



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1I3H
Title : CONCANAVALLIN A-DIMANNOSE STRUCTURE
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Deposited on : 2001-02-15
Resolution : 1.20 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

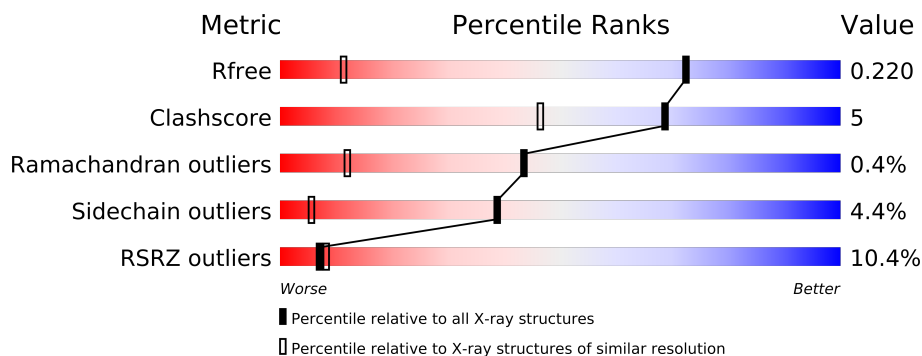
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.20 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}	66092	1038 (1.26-1.14)
Clashscore	79885	1158 (1.26-1.14)
Ramachandran outliers	78287	1106 (1.26-1.14)
Sidechain outliers	78261	1104 (1.26-1.14)
RSRZ outliers	66119	1038 (1.26-1.14)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	237	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	MN	A	240	-	X
4	CA	A	241	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2174 atoms, of which 0 are hydrogen and 0 are deuterium.

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 CONCAVALIN A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	25	11	0
			1896	1193	321	379	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	151	ASP	GLU	SEE REMARK 999	UNP P02866
A	155	GLU	ARG	SEE REMARK 999	UNP P02866

- Molecule 2 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	2	Total	C	O	0	0
			23	12	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	151	ASP	GLU	SEE REMARK 999	UNP P02866
A	155	GLU	ARG	SEE REMARK 999	UNP P02866

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mn	0	0
			1	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Ca 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	253	Total 253	O 253	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	90.90Å 86.41Å 65.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.20 19.51 – 1.20	Depositor EDS
% Data completeness (in resolution range)	95.1 (40.00-1.20) 95.3 (19.51-1.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 1.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.167 , 0.190 0.203 , 0.220	Depositor DCC
R_{free} test set	7747 reflections (10.13%)	DCC
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 52.5	EDS
Estimated twinning fraction	0.007 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 76521 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2174	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, MN, MAN

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	1.87	6/1939 (0.3%)	1.46	19/2639 (0.7%)

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

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	60[A]	ARG	CZ-NH2	50.34	1.98	1.33
1	A	60[B]	ARG	CZ-NH2	50.34	1.98	1.33
1	A	30	LYS	CE-NZ	14.09	1.84	1.49
1	A	69	ASN	CB-CG	10.52	1.75	1.51
1	A	42	MET	SD-CE	-8.20	1.31	1.77
1	A	114	LYS	CE-NZ	7.96	1.69	1.49

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	60[A]	ARG	NH1-CZ-NH2	-29.72	86.70	119.40
1	A	60[B]	ARG	NH1-CZ-NH2	-29.72	86.70	119.40
1	A	120	THR	O-C-N	16.56	149.19	122.70
1	A	69	ASN	CB-CG-ND2	-14.99	80.72	116.70
1	A	60[A]	ARG	NE-CZ-NH1	13.76	127.18	120.30
1	A	60[B]	ARG	NE-CZ-NH1	13.76	127.18	120.30
1	A	120	THR	C-N-CA	13.37	155.12	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	120	THR	CA-C-N	-12.14	90.49	117.20
1	A	69	ASN	CB-CG-OD1	9.43	140.45	121.60
1	A	30	LYS	CD-CE-NZ	-8.40	92.37	111.70
1	A	121	HIS	C-N-CA	6.35	137.56	121.70
1	A	69	ASN	CB-CA-C	5.87	122.14	110.40
1	A	69	ASN	N-CA-CB	-5.70	100.33	110.60
1	A	151	ASP	CA-CB-CG	5.67	125.88	113.40
1	A	158	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	A	134	SER	C-N-CA	-5.52	107.89	121.70
1	A	158	ARG	NE-CZ-NH1	5.27	122.93	120.30
1	A	87	GLU	N-CA-CB	-5.12	101.39	110.60
1	A	136	ASP	CB-CG-OD2	5.10	122.89	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	60[A]	ARG	Sidechain
1	A	69	ASN	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1896	0	0	9	2
2	A	23	0	0	0	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	253	0	0	5	3
All	All	2174	0	0	9	5

