



Full wwPDB X-ray Structure Validation Report ⓘ

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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
A user guide is available at
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

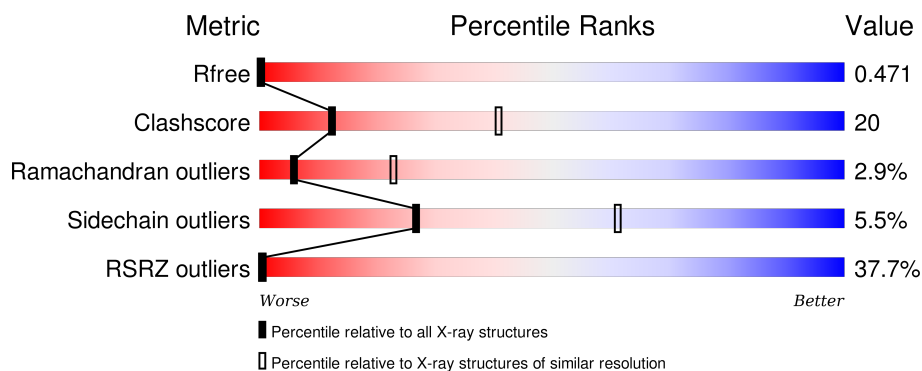
1 Overall quality at a glance

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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (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 ≥ 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 $\leq 5\%$. 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	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.

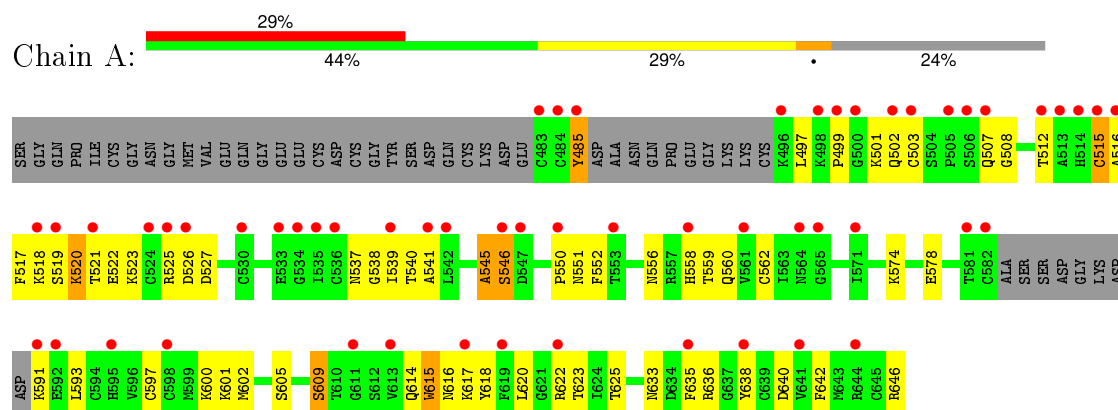
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	146	1099	666	198	209	26	0	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 1: ADAM 10



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 3 2	Depositor
Cell constants a, b, c, α , β , γ	146.78 Å 146.78 Å 146.78 Å 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
$\langle I/\sigma(I) \rangle$ ¹	6.50 (at 2.39 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.261 , 0.289 0.478 , 0.471	Depositor DCC
R_{free} test set	326 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	44.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 18.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 11118 reflections	Xtriage
F_o, F_c correlation	0.67	EDS
Total number of atoms	1109	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage'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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 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

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:523:LYS:NZ	1:A:526:ASP:HA	2.19	0.58
1:A:508:GLY:HA3	1:A:541:ALA:O	2.04	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:HG22	1:A:623:THR:O	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:N	1:A:485:TYR:CD2	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:N	1:A:485:TYR:HD2	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:620:LEU:HB2	1:A:622:ARG:NH1	2.36	0.41
1:A:597:CYS:SG	1:A:609:SER:HA	2.60	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%)	6	23

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%)	27	61

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	0.19	0
2	SO4	A	648	1	4,4,4	0.24	0	6,6,6	0.13	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	SO4	A	647	-	-	0/0/0/0	0/0/0/0
2	SO4	A	648	1	-	0/0/0/0	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.

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 ⓘ

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	146/192 (76%)	1.69	55 (37%) 0 0	21, 40, 52, 60	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	499	PRO	4.8
1	A	611	GLY	4.7
1	A	483	CYS	4.4
1	A	550	PRO	4.4
1	A	536	CYS	3.9
1	A	496	LYS	3.8
1	A	546	SER	3.7
1	A	547	ASP	3.6
1	A	500	GLY	3.3
1	A	513	ALA	3.2
1	A	526	ASP	3.2
1	A	581	THR	3.2
1	A	582	CYS	3.2
1	A	534	GLY	3.1
1	A	505	PRO	3.1
1	A	506	SER	3.0
1	A	516	ALA	3.0
1	A	644	ARG	3.0
1	A	503	CYS	3.0
1	A	535	ILE	3.0
1	A	507	GLN	2.9
1	A	553	THR	2.9
1	A	598	CYS	2.9
1	A	613	VAL	2.8
1	A	591	LYS	2.7
1	A	485	TYR	2.7
1	A	595	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	541	ALA	2.6
1	A	561	VAL	2.6
1	A	622	ARG	2.5
1	A	533	GLU	2.5
1	A	592	GLU	2.5
1	A	558	HIS	2.5
1	A	571	ILE	2.5
1	A	525	ARG	2.5
1	A	514	HIS	2.4
1	A	638	TYR	2.4
1	A	564	ASN	2.4
1	A	521	THR	2.3
1	A	484	CYS	2.3
1	A	498	LYS	2.3
1	A	502	GLN	2.3
1	A	539	ILE	2.3
1	A	565	GLY	2.3
1	A	635	PHE	2.3
1	A	518	LYS	2.3
1	A	617	LYS	2.2
1	A	641	VAL	2.2
1	A	515	CYS	2.2
1	A	524	CYS	2.2
1	A	512	THR	2.1
1	A	619	PHE	2.1
1	A	530	CYS	2.1
1	A	519	SER	2.1
1	A	542	LEU	2.0

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 carbohydrates 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. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	A	647	5/5	0.61	0.37	0.32	61,62,62,63	0
2	SO4	A	648	5/5	0.60	0.23	-	87,87,88,88	0

6.5 Other polymers

There are no such residues in this entry.