wwPDB X-ray Structure Validation Summary Report (i)

Sep 19, 2023 – 02:49 AM EDT

PDB ID	:	5DVX
Title	:	Crystal structure of the catalytic-domain of human carbonic anhydrase IX at 1.6 angstrom resolution
Authors	:	Mahon, B.P.; Socorro, L.; Driscoll, J.M.; McKenna, R.
Deposited on	:	2015-09-21
Resolution	:	1.60 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:

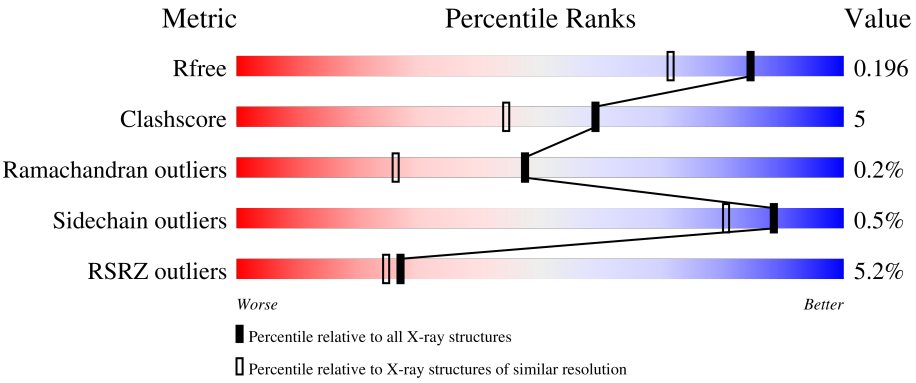
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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	260	7% 91% 8%
1	B	260	4% 90% 8% .

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4847 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 Carbonic anhydrase 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	20	0
			2113	1339	386	384	4			
1	B	255	Total	C	N	O	S	0	16	0
			2042	1295	360	383	4			

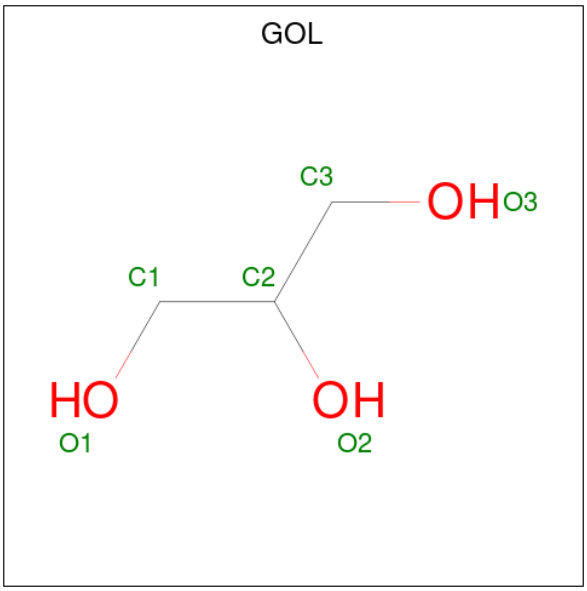
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	174	SER	CYS	engineered mutation	UNP Q16790
A	183	SER	LEU	engineered mutation	UNP Q16790
A	213	LYS	ALA	engineered mutation	UNP Q16790
A	258	LYS	ALA	engineered mutation	UNP Q16790
A	259	TYR	PHE	engineered mutation	UNP Q16790
A	350	SER	MET	engineered mutation	UNP Q16790
B	174	SER	CYS	engineered mutation	UNP Q16790
B	183	SER	LEU	engineered mutation	UNP Q16790
B	213	LYS	ALA	engineered mutation	UNP Q16790
B	258	LYS	ALA	engineered mutation	UNP Q16790
B	259	TYR	PHE	engineered mutation	UNP Q16790
B	350	SER	MET	engineered mutation	UNP Q16790

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Zn	0	0
			3	3		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

