.4
1	A	833	ARG	2.4
1	A	76	GLU	2.3
1	A	20	GLY	2.3
1	A	358	ARG	2.3
1	A	552	GLU	2.3
1	A	335	ILE	2.2
1	A	560	ASN	2.2
1	A	583	VAL	2.2
1	A	346	ILE	2.2
1	A	342	PRO	2.1
1	A	23	ASN	2.1
1	A	72	GLN	2.1
1	A	433	GLU	2.0
1	A	759	LYS	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(\AA^2)	Q<0.9
1	LLP	A	680	24/25	0.98	0.10	-	22,24,26,27	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
3	DMS	A	843	4/4	0.96	0.16	1.23	55,55,55,55	0
2	16F	A	920	24/24	0.90	0.12	0.91	33,36,42,45	0
2	16F	A	998	24/24	0.93	0.12	-0.07	25,32,48,48	0

6.5 Other polymers

There are no such residues in this entry.