



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 02:04 pm BST

PDB ID : 2AO7  
Title : Adam10 Disintegrin and cysteine- rich domain  
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Deposited on : 2005-08-12  
Resolution : 2.90 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](mailto: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.

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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

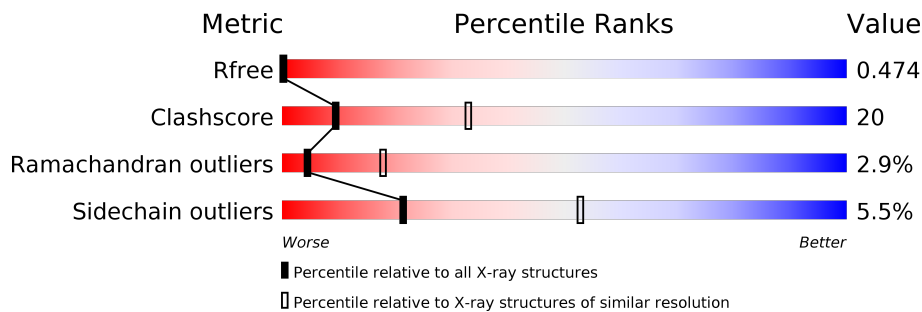
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	192	

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	648	-	-	X	-

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1109 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 ADAM 10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
			Total	C	N	O				S
1	A	146	1099	666	198	209	26	0	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).

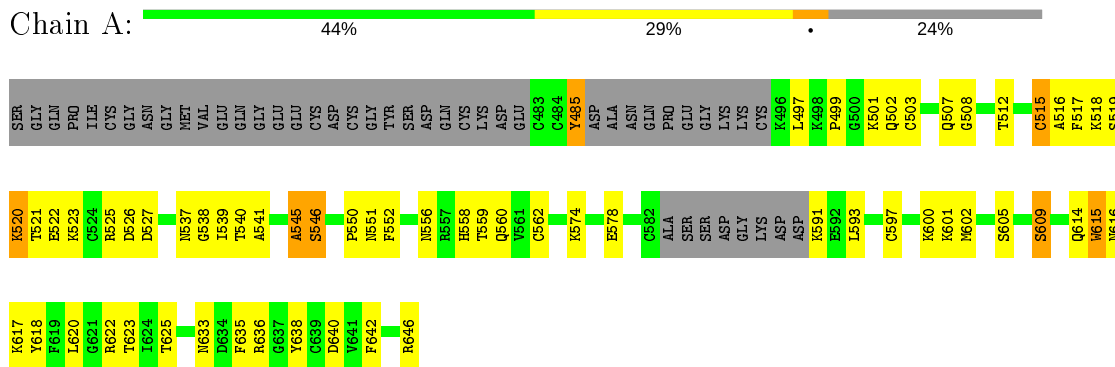


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0

### 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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: ADAM 10



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	146.78Å 146.78Å 146.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.90 25.95 – 2.38	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.90) 98.4 (25.95-2.38)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.50 (at 2.39Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.261 , 0.289 0.478 , 0.474	Depositor DCC
$R_{free}$ test set	574 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.9	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 19.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.67	EDS
Total number of atoms	1109	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [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	0.46	0/1119	0.69	0/1501

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	1099	0	1036	42	11
2	A	10	0	0	1	1
All	All	1109	0	1036	42	11

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.

