wwPDB X-ray Structure Validation Summary Report (i)

Jun 12, 2024 – 09:28 AM EDT

PDB ID	:	2I9U
Title	:	Crystal Structure of Guanine Deaminase from C. acetobutylicum with bound guanine in the active site
Authors	:	Kumaran, D.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on	:	2006-09-06
Resolution	:	2.05 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

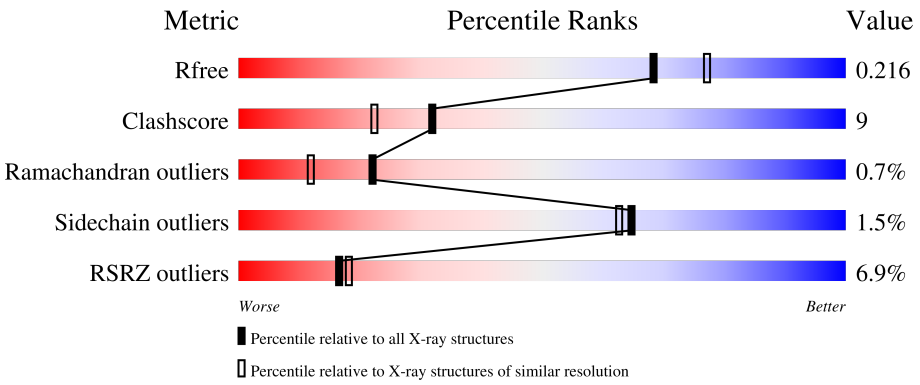
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.05 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}	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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% 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	439	9% 75% 19% • 5%
1	B	439	4% 80% 14% • 5%

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	GOL	A	505	-	X	-	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7136 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 Cytosine/guanine deaminase related protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	419	3343	2149	550	626	18	0	0	0
1	B	419	3343	2149	550	626	18	0	0	0

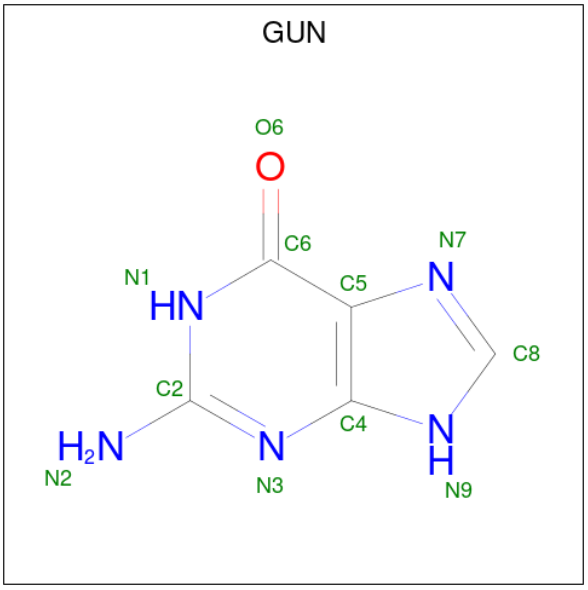
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q97MB6
A	2	SER	-	cloning artifact	UNP Q97MB6
A	3	LEU	-	cloning artifact	UNP Q97MB6
A	4	LEU	-	cloning artifact	UNP Q97MB6
A	432	GLU	-	cloning artifact	UNP Q97MB6
A	433	GLY	-	cloning artifact	UNP Q97MB6
A	434	HIS	-	expression tag	UNP Q97MB6
A	435	HIS	-	expression tag	UNP Q97MB6
A	436	HIS	-	expression tag	UNP Q97MB6
A	437	HIS	-	expression tag	UNP Q97MB6
A	438	HIS	-	expression tag	UNP Q97MB6
A	439	HIS	-	expression tag	UNP Q97MB6
B	1	MET	-	initiating methionine	UNP Q97MB6
B	2	SER	-	cloning artifact	UNP Q97MB6
B	3	LEU	-	cloning artifact	UNP Q97MB6
B	4	LEU	-	cloning artifact	UNP Q97MB6
B	432	GLU	-	cloning artifact	UNP Q97MB6
B	433	GLY	-	cloning artifact	UNP Q97MB6
B	434	HIS	-	expression tag	UNP Q97MB6
B	435	HIS	-	expression tag	UNP Q97MB6
B	436	HIS	-	expression tag	UNP Q97MB6
B	437	HIS	-	expression tag	UNP Q97MB6
B	438	HIS	-	expression tag	UNP Q97MB6
B	439	HIS	-	expression tag	UNP Q97MB6

