

wwPDB X-ray Structure Validation Summary Report (i)

Dec 13, 2023 – 11:17 am GMT

PDB ID 2YDA

> Title Sulfolobus sulfataricus 2-keto-3-deoxygluconate aldolase Y103F, Y130F, A198F

Authors : Crennell, S.J.; Royer, S.F.; Angelopoulou, M.; Hough, D.W.; Danson, M.J.;

Bull, S.D.

Deposited on 2011-03-18

Resolution 1.91 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 (1)) were used in the production of this report:

MolProbity 4.02b-467

> 1.8.4, CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13

EDS 2.36

20191225.v01 (using entries in the PDB archive December 25th 2019) Percentile statistics

> Refmac 5.8.0158

CCP4 7.0.044 (Gargrove)

Ideal geometry (proteins) Engh & Huber (2001) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

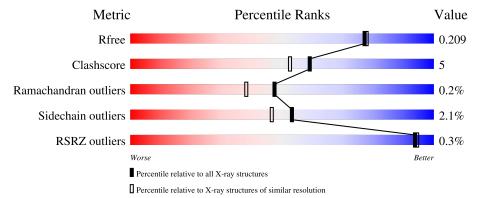
Validation Pipeline (wwPDB-VP) 2.36

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 1.91 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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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	294	89%	10%	
1	В	294	89%	10%	•

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	GOL	A	1294	_	-	X	-



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5275 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.

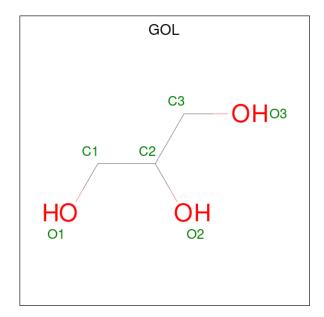
• Molecule 1 is a protein called 2-KETO-3-DEOXY GLUCONATE ALDOLASE.

\mathbf{Mol}	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	292	Total	С	N	О	S	0	16	0
1	11	232	2423	1571	391	455	6	U	10	
1	B	293	Total	С	N	Ο	S	0	18	0
1	D	290	2445	1583	395	461	6		10	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	PHE	TYR	TYR engineered mutation	
A	130	PHE	TYR	engineered mutation	UNP O54288
A	198	PHE	ALA	engineered mutation	UNP O54288
В	103	PHE	TYR	engineered mutation	UNP O54288
В	130	PHE	TYR	engineered mutation	UNP O54288
В	198	PHE	ALA	engineered mutation	UNP O54288

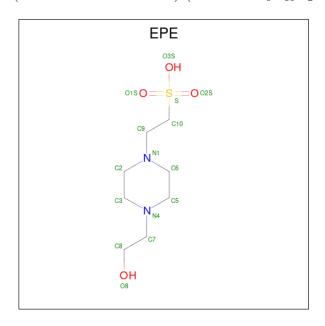
• Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).





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

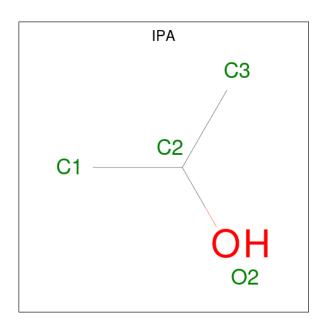
• Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
9	Λ	1	Total	С	N	О	S	0	0
3	A	1	15	8	2	4	1	0	U

• Molecule 4 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C₃H₈O).





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

• Molecule 5 is water.

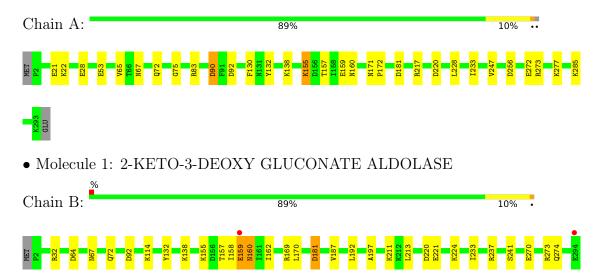
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	173	Total O 173 173	0	0
5	В	181	Total O 181 181	0	0



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: 2-KETO-3-DEOXY GLUCONATE ALDOLASE





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 65 2 2	Depositor	
Cell constants	99.62Å 99.62Å 249.01Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	43.14 - 1.91	Depositor	
rtesolution (A)	43.14 - 1.91	EDS	
% Data completeness	100.0 (43.14-1.91)	Depositor	
(in resolution range)	99.3 (43.14-1.91)	EDS	
R_{merge}	0.10	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.02 (at 1.91Å)	Xtriage	
Refinement program	REFMAC 5.2.0019	Depositor	
D D.	0.172 , 0.210	Depositor	
R, R_{free}	0.172 , 0.209	DCC	
R_{free} test set	2895 reflections (5.07%)	wwPDB-VP	
Wilson B-factor (Å ²)	21.8	Xtriage	
Anisotropy	0.085	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 49.2	EDS	
L-test for twinning ²	$ < L >=0.48, < L^2>=0.31$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
F_o, F_c correlation	0.96	EDS	
Total number of atoms	5275	wwPDB-VP	
Average B, all atoms (Å ²)	20.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.22% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: IPA, EPE, 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	Bo	nd lengths	Bo	nd angles
Mol Chain		RMSZ	# Z > 5	RMSZ	# Z >5
1	A	0.72	0/2512	0.69	0/3391
1	В	1.58	$2/2539 \ (0.1\%)$	0.89	7/3426 (0.2%)
All	All	1.23	$2/5051 \ (0.0\%)$	0.79	7/6817 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
1	В	159[A]	GLU	N-CA	49.76	2.45	1.46
1	В	159[B]	GLU	N-CA	49.76	2.45	1.46

