Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 01:52 AM GMT

PDB ID	:	2ENR
Title	:	CO-CRYSTALS OF DEMETALLIZED CONCANAVALIN A WITH CADMIUM HAVING A CADMIUM ION BOUND IN BOTH THE S1 SITE AND THE S2 SITE
Authors	:	Bouckaert, J.; Loris, R.; Wyns, L.
Deposited on	:	1998-07-14
Resolution	:	2.35 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 (1)) were used in the production of this report:

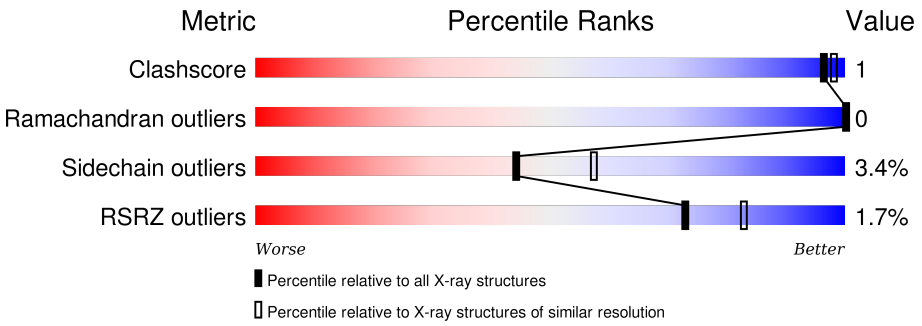
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

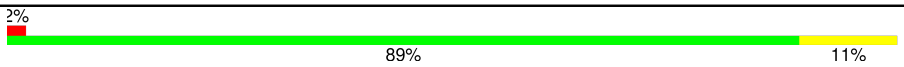
The reported resolution of this entry is 2.35 Å.

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	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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.

Mol	Chain	Length	Quality of chain
1	A	237	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2497 atoms, of which 588 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 CONCANAVALIN A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	237	2202	1141	394	302	363	2	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	97	THR	LEU	CONFLICT	UNP P02866
A	98	GLY	PHE	CONFLICT	UNP P02866
A	100	TYR	PRO	CONFLICT	UNP P02866
A	101	LYS	ILE	CONFLICT	UNP P02866
A	102	GLU	PHE	CONFLICT	UNP P02866
A	104	ASN	-	INSERTION	UNP P02866
A	105	THR	PHE	CONFLICT	UNP P02866
A	107	LEU	THR	CONFLICT	UNP P02866
A	108	SER	MET	CONFLICT	UNP P02866
A	109	TRP	PHE	CONFLICT	UNP P02866
A	110	SER	LEU	CONFLICT	UNP P02866
A	111	PHE	MET	CONFLICT	UNP P02866
A	112	THR	VAL	CONFLICT	UNP P02866
A	113	SER	VAL	CONFLICT	UNP P02866
A	114	LYS	ASN	CONFLICT	UNP P02866
A	115	LEU	LYS	CONFLICT	UNP P02866
A	116	LYS	VAL	CONFLICT	UNP P02866
A	118	ASN	SER	CONFLICT	UNP P02866
A	151	ASP	GLU	CONFLICT	UNP P02866
A	155	GLU	ARG	CONFLICT	UNP P02866

- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cd		
2	A	2	2	2	0	0

- Molecule 3 is water.

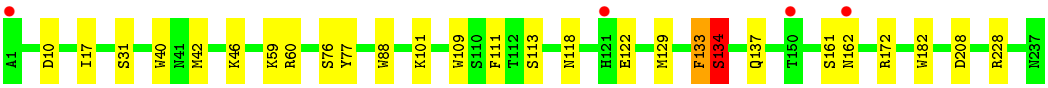
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	H	O		
3	A	99	293	194	99	0	0

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.

- Molecule 1: CONCANAVALIN A

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	63.20Å 87.69Å 89.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.35 9.99 – 2.35	Depositor EDS
% Data completeness (in resolution range)	96.0 (10.00-2.35) 94.6 (9.99-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	7.68 (at 2.36Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.173 , (Not available) 0.163 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	28.2	Xtriage
Anisotropy	0.223	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 46.9	EDS
Estimated twinning fraction	0.013 for -h,-l,-k	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 9923 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	2497	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.01% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CD

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	0.95	6/1850 (0.3%)	1.61	32/2522 (1.3%)

