



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 02:01 PM GMT

PDB ID : 3H2Y
Title : Crystal structure of YqeH GTPase from Bacillus anthracis with dGDP bound
Authors : Brunzelle, J.S.; Anderson, S.M.; Xu, X.; Savchenko, A.; Anderson, W.F.;
Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2009-04-15
Resolution : 1.80 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

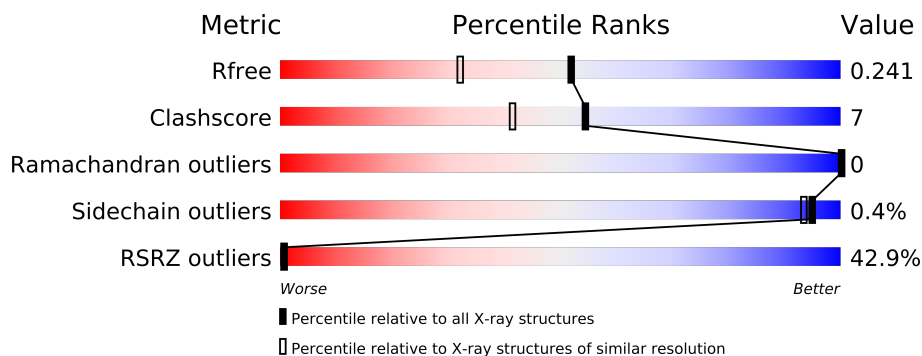
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.80 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}	66092	3513 (1.80-1.80)
Clashscore	79885	4461 (1.80-1.80)
Ramachandran outliers	78287	4404 (1.80-1.80)
Sidechain outliers	78261	4403 (1.80-1.80)
RSRZ outliers	66119	3515 (1.80-1.80)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	368	

2 Entry composition i

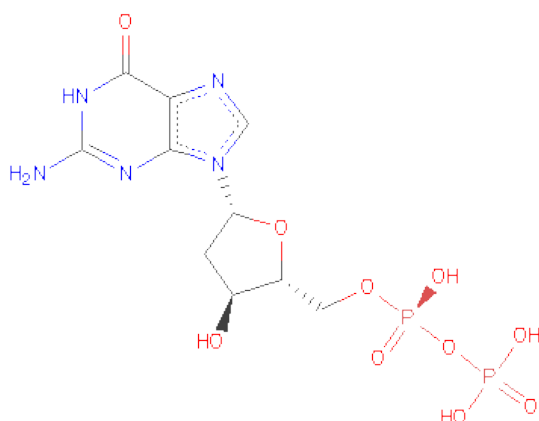
There are 3 unique types of molecules in this entry. The entry contains 2587 atoms, of which 0 are hydrogen and 0 are deuterium.

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 GTPase family protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	309	2434	1561	414	451	3	5	17	2	0

- Molecule 2 is 2'-DEOXYGUANOSINE-5'-DIPHOSPHATE (three-letter code: DGI) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	27	10	5	10	2	0	0

