WORLDWIDE PDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Jan 31, 2016 – 07:41 PM GMT

PDB ID	:	1GTM
Title	:	STRUCTURE OF GLUTAMATE DEHYDROGENASE
Authors	:	Yip, K.S.P.; Stillman, T.J.; Britton, K.L.; Pasquo, A.; Rice, D.W.
Deposited on	:	1996-08-22
Resolution	:	2.20 Å(reported)

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

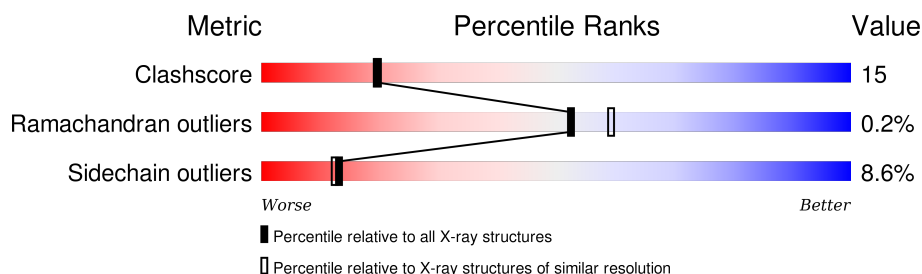|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	Percentile Ranks	Value
Clashscore		15
Ramachandran outliers		0.2%
Sidechain outliers		8.6%

Worse *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)

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 <=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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	419	58% 33% 6% •
1	B	419	66% 27% 6%
1	C	419	65% 28% 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
2	SO4	A	421	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	C	420	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10224 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 GLUTAMATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	S	0	0	0
			3292	2107	554	618	13			
1	B	417	Total	C	N	O	S	0	0	0
			3292	2107	554	618	13			
1	C	417	Total	C	N	O	S	0	0	0
			3292	2107	554	618	13			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	ALA	GLN	CONFLICT	UNP P80319
B	3	ALA	GLN	CONFLICT	UNP P80319
C	3	ALA	GLN	CONFLICT	UNP P80319

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O$_4$S).

SO4
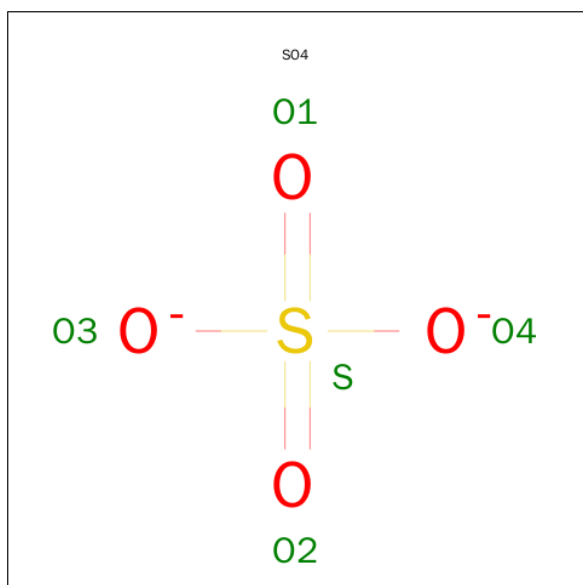
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total O S 5 4 1			0	0
2	B	1	Total O S 5 4 1			0	0
2	C	1	Total O S 5 4 1			0	0
2	B	1	Total O S 5 4 1			0	0
2	A	1	Total O S 5 4 1			0	0
2	C	1	Total O S 5 4 1			0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	107	Total O 107 107		0	0
3	B	112	Total O 112 112		0	0
3	C	99	Total O 99 99		0	0

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.

Note EDS was not executed.

