Full wwPDB X-ray Structure Validation Report (i)

Feb 2, 2016 – 12:01 AM GMT

PDB ID	:	8JDW
Title	:	CRYSTAL STRUCTURE OF HUMAN L-ARGININE:GLYCINE AMIDINO-TRANSFERASE IN COMPLEX WITH L-ALANINE
Authors	:	Fritsche, E.; Humm, A.; Huber, R.
Deposited on	:	1998-10-12
Resolution	:	2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

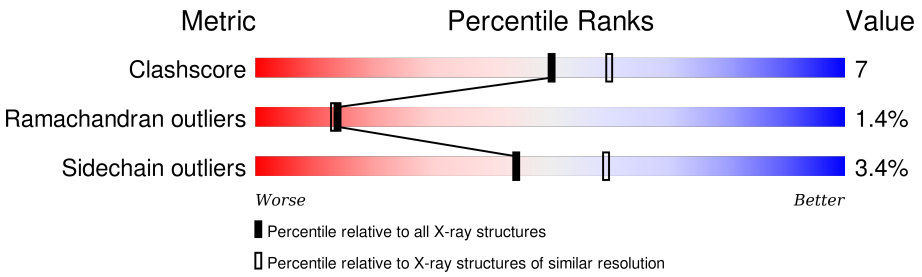
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 2.30 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))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)

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	386	78% 13% • 7%

2 Entry composition (i)

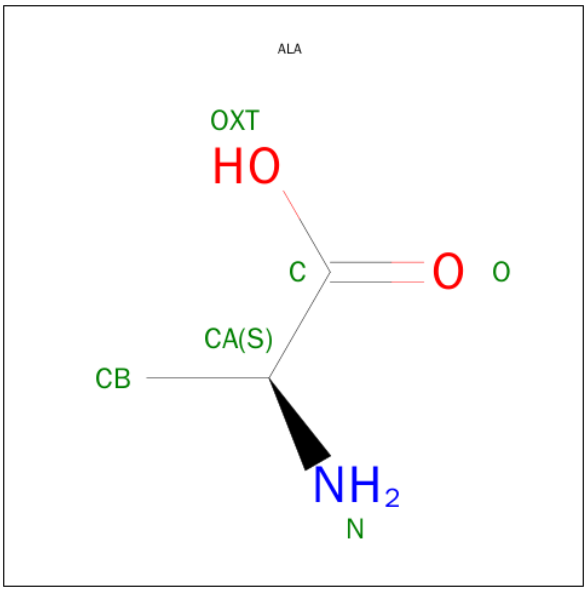
There are 3 unique types of molecules in this entry. The entry contains 3970 atoms, of which 898 are hydrogens and 0 are deuteriums.

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 PROTEIN (L-ARGININE:GLYCINE AMIDINOTRANSFERASE).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	360	3577	1888	639	504	528	18	0	0	0

- Molecule 2 is ALANINE (three-letter code: ALA) (formula: $C_3H_7NO_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
2	A	1	9	3	3	1	2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	H	O		
3	A	128	384	256	128	0	0

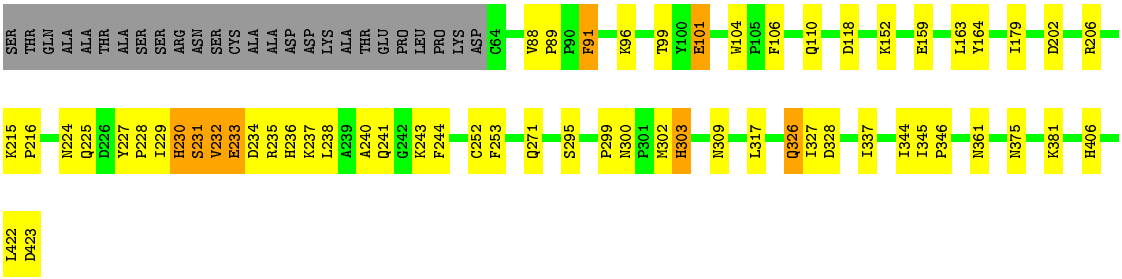
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: PROTEIN (L-ARGININE:GLYCINE AMIDINOTRANSFERASE)

Chain A:



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 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	83.76Å 83.76Å 199.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.30	Depositor
% Data completeness (in resolution range)	91.6 (8.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.84	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.176 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3970	wwPDB-VP
Average B, all atoms ($Å^2$)	24.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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	0.49	0/3027	0.72	0/4114

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	2938	639	2877	41	0
2	A	6	3	4	0	0
3	A	128	256	0	0	0
All	All	3072	898	2881	41	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 7.

