



wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 10:06 am BST

PDB ID : 4YHA
Title : Crystal structure of the complex of Helicobacter pylori alpha-Carbonic Anhydrase with methazolamide
Authors : Roujeinikova, A.; Modak, J.K.
Deposited on : 2015-02-27
Resolution : 2.20 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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	:	2.11
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)	:	2.11

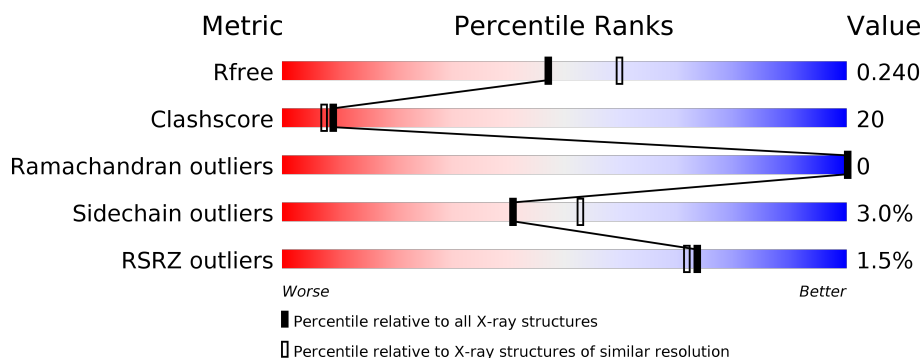
1 Overall quality at a glance

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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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 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 $\leq 5\%$. 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	234	
1	B	234	
1	C	234	
1	D	234	
1	E	234	
1	F	234	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	234	<div> <div>%</div> <div> <div></div> <div>54%</div> <div>41%</div> <div></div> </div> <div>.</div> </div>
1	H	234	<div> <div>%</div> <div> <div></div> <div>56%</div> <div>39%</div> <div></div> </div> <div>..</div> </div>

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	ZN	B	301	-	-	-	X
3	CL	B	302	-	-	X	-
3	CL	H	302	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15354 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 Alpha-carbonic anhydrase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	3	0
			1851	1191	322	334	4			
1	B	221	Total	C	N	O	S	0	1	0
			1807	1160	315	328	4			
1	C	227	Total	C	N	O	S	0	1	0
			1860	1192	326	338	4			
1	D	219	Total	C	N	O	S	0	1	0
			1796	1150	314	328	4			
1	E	225	Total	C	N	O	S	0	1	0
			1847	1185	324	334	4			
1	F	215	Total	C	N	O	S	0	0	0
			1762	1129	309	320	4			
1	G	225	Total	C	N	O	S	0	3	0
			1855	1192	324	335	4			
1	H	225	Total	C	N	O	S	0	0	0
			1841	1180	323	334	4			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	GLY	-	expression tag	UNP K4NGD4
A	15	ILE	-	expression tag	UNP K4NGD4
A	16	ASP	-	expression tag	UNP K4NGD4
A	17	PRO	-	expression tag	UNP K4NGD4
A	18	PHE	-	expression tag	UNP K4NGD4
A	19	THR	-	expression tag	UNP K4NGD4
B	14	GLY	-	expression tag	UNP K4NGD4
B	15	ILE	-	expression tag	UNP K4NGD4
B	16	ASP	-	expression tag	UNP K4NGD4
B	17	PRO	-	expression tag	UNP K4NGD4
B	18	PHE	-	expression tag	UNP K4NGD4
B	19	THR	-	expression tag	UNP K4NGD4
C	14	GLY	-	expression tag	UNP K4NGD4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	15	ILE	-	expression tag	UNP K4NGD4
C	16	ASP	-	expression tag	UNP K4NGD4
C	17	PRO	-	expression tag	UNP K4NGD4
C	18	PHE	-	expression tag	UNP K4NGD4
C	19	THR	-	expression tag	UNP K4NGD4
D	14	GLY	-	expression tag	UNP K4NGD4
D	15	ILE	-	expression tag	UNP K4NGD4
D	16	ASP	-	expression tag	UNP K4NGD4
D	17	PRO	-	expression tag	UNP K4NGD4
D	18	PHE	-	expression tag	UNP K4NGD4
D	19	THR	-	expression tag	UNP K4NGD4
E	14	GLY	-	expression tag	UNP K4NGD4
E	15	ILE	-	expression tag	UNP K4NGD4
E	16	ASP	-	expression tag	UNP K4NGD4
E	17	PRO	-	expression tag	UNP K4NGD4
E	18	PHE	-	expression tag	UNP K4NGD4
E	19	THR	-	expression tag	UNP K4NGD4
F	14	GLY	-	expression tag	UNP K4NGD4
F	15	ILE	-	expression tag	UNP K4NGD4
F	16	ASP	-	expression tag	UNP K4NGD4
F	17	PRO	-	expression tag	UNP K4NGD4
F	18	PHE	-	expression tag	UNP K4NGD4
F	19	THR	-	expression tag	UNP K4NGD4
G	14	GLY	-	expression tag	UNP K4NGD4
G	15	ILE	-	expression tag	UNP K4NGD4
G	16	ASP	-	expression tag	UNP K4NGD4
G	17	PRO	-	expression tag	UNP K4NGD4
G	18	PHE	-	expression tag	UNP K4NGD4
G	19	THR	-	expression tag	UNP K4NGD4
H	14	GLY	-	expression tag	UNP K4NGD4
H	15	ILE	-	expression tag	UNP K4NGD4
H	16	ASP	-	expression tag	UNP K4NGD4
H	17	PRO	-	expression tag	UNP K4NGD4
H	18	PHE	-	expression tag	UNP K4NGD4
H	19	THR	-	expression tag	UNP K4NGD4