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (9) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:150:THR:CG2	5:A:283:HOH:O	2.53	0.56
1:A:117[B]:SER:OG	1:A:119:SER:OG	2.24	0.55
1:A:150:THR:CG2	5:A:402:HOH:O	2.59	0.50
1:A:51[A]:HIS:ND1	5:A:277:HOH:O	2.35	0.47
1:A:162:ASN:C	1:A:162:ASN:ND2	2.69	0.46
1:A:136:ASP:CG	1:A:136:ASP:O	2.55	0.45
1:A:135:LYS:NZ	5:A:398:HOH:O	2.51	0.43
1:A:43:GLN:NE2	5:A:334:HOH:O	2.54	0.40
1:A:96[B]:SER:OG	1:A:169:SER:O	2.40	0.40

All (5) 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	Distance(Å)	Clash(Å)
5:A:477:HOH:O	5:A:477:HOH:O[4_565]	1.59	0.61
5:A:291:HOH:O	5:A:479:HOH:O[2_665]	1.72	0.48
1:A:58:ASP:OD1	1:A:60[A]:ARG:NH1[4_565]	1.76	0.44
5:A:332:HOH:O	5:A:454:HOH:O[6_554]	1.80	0.40
1:A:69:ASN:O	1:A:228[A]:ARG:NH1[6_554]	2.00	0.20

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	246/237 (104%)	239 (97%)	6 (2%)	1 (0%)	43 12

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	GLU

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	214/203 (105%)	205 (96%)	9 (4%)	40 6

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	LYS
1	A	118	ASN
1	A	119	SER
1	A	122	GLU
1	A	135	LYS
1	A	150	THR
1	A	151	ASP
1	A	158	ARG
1	A	162	ASN

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

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

2 carbohydrates 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	MAN	A	238	2	12,12,12	0.75	0	17,17,17	1.91	4 (23%)
2	MAN	A	239	2	10,11,12	0.42	0	11,15,17	0.56	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	MAN	A	238	2	-	0/2/22/22	0/1/1/1
2	MAN	A	239	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	238	MAN	O5-C1-C2	4.65	117.07	109.86
2	A	238	MAN	C1-C2-C3	-4.54	103.34	110.53
2	A	238	MAN	C1-O5-C5	-2.82	108.35	113.40
2	A	238	MAN	O1-C1-C2	2.09	115.38	109.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	236/237 (99%)	0.68	25 (10%) 7 8	18, 20, 28, 39	7 (2%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	150	THR	8.1
1	A	120	THR	7.5
1	A	161	SER	6.1
1	A	162	ASN	5.3
1	A	160	SER	4.5
1	A	122	GLU	4.5
1	A	163	GLY	4.3
1	A	119	SER	3.9
1	A	149	GLY	3.6
1	A	136	ASP	3.4
1	A	117[A]	SER	3.3
1	A	1	ALA	3.2
1	A	202	PRO	3.2
1	A	118	ASN	3.1
1	A	156	LEU	3.1
1	A	123	THR	2.9
1	A	151	ASP	2.7
1	A	6	ALA	2.6
1	A	184	SER	2.6
1	A	27[A]	ILE	2.5
1	A	203	ASP	2.4
1	A	232	LEU	2.4
1	A	69	ASN	2.2
1	A	199	ILE	2.1
1	A	223	SER	2.0

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 ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	MAN	A	239	11/12	0.14	1.92	24,25,27,27	0
2	MAN	A	238	12/12	0.11	-0.23	27,29,30,33	0

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. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	MN	A	240	1/1	0.15	4.96	23,23,23,23	0
4	CA	A	241	1/1	0.17	2.99	25,25,25,25	0

6.5 Other polymers ⓘ

There are no such residues in this entry.