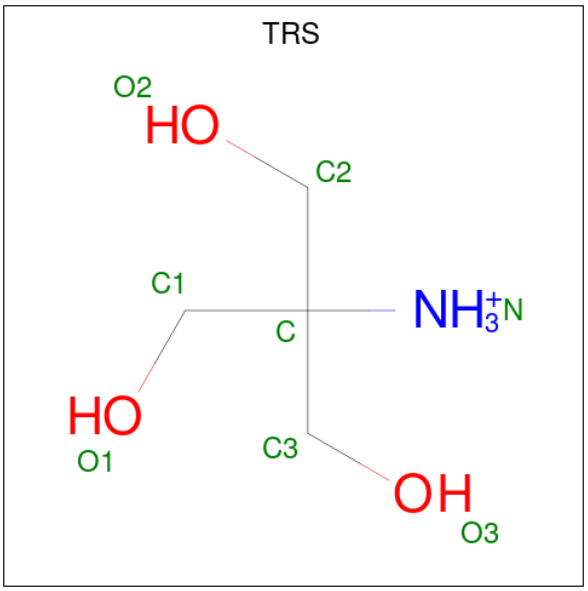


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O 8 4 1 3	0	0

- Molecule 6 is water.

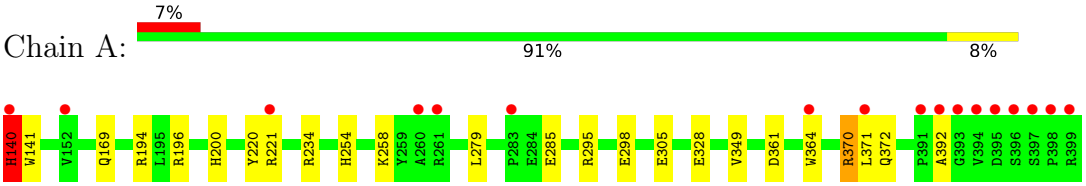
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	355	Total O 362 362	0	7
6	B	271	Total O 279 279	0	8

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.

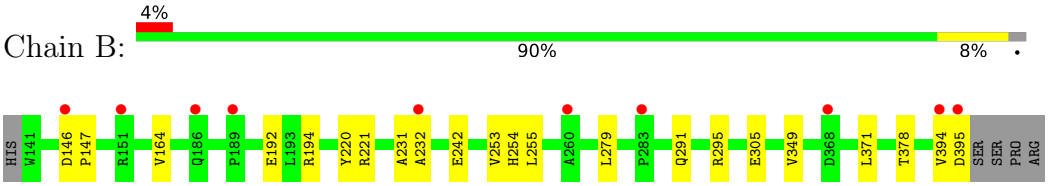
• Molecule 1: Carbonic anhydrase 9

Chain A:



• Molecule 1: Carbonic anhydrase 9

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	57.88Å 102.74Å 108.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.84 – 1.60 19.84 – 1.60	Depositor EDS
% Data completeness (in resolution range)	93.6 (19.84-1.60) 94.6 (19.84-1.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.99 (at 1.60Å)	Xtriage
Refinement program	PHENIX dev_1839	Depositor
R, R_{free}	0.168 , 0.191 0.170 , 0.196	Depositor DCC
R_{free} test set	2000 reflections (2.31%)	wwPDB-VP
Wilson B-factor (Å^2)	12.8	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 57.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4847	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TRS, CL, ZN, 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	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.65	6/2255 (0.3%)	0.62	2/3071 (0.1%)
1	B	0.34	0/2160	0.53	0/2948
All	All	0.53	6/4415 (0.1%)	0.58	2/6019 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	140[A]	HIS	C-O	8.48	1.39	1.23
1	A	140[B]	HIS	C-O	8.48	1.39	1.23
1	A	140[A]	HIS	CG-ND1	-6.50	1.24	1.38
1	A	140[B]	HIS	CG-ND1	-6.50	1.24	1.38
1	A	140[A]	HIS	CG-CD2	6.06	1.46	1.35

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	370[A]	ARG	CB-CA-C	5.16	120.71	110.40
1	A	370[B]	ARG	CB-CA-C	5.16	120.71	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	140[A]	HIS	Peptide
1	A	140[B]	HIS	Peptide