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0

Continued on next page...

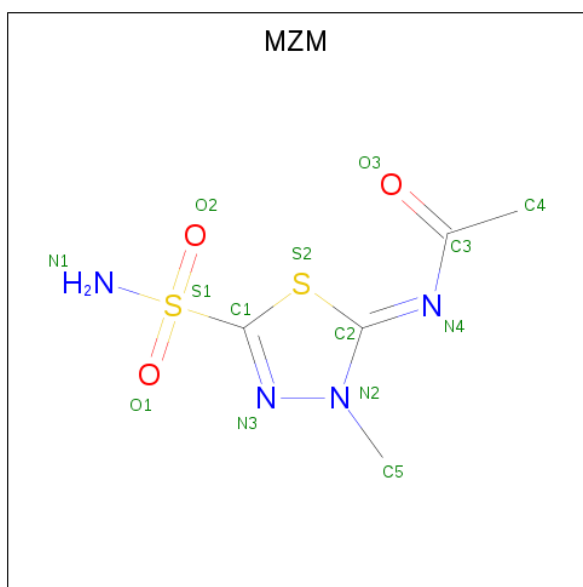
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	1	Total 1	Zn 1	0	0
2	H	1	Total 1	Zn 1	0	0
2	B	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0
2	A	1	Total 1	Zn 1	0	0
2	F	1	Total 1	Zn 1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total 1	Cl 1	0	0
3	E	1	Total 1	Cl 1	0	0
3	H	1	Total 1	Cl 1	0	0
3	B	1	Total 1	Cl 1	0	0
3	C	1	Total 1	Cl 1	0	0
3	A	1	Total 1	Cl 1	0	0

- Molecule 4 is N-(3-methyl-5-sulfamoyl-1,3,4-thiadiazol-2(3H)-ylidene)acetamide (three-letter code: MZM) (formula: C₅H₈N₄O₃S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			14	5	4	3	2		
4	B	1	Total	C	N	O	S	0	0
			14	5	4	3	2		
4	C	1	Total	C	N	O	S	0	0
			14	5	4	3	2		
4	D	1	Total	C	N	O	S	0	0
			14	5	4	3	2		
4	E	1	Total	C	N	O	S	0	0
			14	5	4	3	2		
4	F	1	Total	C	N	O	S	0	0
			14	5	4	3	2		
4	G	1	Total	C	N	O	S	0	0
			14	5	4	3	2		
4	H	1	Total	C	N	O	S	0	0
			14	5	4	3	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		
5	E	1	Total	C	O	0	0
			6	3	3		
5	G	1	Total	C	O	0	0
			6	3	3		