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

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	В	159[A]	GLU	N-CA-CB	-21.59	71.74	110.60
1	В	159[B]	GLU	N-CA-CB	-21.59	71.74	110.60
1	В	158	ILE	O-C-N	-8.23	109.53	122.70
1	В	158	ILE	CA-C-N	6.21	130.86	117.20
1	В	158	ILE	C-N-CA	-5.52	107.90	121.70

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	2423	0	2514	26	0
1	В	2445	0	2532	23	0
2	A	12	0	16	6	0
2	В	18	0	24	1	0
3	A	15	0	17	0	0
4	В	8	0	16	2	0
5	A	173	0	0	2	0
5	В	181	0	0	1	0
All	All	5275	0	5119	47	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 5.

The worst 5 of 47 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash	
Atom-1	Atom-2	${ m distance}({ m \AA})$	$-$ overlap (\AA)	
1:B:270:GLU:OE1	1:B:273:ARG:NH1	2.02	0.90	
1:A:155:LYS:NZ	1:A:157:THR:OG1	2.09	0.83	
1:A:171:ASN:HA	2:A:1294:GOL:H12	1.60	0.83	
1:B:159[A]:GLU:CB	1:B:159[A]:GLU:N	2.45	0.79	
1:B:159[A]:GLU:N	1:B:159[A]:GLU:CA	2.45	0.79	

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	Perce	ntiles
1	A	$306/294\ (104\%)$	302 (99%)	4 (1%)	0	100	100
1	В	308/294~(105%)	303 (98%)	4 (1%)	1 (0%)	41	31
All	All	$614/588 \; (104\%)$	605 (98%)	8 (1%)	1 (0%)	47	38

All (1) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	В	160	ASN

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	$274/260\ (105\%)$	268 (98%)	6 (2%)	52 45		
1	В	277/260 (106%)	271 (98%)	6 (2%)	52 45		
All	All	551/520 (106%)	539 (98%)	12 (2%)	53 45		

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	72	GLN
1	В	132	TYR
1	В	211	LYS
1	В	138	LYS
1	A	132	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

8 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	Во	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
2	GOL	В	1297	-	5,5,5	0.36	0	5,5,5	0.35	0	
4	IPA	В	1299	-	3,3,3	0.52	0	3,3,3	0.36	0	
2	GOL	В	1296	_	5,5,5	0.32	0	5,5,5	0.67	0	
3	EPE	A	1296	-	15,15,15	1.48	1 (6%)	18,20,20	1.36	2 (11%)	
2	GOL	A	1295	-	5,5,5	0.37	0	5,5,5	0.40	0	
4	IPA	В	1298	-	3,3,3	0.66	0	3,3,3	0.71	0	
2	GOL	A	1294	-	5,5,5	0.53	0	5,5,5	1.08	0	
2	GOL	В	1295	-	5,5,5	0.38	0	5,5,5	0.28	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	В	1297	-	-	2/4/4/4	-
2	GOL	В	1296	-	-	2/4/4/4	-
3	EPE	A	1296	-	-	2/9/19/19	0/1/1/1
2	GOL	A	1295	-	-	4/4/4/4	-
2	GOL	A	1294	-	-	2/4/4/4	-
2	GOL	В	1295	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\textup{\AA})$	$\operatorname{Ideal}(ext{\AA})$
3	A	1296	EPE	C10-S	4.70	1.84	1.77

All (2) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
3	A	1296	EPE	O2S-S-C10	3.49	111.12	106.92
3	A	1296	EPE	C5-N4-C3	2.18	113.75	108.83

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1295	GOL	O1-C1-C2-O2
2	A	1295	GOL	O1-C1-C2-C3
2	A	1295	GOL	C1-C2-C3-O3
2	В	1297	GOL	O1-C1-C2-O2
2	В	1297	GOL	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	1297	GOL	1	0
2	A	1295	GOL	2	0
4	В	1298	IPA	2	0
2	A	1294	GOL	4	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)

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, 95^{th} 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	$OWAB(A^2)$	Q<0.9
1	A	292/294 (99%)	-0.43	0 100 100	13, 19, 31, 44	0
1	В	293/294~(99%)	-0.48	2 (0%) 87 89	12, 17, 26, 45	0
All	All	585/588~(99%)	-0.46	2 (0%) 94 94	12, 18, 30, 45	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	294[A]	GLU	3.5
1	В	159[A]	GLU	2.5

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, 95^{th} 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	${f B-factors}({f A}^2)$	Q<0.9
2	GOL	В	1297	6/6	0.76	0.14	49,52,53,53	0
2	GOL	В	1296	6/6	0.85	0.14	47,47,47,49	0
2	GOL	A	1294	6/6	0.87	0.21	37,39,40,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B-factors}({f \AA}^2)$	Q < 0.9
3	EPE	A	1296	15/15	0.88	0.20	55,56,58,58	0
4	IPA	В	1298	4/4	0.90	0.18	26,27,28,30	0
4	IPA	В	1299	4/4	0.90	0.10	34,35,36,36	0
2	GOL	A	1295	6/6	0.91	0.17	33,38,39,40	0
2	GOL	В	1295	6/6	0.97	0.09	19,22,23,23	0

6.5 Other polymers (i)

There are no such residues in this entry.