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

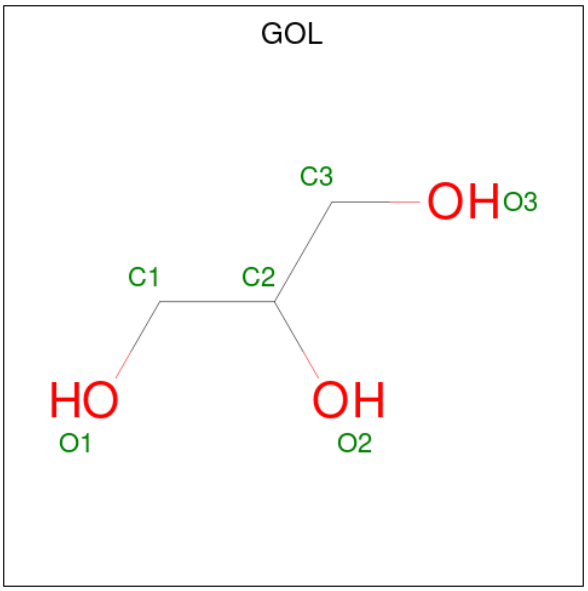
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe 1 1	0	0
2	B	1	Total Fe 1 1	0	0

- Molecule 3 is GUANINE (three-letter code: GUN) (formula: $C_5H_5N_5O$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 11 5 5 1	0	0
3	B	1	Total C N O 11 5 5 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	205	205	205	0	0
			Total	O		
5	B	215	215	215	0	0

3 Residue-property plots (i)

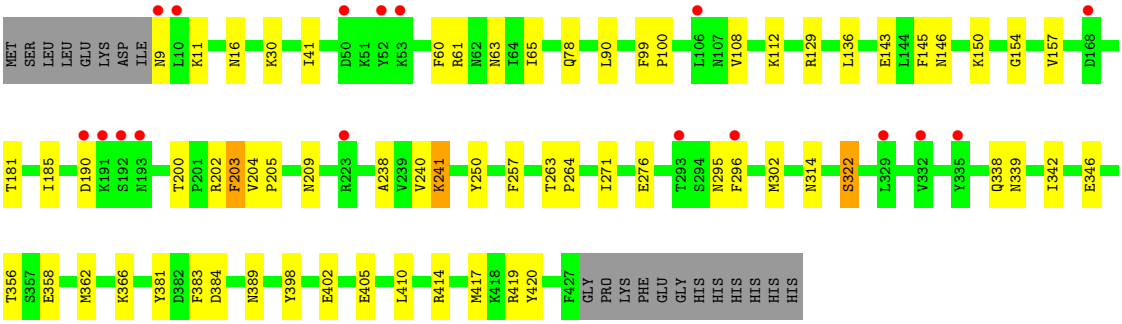
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Cytosine/guanine deaminase related protein

Chain A:

• Molecule 1: Cytosine/guanine deaminase related protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	87.39Å 88.99Å 139.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.50 – 2.05 46.50 – 2.04	Depositor EDS
% Data completeness (in resolution range)	89.8 (46.50-2.05) 89.1 (46.50-2.04)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.39 (at 2.05Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.194 , 0.224 0.189 , 0.216	Depositor DCC
R_{free} test set	2499 reflections (3.85%)	wwPDB-VP
Wilson B-factor (Å^2)	27.3	Xtriage
Anisotropy	0.342	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 45.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7136	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 3.68% 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: GUN, GOL, FE

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	0.33	0/3414	0.61	0/4605
1	B	0.32	0/3414	0.61	0/4605
All	All	0.33	0/6828	0.61	0/9210

There are no bond length outliers.