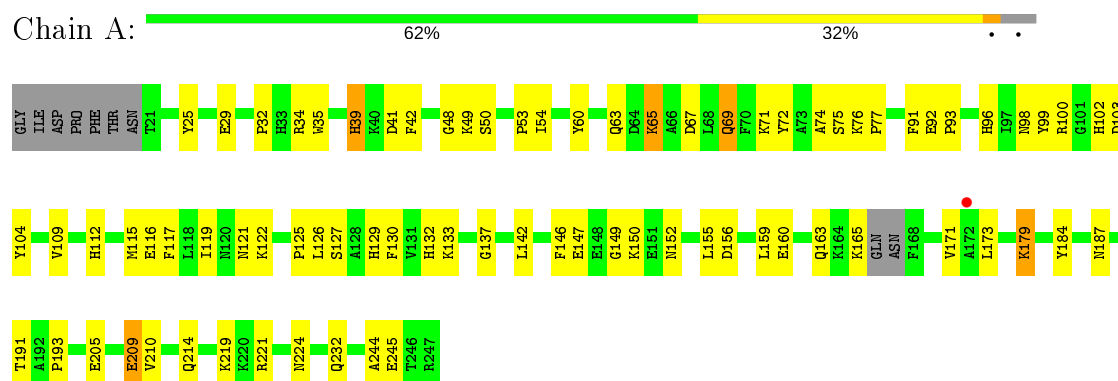
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	78	Total	O	0	0
			78	78		
6	B	66	Total	O	0	0
			66	66		
6	C	129	Total	O	0	0
			129	129		
6	D	31	Total	O	0	0
			31	31		
6	E	121	Total	O	0	0
			121	121		
6	F	34	Total	O	0	0
			34	34		
6	G	58	Total	O	0	0
			58	58		
6	H	68	Total	O	0	0
			68	68		

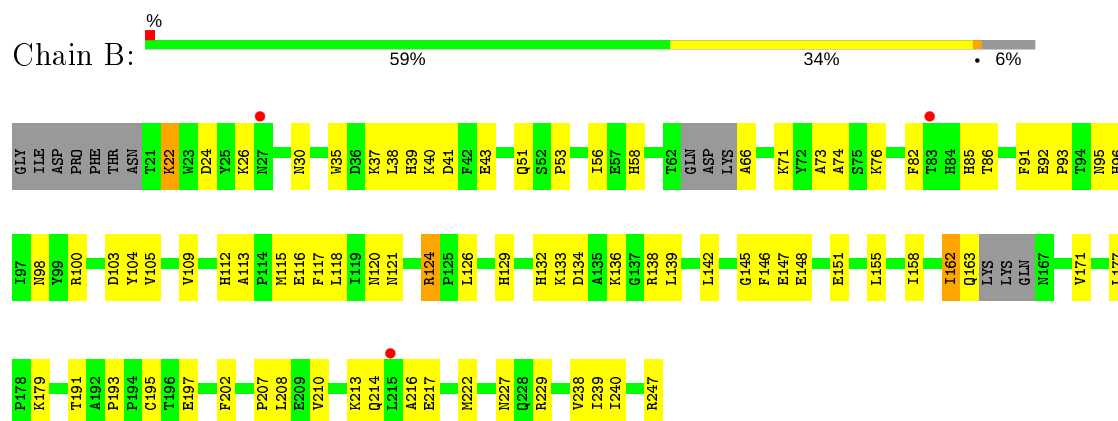
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