- Molecule 1: GLUTAMATE DEHYDROGENASE

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4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α, β, γ	167.20Å 167.20Å 172.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.20	Depositor
% Data completeness (in resolution range)	93.2 (10.00-2.20)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.174 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10224	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

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: SO4

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	0.99	25/3365 (0.7%)	1.65	53/4560 (1.2%)
1	B	0.99	26/3365 (0.8%)	1.71	73/4560 (1.6%)
1	C	1.00	26/3365 (0.8%)	1.69	58/4560 (1.3%)
All	All	0.99	77/10095 (0.8%)	1.68	184/13680 (1.3%)

The worst 5 of 77 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	282	GLU	CD-OE2	8.64	1.35	1.25
1	A	282	GLU	CD-OE1	8.25	1.34	1.25
1	B	7	GLU	CD-OE2	8.24	1.34	1.25
1	B	282	GLU	CD-OE1	7.84	1.34	1.25
1	C	371	GLU	CD-OE2	7.78	1.34	1.25

The worst 5 of 184 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	32	ARG	NE-CZ-NH1	16.34	128.47	120.30
1	A	64	ARG	NE-CZ-NH2	-15.60	112.50	120.30
1	B	64	ARG	NE-CZ-NH2	-15.24	112.68	120.30
1	C	406	ARG	NE-CZ-NH1	13.17	126.89	120.30
1	B	64	ARG	NE-CZ-NH1	12.90	126.75	120.30

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	3292	0	3290	109	0
1	B	3292	0	3290	89	0
1	C	3292	0	3290	97	0
2	A	10	0	0	3	0
2	B	10	0	0	0	0
2	C	10	0	0	3	0
3	A	107	0	0	0	0
3	B	112	0	0	0	0
3	C	99	0	0	0	0
All	All	10224	0	9870	294	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 15.

The worst 5 of 294 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:8:ILE:CD1	1:B:9:VAL:N	1.99	1.25
1:B:8:ILE:HD12	1:B:9:VAL:N	1.52	1.23
1:B:8:ILE:HD13	1:B:8:ILE:C	1.55	1.19
1:B:8:ILE:CD1	1:B:8:ILE:C	2.03	1.18
1:A:25:GLU:OE1	1:A:419:HIS:HD2	1.28	1.16

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	415/419 (99%)	393 (95%)	20 (5%)	2 (0%)	34	35
1	B	415/419 (99%)	401 (97%)	14 (3%)	0	100	100
1	C	415/419 (99%)	396 (95%)	18 (4%)	1 (0%)	52	59
All	All	1245/1257 (99%)	1190 (96%)	52 (4%)	3 (0%)	52	59

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	ASP
1	C	4	ASP
1	A	304	LYS

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	343/345 (99%)	314 (92%)	29 (8%)	13	13
1	B	343/345 (99%)	312 (91%)	31 (9%)	12	11
1	C	343/345 (99%)	315 (92%)	28 (8%)	14	13
All	All	1029/1035 (99%)	941 (91%)	88 (9%)	13	12

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	117	ARG
1	B	264	LYS
1	C	303	LYS
1	B	132	ASP
1	B	222	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	386	ASN
1	A	419	HIS
1	B	386	ASN
1	A	358	ASN
1	B	265	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

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	SO4	A	420	-	4,4,4	1.00	0	6,6,6	0.23	0
2	SO4	A	421	-	4,4,4	1.81	1 (25%)	6,6,6	0.27	0
2	SO4	B	420	-	4,4,4	0.83	0	6,6,6	0.82	0
2	SO4	B	421	-	4,4,4	0.72	0	6,6,6	0.53	0
2	SO4	C	420	-	4,4,4	0.91	0	6,6,6	0.28	0
2	SO4	C	421	-	4,4,4	1.18	0	6,6,6	0.16	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	SO4	A	420	-	-	0/0/0/0	0/0/0/0
2	SO4	A	421	-	-	0/0/0/0	0/0/0/0
2	SO4	B	420	-	-	0/0/0/0	0/0/0/0
2	SO4	B	421	-	-	0/0/0/0	0/0/0/0
2	SO4	C	420	-	-	0/0/0/0	0/0/0/0
2	SO4	C	421	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	421	SO4	O1-S	2.11	1.54	1.47

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	421	SO4	3	0
2	C	420	SO4	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)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates (i)

EDS was not executed - this section will therefore be empty.

6.4 Ligands (i)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers (i)

EDS was not executed - this section will therefore be empty.