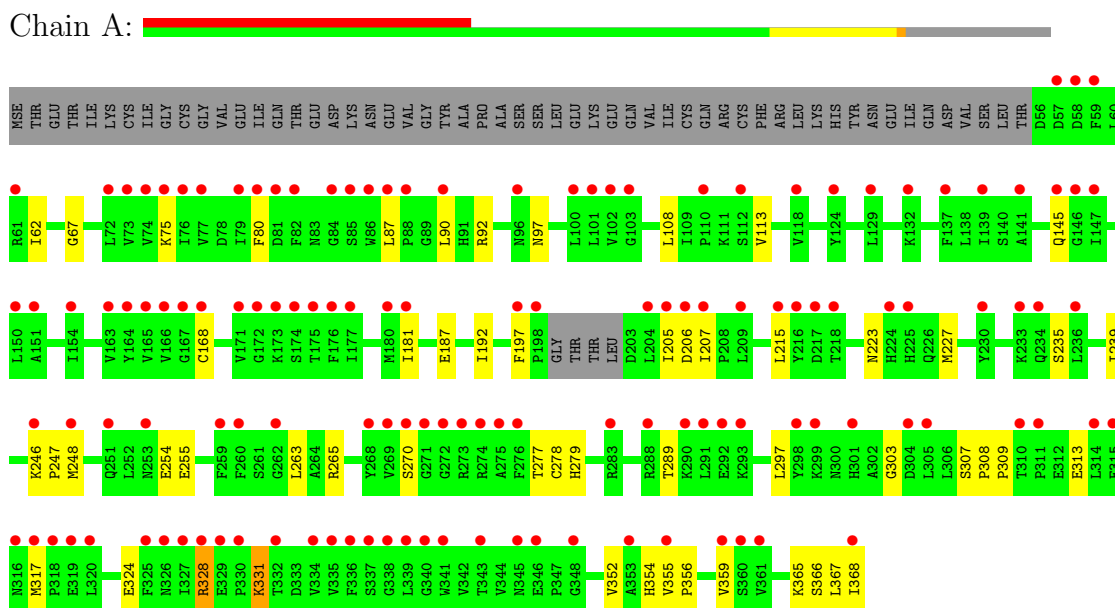
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	126	Total	O	0	0
			126	126		

3 Residue-property plots

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: GTPase family protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	83.13Å 58.99Å 77.72Å 90.00° 99.38° 90.00°	Depositor
Resolution (Å)	30.00 – 1.80 29.49 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.4 (30.00-1.80) 98.5 (29.49-1.80)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.67 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.215 , 0.242 0.214 , 0.241	Depositor DCC
R_{free} test set	1714 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	35.1	Xtriage
Anisotropy	0.546	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 34009 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2587	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.47% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: DGI

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	2/2485 (0.1%)	0.63	5/3359 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	331	LYS	CG-CD	-10.30	1.17	1.52
1	A	328	ARG	CB-CG	-9.22	1.27	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	328	ARG	CA-CB-CG	8.76	132.68	113.40
1	A	331	LYS	CB-CG-CD	7.36	130.74	111.60
1	A	328	ARG	CB-CG-CD	5.89	126.92	111.60
1	A	365	LYS	CA-CB-CG	5.62	125.75	113.40
1	A	90	LEU	CA-CB-CG	5.25	127.37	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2434	0	2400	33	1
2	A	27	0	12	0	0
3	A	126	0	0	4	1
All	All	2587	0	2412	33	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (33) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:227:MSE:HE2	1:A:359:VAL:HG11	1.72	0.70
1:A:265:ARG:HB3	1:A:354:HIS:HB2	1.76	0.65
1:A:324:GLU:HG2	1:A:352:VAL:HG22	1.83	0.60
1:A:181:ILE:HD11	1:A:205:ILE:HD13	1.83	0.58
1:A:62:ILE:HG21	1:A:197:PHE:CE1	2.44	0.53
1:A:80:PHE:CE2	1:A:108:LEU:HB2	2.44	0.53
1:A:235:SER:O	1:A:239:ILE:HD12	2.09	0.53
1:A:355:VAL:HG22	1:A:356:PRO:HD2	1.93	0.50
1:A:355:VAL:HG22	1:A:359:VAL:HB	1.95	0.49
1:A:168[B]:CYS:SG	1:A:223:ASN:ND2	2.85	0.49
1:A:207:ILE:HD12	1:A:215:LEU:HD22	1.95	0.48
1:A:254:GLU:HG2	1:A:255:GLU:HG2	1.96	0.47
1:A:368:ILE:HD11	3:A:458:HOH:O	2.14	0.46
1:A:67:GLY:HA2	1:A:97:ASN:HD21	1.79	0.46
1:A:206:ASP:HB3	3:A:465:HOH:O	2.14	0.46
1:A:331:LYS:HB3	1:A:366:SER:HB2	1.97	0.46
1:A:289:THR:HG21	1:A:297:LEU:HD22	1.96	0.46
1:A:368:ILE:N	1:A:368:ILE:HD12	2.31	0.45
1:A:87:LEU:CD2	1:A:168[B]:CYS:SG	3.05	0.45
1:A:187:GLU:HG3	3:A:493:HOH:O	2.16	0.45
1:A:263:LEU:HD22	1:A:317:MSE:HE1	2.00	0.44
1:A:313:GLU:O	1:A:317:MSE:HB2	2.18	0.44
1:A:317:MSE:HE2	1:A:356:PRO:HG2	2.00	0.44
1:A:254:GLU:HG3	1:A:270:SER:HA	2.00	0.43
1:A:75:LYS:NZ	1:A:87:LEU:H	2.17	0.43
1:A:307:SER:HA	1:A:308:PRO:C	2.39	0.42
1:A:246:LYS:HA	1:A:247:PRO:HD3	1.90	0.42
1:A:248:MSE:HB2	1:A:278:CYS:SG	2.60	0.42
1:A:113:VAL:HG13	1:A:367:LEU:HB2	2.01	0.42
1:A:145:GLN:HB2	3:A:459:HOH:O	2.20	0.41
1:A:192:ILE:HD13	1:A:205:ILE:HD11	2.01	0.41
1:A:303:GLY:HA2	1:A:309:PRO:O	2.19	0.41
1:A:277:THR:HG22	1:A:279:HIS:CE1	2.57	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:92:ARG:NH2	3:A:493:HOH:O[4_455]	2.12	0.08