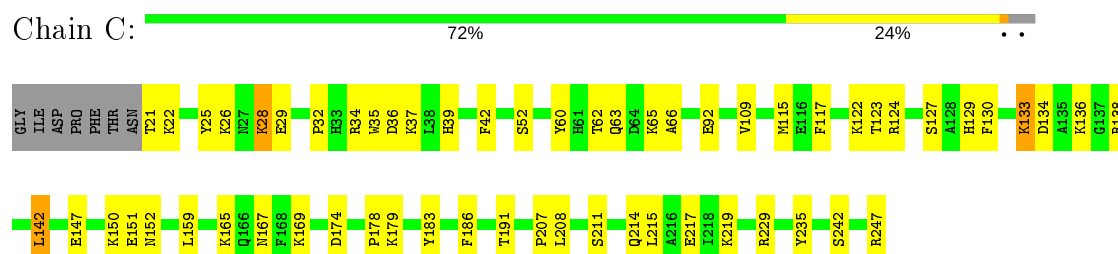
- Molecule 1: Alpha-carbonic anhydrase



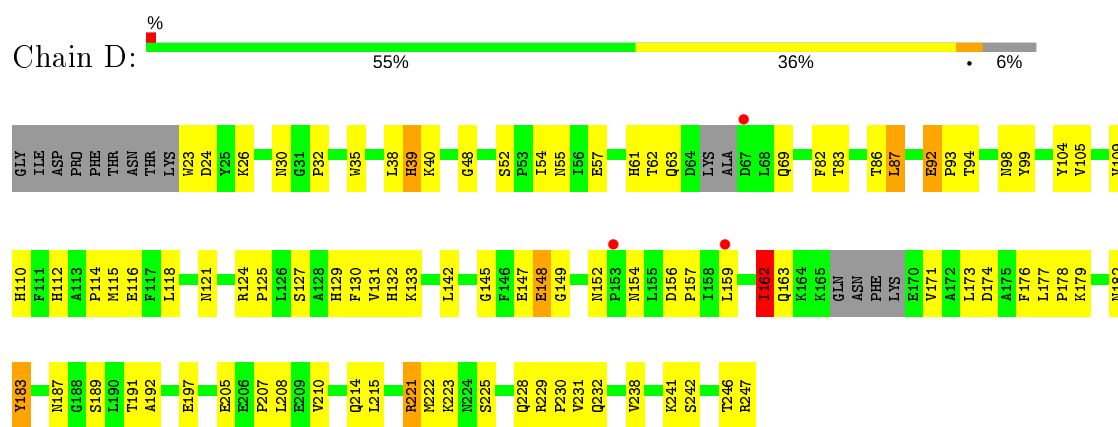
- Molecule 1: Alpha-carbonic anhydrase



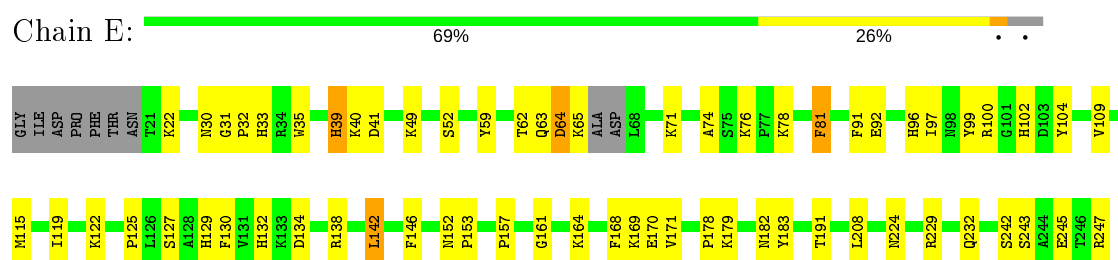
- Molecule 1: Alpha-carbonic anhydrase



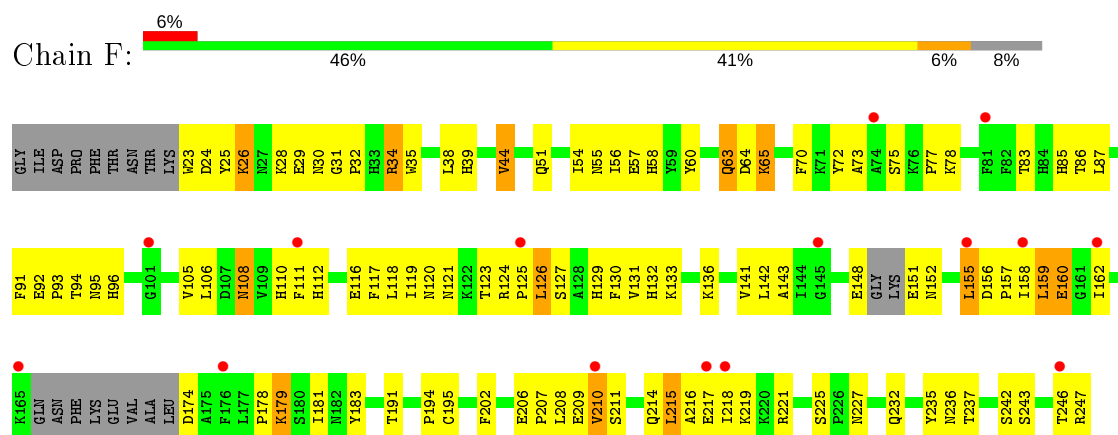
- Molecule 1: Alpha-carbonic anhydrase



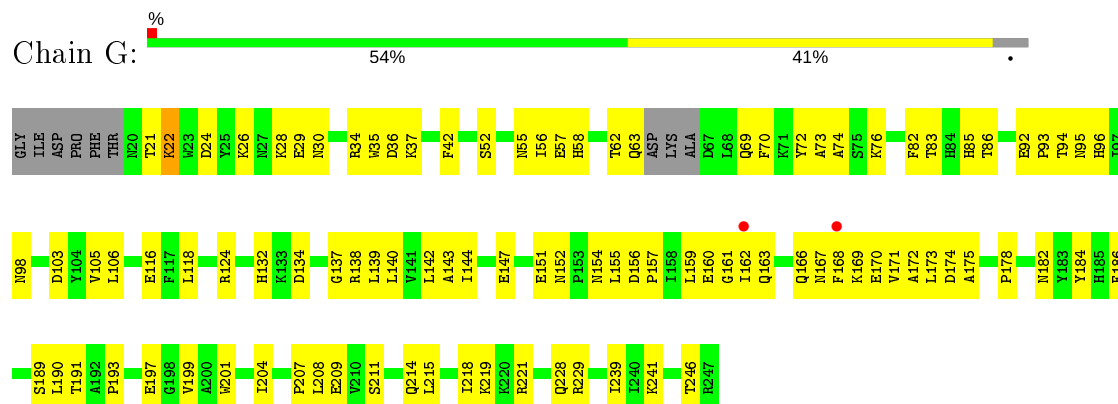
- Molecule 1: Alpha-carbonic anhydrase



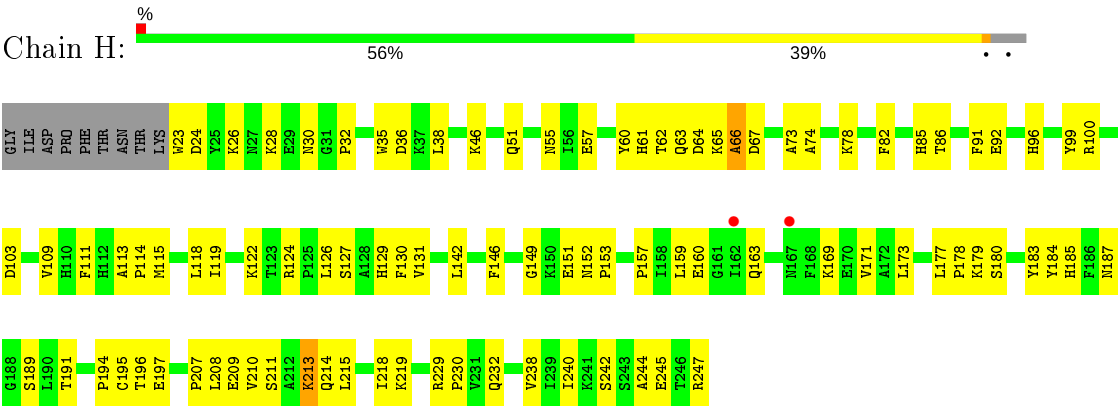
- Molecule 1: Alpha-carbonic anhydrase



- Molecule 1: Alpha-carbonic anhydrase



● Molecule 1: Alpha-carbonic anhydrase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.45Å 135.65Å 166.58Å 90.00° 90.05° 90.00°	Depositor
Resolution (Å)	29.90 – 2.20 29.90 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.1 (29.90-2.20) 97.9 (29.90-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.73 (at 2.20Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.208 , 0.245 0.206 , 0.240	Depositor DCC
R_{free} test set	4703 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtriage
Anisotropy	0.433	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 34.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.460 for h,-k,-l	Xtriage