All (41) 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:295:SER:H	1:A:326:GLN:HE22	1.29	0.78
1:A:344:ILE:HD11	1:A:375:ASN:O	1.89	0.73
1:A:152:LYS:HE2	1:A:159:GLU:HG2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:LYS:HB3	1:A:229:ILE:HD13	1.80	0.63
1:A:327:ILE:HD11	1:A:337:ILE:HG12	1.81	0.63
1:A:91:PHE:CZ	1:A:96:LYS:HG2	2.37	0.59
1:A:236:HIS:CD2	1:A:299:PRO:HB3	2.40	0.57
1:A:234:ASP:O	1:A:237:LYS:HG2	2.07	0.55
1:A:238:LEU:HB3	1:A:243:LYS:O	2.07	0.55
1:A:295:SER:H	1:A:326:GLN:NE2	2.02	0.55
1:A:228:PRO:HB2	1:A:232:VAL:HG11	1.89	0.54
1:A:104:TRP:CH2	1:A:229:ILE:HD12	2.43	0.54
1:A:229:ILE:HG13	1:A:230:HIS:N	2.24	0.53
1:A:227:TYR:HD2	1:A:229:ILE:HG22	1.75	0.50
1:A:233:GLU:C	1:A:235:ARG:H	2.14	0.49
1:A:234:ASP:C	1:A:236:HIS:N	2.67	0.48
1:A:227:TYR:HD2	1:A:229:ILE:CG2	2.25	0.48
1:A:233:GLU:HA	1:A:235:ARG:HG3	1.96	0.47
1:A:202:ASP:O	1:A:206:ARG:HG3	2.14	0.47
1:A:237:LYS:O	1:A:240:ALA:HB3	2.15	0.47
1:A:236:HIS:CE1	1:A:299:PRO:HD3	2.51	0.45
1:A:422:LEU:O	1:A:423:ASP:HB2	2.15	0.45
1:A:244:PHE:HB3	1:A:271:GLN:OE1	2.17	0.45
1:A:233:GLU:C	1:A:235:ARG:N	2.70	0.45
1:A:244:PHE:N	1:A:244:PHE:CD1	2.85	0.44
1:A:252:CYS:O	1:A:253:PHE:HB3	2.18	0.43
1:A:361:ASN:ND2	1:A:406:HIS:HB3	2.34	0.43
1:A:345:ILE:HA	1:A:346:PRO:HD3	1.87	0.43
1:A:89:PRO:HD3	1:A:163:LEU:CD1	2.49	0.43
1:A:88:VAL:HG21	1:A:110:GLN:HB3	2.02	0.42
1:A:229:ILE:HG13	1:A:230:HIS:H	1.83	0.42
1:A:99:THR:HB	1:A:104:TRP:NE1	2.34	0.42
1:A:381:LYS:HD3	1:A:381:LYS:HA	1.89	0.42
1:A:235:ARG:NH2	1:A:300:ASN:HB2	2.35	0.41
1:A:229:ILE:C	1:A:231:SER:H	2.24	0.41
1:A:106:PHE:CE1	1:A:110:GLN:HG3	2.55	0.41
1:A:215:LYS:HA	1:A:216:PRO:HD3	1.86	0.41
1:A:236:HIS:O	1:A:240:ALA:N	2.52	0.40
1:A:241:GLN:HB2	1:A:243:LYS:HG3	2.03	0.40
1:A:101:GLU:OE2	1:A:231:SER:HB2	2.20	0.40
1:A:302:MET:O	1:A:303:HIS:HB2	2.20	0.40

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	358/386 (93%)	329 (92%)	24 (7%)	5 (1%)	14 13

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230	HIS
1	A	232	VAL
1	A	231	SER
1	A	233	GLU
1	A	303	HIS

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	319/339 (94%)	308 (97%)	11 (3%)	44 59

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	PHE
1	A	101	GLU
1	A	118	ASP
1	A	164	TYR
1	A	179	ILE
1	A	224	ASN

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Mol	Chain	Res	Type
1	A	225	GLN
1	A	309	ASN
1	A	317	LEU
1	A	326	GLN
1	A	328	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	132	ASN
1	A	205	HIS
1	A	225	GLN
1	A	236	HIS
1	A	284	HIS
1	A	309	ASN
1	A	326	GLN
1	A	349	HIS

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)

1 ligand is 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	ALA	A	500	-	2,5,5	0.85	0	0,6,6	0.00	-

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	ALA	A	500	-	-	0/0/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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)

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.