There are no bond angle outliers.

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	3343	0	3355	78	0
1	B	3343	0	3355	44	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	11	0	5	0	0
3	B	11	0	5	0	0
4	A	6	0	4	0	0
5	A	205	0	0	4	0
5	B	215	0	0	2	0
All	All	7136	0	6724	119	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 9.

The worst 5 of 119 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:93:TRP:HA	5:A:584:HOH:O	1.81	0.79
1:B:9:ASN:HD21	1:B:11:LYS:HE3	1.48	0.78
1:A:303:MET:HE2	1:A:305:VAL:HG22	1.66	0.78
1:A:78:GLN:HB3	1:A:322:SER:HB2	1.67	0.76
1:A:250:TYR:O	1:A:253:VAL:HG22	1.89	0.72

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	417/439 (95%)	399 (96%)	15 (4%)	3 (1%)	22 12
1	B	417/439 (95%)	399 (96%)	15 (4%)	3 (1%)	22 12
All	All	834/878 (95%)	798 (96%)	30 (4%)	6 (1%)	22 12

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	322	SER
1	B	322	SER
1	B	190	ASP
1	A	203	PHE
1	B	90	LEU

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	374/392 (95%)	368 (98%)	6 (2%)	62	59
1	B	374/392 (95%)	369 (99%)	5 (1%)	69	67
All	All	748/784 (95%)	737 (98%)	11 (2%)	65	62

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	241	LYS
1	B	250	TYR
1	B	419	ARG
1	B	410	LEU
1	A	345	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	161	ASN
1	B	262	ASN
1	B	339	ASN
1	B	314	ASN
1	A	339	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
3	GUN	A	503	2	7,12,12	1.46	2 (28%)	8,17,17	2.58	2 (25%)
3	GUN	B	504	2	7,12,12	1.28	1 (14%)	8,17,17	2.16	2 (25%)
4	GOL	A	505	-	5,5,5	4.75	5 (100%)	5,5,5	6.19	3 (60%)

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	GUN	A	503	2	-	-	0/2/2/2
3	GUN	B	504	2	-	-	0/2/2/2
4	GOL	A	505	-	-	3/4/4/4	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	505	GOL	C3-C2	-8.07	1.21	1.51
4	A	505	GOL	O1-C1	4.54	1.61	1.42
4	A	505	GOL	O3-C3	3.27	1.56	1.42
4	A	505	GOL	C1-C2	-2.95	1.40	1.51
4	A	505	GOL	O2-C2	-2.76	1.35	1.43

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	505	GOL	O3-C3-C2	11.34	161.43	110.38
4	A	505	GOL	O2-C2-C3	7.00	138.16	109.18
3	A	503	GUN	O6-C6-N1	6.27	128.06	120.62
3	B	504	GUN	O6-C6-N1	5.30	126.91	120.62
4	A	505	GOL	O1-C1-C2	3.55	126.35	110.38

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	505	GOL	O1-C1-C2-C3
4	A	505	GOL	C1-C2-C3-O3
4	A	505	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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	419/439 (95%)	0.36	41 (9%)	7	8	16, 29, 52, 66	0
1	B	419/439 (95%)	0.16	17 (4%)	37	40	17, 29, 46, 66	0
All	All	838/878 (95%)	0.26	58 (6%)	16	18	16, 29, 51, 66	0

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	91	LEU	7.8
1	A	245	LYS	5.1
1	A	246	LYS	5.0
1	A	241	LYS	4.3
1	A	242	SER	4.1

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
3	GUN	A	503	11/11	0.71	0.37	32,36,38,40	0
4	GOL	A	505	6/6	0.83	0.32	42,44,45,49	0
2	FE	B	502	1/1	0.92	0.12	45,45,45,45	1
3	GUN	B	504	11/11	0.94	0.14	27,32,34,38	0
2	FE	A	501	1/1	0.99	0.04	41,41,41,41	0

6.5 Other polymers (i)

There are no such residues in this entry.