Reported twinning fraction	0.500 for h,-k,-l	Depositor
Outliers	0 of 93642 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15354	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: GOL, ZN, CL, MZM

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	0.53	0/1914	0.65	0/2588
1	B	0.52	0/1863	0.68	0/2520
1	C	0.57	1/1918 (0.1%)	0.69	2/2594 (0.1%)
1	D	0.47	0/1848	0.73	4/2499 (0.2%)
1	E	0.54	0/1904	0.68	1/2573 (0.0%)
1	F	0.50	0/1814	0.72	0/2453
1	G	0.49	0/1918	0.66	0/2594
1	H	0.50	0/1896	0.69	1/2565 (0.0%)
All	All	0.52	1/15075 (0.0%)	0.69	8/20386 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	35	TRP	CB-CG	-5.04	1.41	1.50

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	87	LEU	CB-CG-CD1	-6.94	99.20	111.00
1	D	221	ARG	NE-CZ-NH1	-6.69	116.95	120.30
1	D	221	ARG	NE-CZ-NH2	6.55	123.57	120.30
1	C	142	LEU	CA-CB-CG	6.46	130.15	115.30
1	D	162	ILE	CG1-CB-CG2	-6.11	97.96	111.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	1851	0	1826	66	0
1	B	1807	0	1762	78	0
1	C	1860	0	1823	46	0
1	D	1796	0	1746	84	0
1	E	1847	0	1813	52	0
1	F	1762	0	1713	109	0
1	G	1855	0	1826	98	0