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	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	133	PHE	CB-CG	9.70	1.67	1.51
1	A	133	PHE	CG-CD1	6.77	1.49	1.38
1	A	134	SER	CA-CB	-6.71	1.42	1.52
1	A	133	PHE	CG-CD2	5.56	1.47	1.38
1	A	133	PHE	C-O	5.08	1.33	1.23
1	A	133	PHE	CA-C	5.08	1.66	1.52

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	ARG	NE-CZ-NH2	-12.53	114.03	120.30
1	A	133	PHE	O-C-N	-12.18	103.22	122.70
1	A	133	PHE	CB-CG-CD1	11.77	129.04	120.80
1	A	133	PHE	CD1-CG-CD2	-11.51	103.33	118.30
1	A	133	PHE	CA-C-O	10.71	142.60	120.10
1	A	133	PHE	CA-C-N	-10.16	94.84	117.20
1	A	133	PHE	CB-CG-CD2	8.98	127.08	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	88	TRP	CD1-CG-CD2	8.45	113.06	106.30
1	A	133	PHE	CG-CD1-CE1	8.39	130.03	120.80
1	A	172	ARG	NE-CZ-NH1	7.58	124.09	120.30
1	A	208	ASP	N-CA-CB	-7.48	97.13	110.60
1	A	88	TRP	CE2-CD2-CG	-7.48	101.32	107.30
1	A	134	SER	CA-CB-OG	7.26	130.81	111.20
1	A	133	PHE	CG-CD2-CE2	7.20	128.72	120.80
1	A	40	TRP	CD1-CG-CD2	7.16	112.03	106.30
1	A	172	ARG	CB-CG-CD	-7.01	93.37	111.60
1	A	182	TRP	CE2-CD2-CG	-6.97	101.72	107.30
1	A	182	TRP	CD1-CG-CD2	6.82	111.75	106.30
1	A	109	TRP	CE2-CD2-CG	-6.47	102.12	107.30
1	A	109	TRP	CD1-CG-CD2	6.47	111.47	106.30
1	A	40	TRP	CE2-CD2-CG	-6.35	102.22	107.30
1	A	129	MET	CG-SD-CE	-6.34	90.06	100.20
1	A	77	TYR	CB-CG-CD2	-6.07	117.36	121.00
1	A	88	TRP	CG-CD2-CE3	6.01	139.31	133.90
1	A	42	MET	CG-SD-CE	-5.93	90.71	100.20
1	A	133	PHE	CA-CB-CG	5.88	128.02	113.90
1	A	10	ASP	CB-CG-OD2	-5.86	113.02	118.30
1	A	182	TRP	CG-CD2-CE3	5.61	138.95	133.90
1	A	59	LYS	CA-CB-CG	5.49	125.47	113.40
1	A	182	TRP	CB-CG-CD1	-5.31	120.09	127.00
1	A	134	SER	CB-CA-C	-5.18	100.26	110.10
1	A	88	TRP	CG-CD1-NE1	-5.08	105.02	110.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	133	PHE	Mainchain

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	1808	394	1755	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2	0	0	0	0
3	A	99	194	0	0	0
All	All	1909	588	1755	5	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 1.

All (5) 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:134:SER:HB2	1:A:137:GLN:OE1	2.00	0.61
1:A:17:ILE:HD13	1:A:228:ARG:HD3	1.92	0.51
1:A:60:ARG:HD2	1:A:76:SER:HB3	1.94	0.49
1:A:111:PHE:CE2	1:A:113:SER:HB2	2.49	0.46
1:A:46:LYS:HD3	1:A:46:LYS:HA	1.96	0.42

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	235/237 (99%)	223 (95%)	12 (5%)	0	100 100

There are no Ramachandran outliers to report.

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	203/203 (100%)	196 (97%)	7 (3%)	44 57

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

Mol	Chain	Res	Type
1	A	31	SER
1	A	101	LYS
1	A	118	ASN
1	A	122	GLU
1	A	134	SER
1	A	161	SER
1	A	162	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	ASN
1	A	162	ASN

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 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.

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)

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	237/237 (100%)	-0.52	4 (1%)	73	83	7, 19, 46, 68	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	162	ASN	3.5
1	A	150	THR	3.0
1	A	1	ALA	3.0
1	A	121	HIS	2.1

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	CD	A	242	1/1	1.00	0.01	-4.92	32,32,32,32	0
2	CD	A	241	1/1	1.00	0.02	-5.82	28,28,28,28	0

6.5 Other polymers (i)

There are no such residues in this entry.