CLOSE-CONTACTS INFOmissingINFO

5.2 Torsion angles (i)

5.2.1 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	277/260 (106%)	270 (98%)	6 (2%)	1 (0%)	34 15
1	B	269/260 (104%)	266 (99%)	3 (1%)	0	100 100
All	All	546/520 (105%)	536 (98%)	9 (2%)	1 (0%)	47 26

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	392	ALA

5.2.2 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	234/214 (109%)	233 (100%)	1 (0%)	91 84
1	B	224/214 (105%)	223 (100%)	1 (0%)	91 84
All	All	458/428 (107%)	456 (100%)	2 (0%)	88 84

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	371	LEU
1	B	371	LEU

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

5.2.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.4 Carbohydrates (i)

There are no monosaccharides in this entry.

5.5 Ligand geometry (i)

Of 14 ligands modelled in this entry, 7 are monoatomic - leaving 7 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	GOL	A	404	-	5,5,5	0.39	0	5,5,5	0.37	0
3	GOL	A	405	-	5,5,5	0.36	0	5,5,5	0.35	0
3	GOL	B	402	-	5,5,5	0.38	0	5,5,5	0.31	0
3	GOL	B	404	-	5,5,5	0.36	0	5,5,5	0.27	0
3	GOL	B	403	-	5,5,5	0.43	0	5,5,5	0.13	0
3	GOL	A	403	-	5,5,5	0.37	0	5,5,5	0.30	0
5	TRS	A	408	-	7,7,7	0.34	0	9,9,9	0.44	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
3	GOL	A	404	-	-	4/4/4/4	-
3	GOL	A	405	-	-	2/4/4/4	-
3	GOL	B	402	-	-	2/4/4/4	-
3	GOL	B	404	-	-	2/4/4/4	-
3	GOL	B	403	-	-	4/4/4/4	-
3	GOL	A	403	-	-	2/4/4/4	-
5	TRS	A	408	-	-	7/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	404	GOL	O1-C1-C2-C3
3	A	405	GOL	O1-C1-C2-C3
3	B	402	GOL	O1-C1-C2-C3
3	B	403	GOL	O1-C1-C2-C3
3	B	404	GOL	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	404	GOL	1	0
3	B	402	GOL	1	0

5.6 Other polymers (i)

There are no such residues in this entry.

5.7 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, 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(Å^2)	Q<0.9
1	A	260/260 (100%)	0.24	17 (6%)	18	17	7, 14, 38, 74	0
1	B	255/260 (98%)	0.24	10 (3%)	39	36	9, 18, 36, 92	0
All	All	515/520 (99%)	0.24	27 (5%)	27	24	7, 16, 38, 92	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140[A]	HIS	9.8
1	A	392	ALA	7.9
1	B	395	ASP	6.5
1	A	371	LEU	6.4
1	A	395	ASP	5.4

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 monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
5	TRS	A	408	8/8	0.53	0.31	52,62,69,71	0
3	GOL	B	404	6/6	0.64	0.20	54,55,57,58	0
3	GOL	B	403	6/6	0.73	0.39	52,56,58,59	0
3	GOL	A	405	6/6	0.78	0.29	47,56,58,59	0
3	GOL	A	403	6/6	0.85	0.12	25,38,43,47	0
3	GOL	A	404	6/6	0.86	0.26	36,56,58,66	0
3	GOL	B	402	6/6	0.94	0.08	25,42,45,46	0
4	CL	A	407	1/1	0.98	0.04	21,21,21,21	0
4	CL	A	406	1/1	0.99	0.04	22,22,22,22	0
2	ZN	A	402	1/1	1.00	0.04	11,11,11,11	0
2	ZN	A	409	1/1	1.00	0.03	12,12,12,12	0
2	ZN	B	401	1/1	1.00	0.04	10,10,10,10	0
4	CL	B	405	1/1	1.00	0.06	14,14,14,14	0
2	ZN	A	401	1/1	1.00	0.04	8,8,8,8	0

6.5 Other polymers (i)

There are no such residues in this entry.