All (42) 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:556:ASN:HD22	1:A:560:GLN:HE21	1.09	0.94
1:A:559:THR:HG22	1:A:560:GLN:HG3	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:556:ASN:HD22	1:A:560:GLN:NE2	1.75	0.84
1:A:545:ALA:O	1:A:546:SER:HB2	1.90	0.71
1:A:556:ASN:ND2	1:A:560:GLN:HE21	1.89	0.68
1:A:502:GLN:HE21	1:A:516:ALA:HA	1.61	0.65
1:A:518:LYS:HB3	1:A:522:GLU:HG3	1.82	0.61
1:A:545:ALA:O	1:A:546:SER:CB	2.51	0.59
1:A:508:GLY:HA3	1:A:541:ALA:O	2.04	0.58
1:A:523:LYS:NZ	1:A:526:ASP:HA	2.19	0.58
1:A:559:THR:HG22	1:A:560:GLN:CG	2.33	0.57
1:A:633:ASN:O	1:A:636:ARG:HB2	2.06	0.56
1:A:485:TYR:HD2	1:A:485:TYR:H	1.52	0.56
1:A:614:GLN:O	1:A:615:TRP:HB2	2.07	0.55
1:A:556:ASN:O	1:A:559:THR:HB	2.06	0.54
1:A:519:SER:C	1:A:521:THR:H	2.10	0.54
1:A:485:TYR:HA	1:A:497:LEU:HA	1.91	0.53
1:A:622:ARG:HG2	1:A:622:ARG:HH11	1.73	0.53
1:A:623:THR:O	1:A:623:THR:HG22	2.09	0.53
1:A:502:GLN:NE2	1:A:517:PHE:H	2.08	0.51
1:A:552:PHE:CD2	1:A:574:LYS:HA	2.47	0.50
1:A:525:ARG:NH1	2:A:648:SO4:S	2.86	0.49
1:A:518:LYS:O	1:A:538:GLY:HA2	2.13	0.48
1:A:578:GLU:HG3	1:A:601:LYS:HG2	1.96	0.48
1:A:537:ASN:HD21	1:A:540:THR:HG22	1.80	0.47
1:A:485:TYR:CD2	1:A:485:TYR:N	2.83	0.46
1:A:640:ASP:HB3	1:A:642:PHE:H	1.83	0.44
1:A:503:CYS:O	1:A:515:CYS:HB3	2.18	0.43
1:A:616:ASN:OD1	1:A:620:LEU:HA	2.18	0.43
1:A:646:ARG:HD2	1:A:646:ARG:HA	1.84	0.43
1:A:485:TYR:HD2	1:A:485:TYR:N	2.14	0.43
1:A:523:LYS:HZ1	1:A:526:ASP:HA	1.84	0.42
1:A:519:SER:O	1:A:521:THR:N	2.51	0.42
1:A:552:PHE:HB3	1:A:574:LYS:HG3	2.01	0.42
1:A:551:ASN:O	1:A:562:CYS:O	2.38	0.42
1:A:640:ASP:CB	1:A:642:PHE:H	2.33	0.41
1:A:591:LYS:C	1:A:593:LEU:H	2.23	0.41
1:A:597:CYS:SG	1:A:609:SER:HA	2.60	0.41
1:A:620:LEU:HB2	1:A:622:ARG:NH1	2.36	0.41
1:A:519:SER:C	1:A:521:THR:N	2.74	0.40
1:A:507:GLN:HG3	1:A:507:GLN:H	1.66	0.40
1:A:616:ASN:C	1:A:618:TYR:N	2.74	0.40

All (11) 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)
1:A:512:THR:OG1	1:A:605:SER:OG[33_554]	1.66	0.54
1:A:501:LYS:NZ	1:A:635:PHE:O[10_655]	1.96	0.24
1:A:502:GLN:CD	1:A:635:PHE:CZ[10_655]	1.99	0.21
1:A:525:ARG:CG	1:A:622:ARG:NH2[24_555]	2.03	0.17
1:A:521:THR:OG1	1:A:602:MET:SD[33_554]	2.07	0.13
1:A:502:GLN:CG	1:A:635:PHE:CE2[10_655]	2.09	0.11
1:A:502:GLN:CG	1:A:635:PHE:CZ[10_655]	2.12	0.08
1:A:600:LYS:CE	1:A:617:LYS:CE[43_655]	2.14	0.06
1:A:622:ARG:NE	2:A:648:SO4:O2[24_555]	2.17	0.03
1:A:499:PRO:CB	1:A:638:TYR:CD2[10_655]	2.18	0.02
1:A:527:ASP:O	1:A:558:HIS:NE2[24_555]	2.18	0.02

### 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	140/192 (73%)	123 (88%)	13 (9%)	4 (3%)	<b>4</b> <b>18</b>

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	545	ALA
1	A	546	SER
1	A	520	LYS
1	A	550	PRO

#### 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	128/165 (78%)	121 (94%)	7 (6%)	21 53

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	485	TYR
1	A	515	CYS
1	A	520	LYS
1	A	539	ILE
1	A	609	SER
1	A	615	TRP
1	A	625	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	502	GLN
1	A	507	GLN
1	A	560	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](#)

2 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	647	-	4,4,4	0.26	0	6,6,6	0.15	0
2	SO4	A	648	1	4,4,4	0.28	0	6,6,6	0.08	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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	648	SO4	1	1

## 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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.