1	H	1841	0	1798	78	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	1	0	0	1	0
3	B	1	0	0	3	0
3	C	1	0	0	1	0
3	E	1	0	0	0	0
3	G	1	0	0	1	0
3	H	1	0	0	2	0
4	A	14	0	8	1	0
4	B	14	0	8	0	0
4	C	14	0	8	0	0
4	D	14	0	8	2	0
4	E	14	0	8	1	0
4	F	14	0	8	3	0
4	G	14	0	8	1	0
4	H	14	0	8	2	0
5	C	6	0	8	0	0
5	D	6	0	8	0	0
5	E	6	0	8	0	0
5	G	6	0	8	1	0
6	A	78	0	0	11	0
6	B	66	0	0	8	2
6	C	129	0	0	13	3

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	31	0	0	3	0
6	E	121	0	0	9	1
6	F	34	0	0	5	0
6	G	58	0	0	8	0
6	H	68	0	0	4	1
All	All	15354	0	14403	587	4

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 20.

The worst 5 of 587 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:G:162:ILE:HG12	1:G:221:ARG:HH21	1.26	1.01
1:G:162:ILE:HG13	1:G:221:ARG:HE	1.30	0.97
1:H:129:HIS:NE2	3:H:302:CL:CL	2.36	0.94
1:G:163:GLN:HE22	1:G:221:ARG:NH1	1.67	0.91
1:G:159:LEU:HA	1:G:221:ARG:HH12	1.35	0.90

All (4) 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	Interatomic distance (Å)	Clash overlap (Å)
6:B:451:HOH:O	6:C:529:HOH:O[2_846]	1.99	0.21
6:C:511:HOH:O	6:E:500:HOH:O[2_856]	2.04	0.16
6:B:450:HOH:O	6:C:523:HOH:O[2_846]	2.05	0.15
6:H:456:HOH:O	6:H:465:HOH:O[1_655]	2.19	0.01