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	307/368 (83%)	298 (97%)	9 (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	265/318 (83%)	264 (100%)	1 (0%)	95	93

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	328	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	ASN
1	A	223	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand 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	$\# Z > 2$
2	DGI	A	369	-	29,29,29	1.45	5 (17%)	42,45,45	3.53	7 (16%)

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	DGI	A	369	-	-	0/14/28/28	0/1/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	369	DGI	C6-C5	4.22	1.48	1.41
2	A	369	DGI	C4-N9	-3.48	1.32	1.37
2	A	369	DGI	C5-C4	2.88	1.47	1.40
2	A	369	DGI	C2-N2	2.62	1.36	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	369	DGI	C2-N3	2.16	1.36	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	369	DGI	C6-C5-N7	20.28	136.87	134.14
2	A	369	DGI	N3-C4-N9	4.93	134.14	126.91
2	A	369	DGI	C5-C4-N3	-4.32	119.68	125.94
2	A	369	DGI	C2-N3-C4	4.00	120.72	115.09
2	A	369	DGI	C4-C5-N7	-3.30	106.69	109.52
2	A	369	DGI	C8-N9-C4	2.94	109.14	106.90
2	A	369	DGI	PA-O3A-PB	-2.03	125.73	131.68

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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 ⓘ

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	309/368 (83%)	1.90	133 (43%) 1 1	42, 54, 70, 73	4 (1%)