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	224/234 (96%)	216 (96%)	8 (4%)	0	100	100
1	B	216/234 (92%)	206 (95%)	10 (5%)	0	100	100
1	C	226/234 (97%)	212 (94%)	14 (6%)	0	100	100
1	D	214/234 (92%)	200 (94%)	14 (6%)	0	100	100
1	E	222/234 (95%)	213 (96%)	9 (4%)	0	100	100
1	F	209/234 (89%)	194 (93%)	15 (7%)	0	100	100
1	G	224/234 (96%)	210 (94%)	14 (6%)	0	100	100
1	H	223/234 (95%)	209 (94%)	14 (6%)	0	100	100
All	All	1758/1872 (94%)	1660 (94%)	98 (6%)	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	203/208 (98%)	198 (98%)	5 (2%)	47	60
1	B	197/208 (95%)	193 (98%)	4 (2%)	55	69
1	C	203/208 (98%)	200 (98%)	3 (2%)	65	78
1	D	196/208 (94%)	186 (95%)	10 (5%)	24	29
1	E	202/208 (97%)	199 (98%)	3 (2%)	65	78
1	F	192/208 (92%)	174 (91%)	18 (9%)	8	8
1	G	204/208 (98%)	202 (99%)	2 (1%)	76	86
1	H	200/208 (96%)	198 (99%)	2 (1%)	76	86
All	All	1597/1664 (96%)	1550 (97%)	47 (3%)	41	54

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	215	LEU
1	F	34	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	22	LYS
1	E	64	ASP
1	F	44	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	95	ASN
1	F	63	GLN
1	E	232	GLN
1	B	30	ASN
1	C	63	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 14 are monoatomic - leaving 12 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	$\# Z > 2$
4	MZM	C	303	2	8,14,14	1.75	2 (25%)	10,21,21	3.07	4 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MZM	A	303	2	8,14,14	2.04	3 (37%)	10,21,21	3.54	6 (60%)
5	GOL	E	304	-	5,5,5	0.47	0	5,5,5	0.79	0
4	MZM	G	303	2	8,14,14	1.89	3 (37%)	10,21,21	3.91	6 (60%)
5	GOL	G	304	-	5,5,5	0.38	0	5,5,5	0.81	0
4	MZM	E	303	2	8,14,14	1.87	3 (37%)	10,21,21	3.50	6 (60%)
5	GOL	C	304	-	5,5,5	0.33	0	5,5,5	0.85	0
4	MZM	F	302	2	8,14,14	1.79	2 (25%)	10,21,21	4.21	6 (60%)
4	MZM	H	303	2	8,14,14	1.84	2 (25%)	10,21,21	3.38	5 (50%)
4	MZM	D	302	2	8,14,14	1.80	2 (25%)	10,21,21	4.16	5 (50%)
5	GOL	D	303	-	5,5,5	0.45	0	5,5,5	0.39	0
4	MZM	B	303	2	8,14,14	1.58	2 (25%)	10,21,21	4.20	7 (70%)

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
4	MZM	C	303	2	-	0/2/10/10	0/1/1/1
4	MZM	A	303	2	-	0/2/10/10	0/1/1/1
5	GOL	E	304	-	-	2/4/4/4	-
4	MZM	G	303	2	-	0/2/10/10	0/1/1/1
5	GOL	G	304	-	-	2/4/4/4	-
4	MZM	E	303	2	-	0/2/10/10	0/1/1/1
5	GOL	C	304	-	-	2/4/4/4	-
4	MZM	F	302	2	-	0/2/10/10	0/1/1/1
4	MZM	H	303	2	-	0/2/10/10	0/1/1/1
4	MZM	D	302	2	-	0/2/10/10	0/1/1/1
5	GOL	D	303	-	-	2/4/4/4	-
4	MZM	B	303	2	-	0/2/10/10	0/1/1/1

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	303	MZM	C2-N4	3.49	1.43	1.33
4	F	302	MZM	C2-N4	3.48	1.43	1.33
4	H	303	MZM	C2-N4	3.45	1.43	1.33
4	D	302	MZM	C2-N4	3.39	1.43	1.33
4	G	303	MZM	C2-N4	3.36	1.43	1.33

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	302	MZM	O2-S1-O1	-10.44	101.60	118.76
4	D	302	MZM	O2-S1-O1	-10.37	101.71	118.76
4	G	303	MZM	O2-S1-O1	-9.98	102.35	118.76
4	B	303	MZM	O2-S1-O1	-8.74	104.39	118.76
4	A	303	MZM	O2-S1-O1	-8.49	104.80	118.76

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	304	GOL	O1-C1-C2-C3
5	G	304	GOL	C1-C2-C3-O3
5	E	304	GOL	O1-C1-C2-C3
5	D	303	GOL	O1-C1-C2-C3
5	D	303	GOL	O1-C1-C2-O2

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	303	MZM	1	0
4	G	303	MZM	1	0
5	G	304	GOL	1	0
4	E	303	MZM	1	0
4	F	302	MZM	3	0
4	H	303	MZM	2	0
4	D	302	MZM	2	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 ⓘ

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	225/234 (96%)	-0.17	1 (0%) 92 91	16, 36, 56, 64	0
1	B	221/234 (94%)	-0.04	3 (1%) 75 73	16, 38, 54, 66	0
1	C	227/234 (97%)	-0.44	0 100 100	12, 24, 43, 59	0
1	D	219/234 (93%)	0.04	3 (1%) 75 73	22, 42, 57, 67	0
1	E	225/234 (96%)	-0.53	0 100 100	10, 21, 38, 51	0
1	F	215/234 (91%)	0.51	15 (6%) 16 15	22, 53, 67, 81	0
1	G	225/234 (96%)	-0.02	2 (0%) 84 83	20, 42, 67, 83	0
1	H	225/234 (96%)	-0.27	2 (0%) 84 83	20, 34, 45, 61	0
All	All	1782/1872 (95%)	-0.12	26 (1%) 73 72	10, 36, 61, 83	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	125	PRO	4.1
1	F	101	GLY	3.8
1	F	81	PHE	3.6
1	G	168	PHE	3.1
1	F	218	ILE	2.9

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. 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
2	ZN	B	301	1/1	0.61	0.52	257,257,257,257	0
3	CL	B	302	1/1	0.89	0.11	29,29,29,29	0
5	GOL	C	304	6/6	0.92	0.12	21,26,28,34	0
2	ZN	F	301	1/1	0.92	0.06	102,102,102,102	0
5	GOL	D	303	6/6	0.94	0.10	32,33,35,41	0
5	GOL	E	304	6/6	0.94	0.13	19,22,31,39	0
2	ZN	D	301	1/1	0.95	0.09	62,62,62,62	0
4	MZM	F	302	14/14	0.95	0.12	48,55,64,72	0
2	ZN	H	301	1/1	0.96	0.12	29,29,29,29	0
4	MZM	D	302	14/14	0.96	0.10	30,36,51,54	0
4	MZM	B	303	14/14	0.96	0.13	26,35,55,62	0
3	CL	H	302	1/1	0.96	0.07	36,36,36,36	0
5	GOL	G	304	6/6	0.96	0.15	32,35,39,51	0
2	ZN	A	301	1/1	0.98	0.12	35,35,35,35	0
4	MZM	C	303	14/14	0.98	0.11	12,18,30,36	0
4	MZM	G	303	14/14	0.98	0.12	28,37,45,45	0
4	MZM	E	303	14/14	0.98	0.09	10,18,21,28	0
3	CL	G	302	1/1	0.98	0.09	33,33,33,33	0
4	MZM	H	303	14/14	0.98	0.10	22,33,42,42	0
3	CL	A	302	1/1	0.98	0.07	22,22,22,22	0
4	MZM	A	303	14/14	0.98	0.12	16,23,34,40	0
3	CL	C	302	1/1	0.99	0.12	19,19,19,19	0
2	ZN	G	301	1/1	0.99	0.14	33,33,33,33	0
3	CL	E	302	1/1	0.99	0.09	10,10,10,10	0
2	ZN	C	301	1/1	1.00	0.14	16,16,16,16	0
2	ZN	E	301	1/1	1.00	0.16	20,20,20,20	0

6.5 Other polymers ⓘ

There are no such residues in this entry.