All (133) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	PHE	7.4
1	A	272	GLY	6.1
1	A	77	VAL	6.1
1	A	233	LYS	6.1
1	A	102	VAL	5.7
1	A	76	ILE	5.6
1	A	320	LEU	5.5
1	A	198	PRO	5.5
1	A	346	GLU	5.0
1	A	269	VAL	4.9
1	A	166	VAL	4.9
1	A	276	PHE	4.7
1	A	340	GLY	4.6
1	A	165	VAL	4.6
1	A	171	VAL	4.5
1	A	154	ILE	4.5
1	A	79	ILE	4.5
1	A	74	VAL	4.4
1	A	326	ASN	4.2
1	A	163	VAL	4.0
1	A	319	GLU	3.9
1	A	177	ILE	3.9
1	A	248	MSE	3.9
1	A	205	ILE	3.9
1	A	80	PHE	3.8
1	A	251	GLN	3.8
1	A	339	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	316	ASN	3.7
1	A	292	GLU	3.7
1	A	139	ILE	3.7
1	A	335	VAL	3.7
1	A	176	PHE	3.7
1	A	311	PRO	3.6
1	A	59[A]	PHE	3.6
1	A	82	PHE	3.6
1	A	207	ILE	3.5
1	A	314	LEU	3.5
1	A	336	PHE	3.5
1	A	215	LEU	3.5
1	A	168[A]	CYS	3.5
1	A	328	ARG	3.5
1	A	268	TYR	3.5
1	A	87	LEU	3.5
1	A	291	LEU	3.4
1	A	315	GLU	3.4
1	A	225	HIS	3.4
1	A	337	SER	3.4
1	A	72	LEU	3.4
1	A	218	THR	3.3
1	A	329	GLU	3.3
1	A	61	ARG	3.3
1	A	150	LEU	3.2
1	A	341	TRP	3.2
1	A	85	SER	3.1
1	A	327	ILE	3.1
1	A	271	GLY	3.1
1	A	86	TRP	3.1
1	A	317	MSE	3.1
1	A	103	GLY	3.1
1	A	253	ASN	3.0
1	A	262	GLY	3.0
1	A	73	VAL	3.0
1	A	270	SER	3.0
1	A	236	LEU	2.9
1	A	216	TYR	2.9
1	A	124	TYR	2.9
1	A	348	GLY	2.9
1	A	290	LYS	2.9
1	A	288	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	273	ARG	2.9
1	A	234	GLN	2.9
1	A	259	PHE	2.9
1	A	275	ALA	2.8
1	A	283	ARG	2.8
1	A	204	LEU	2.7
1	A	334	VAL	2.7
1	A	361	VAL	2.7
1	A	75	LYS	2.7
1	A	57	ASP	2.7
1	A	100	LEU	2.7
1	A	172	GLY	2.6
1	A	345	ASN	2.6
1	A	110	PRO	2.6
1	A	230	TYR	2.6
1	A	96	ASN	2.6
1	A	368	ILE	2.6
1	A	301	HIS	2.5
1	A	137	PHE	2.5
1	A	325	PHE	2.5
1	A	84	GLY	2.5
1	A	206	ASP	2.5
1	A	145	GLN	2.5
1	A	304	ASP	2.4
1	A	174	SER	2.4
1	A	332	THR	2.4
1	A	167	GLY	2.4
1	A	224	HIS	2.4
1	A	355	VAL	2.4
1	A	359	VAL	2.4
1	A	299	LYS	2.4
1	A	338	GLY	2.4
1	A	175	THR	2.4
1	A	353	ALA	2.4
1	A	173	LYS	2.4
1	A	164	TYR	2.3
1	A	132	LYS	2.3
1	A	260	PHE	2.3
1	A	101	LEU	2.3
1	A	58	ASP	2.3
1	A	246	LYS	2.3
1	A	305	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	343	THR	2.2
1	A	88	PRO	2.2
1	A	118	VAL	2.2
1	A	90	LEU	2.2
1	A	181	ILE	2.2
1	A	274	ARG	2.2
1	A	360	SER	2.2
1	A	217	ASP	2.1
1	A	298	TYR	2.1
1	A	310	THR	2.1
1	A	146	GLY	2.1
1	A	147	ILE	2.1
1	A	129	LEU	2.1
1	A	141	ALA	2.1
1	A	151	ALA	2.1
1	A	330	PRO	2.1
1	A	293	LYS	2.1
1	A	112	SER	2.0
1	A	180	MSE	2.0
1	A	209	LEU	2.0
1	A	318	PRO	2.0
1	A	81	ASP	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	DGI	A	369	27/27	0.10	-1.74	34,39,42,46	0

6.5 Other polymers ⓘ

There are no such residues in this entry.