



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2018 – 05:22 am GMT

PDB ID : 2CB8
Title : High resolution crystal structure of liganded human L-ACBP
Authors : Taskinen, J.P.; van Aalten, D.M.; Knudsen, J.; Wierenga, R.K.
Deposited on : 2006-01-03
Resolution : 1.40 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

<https://www.wwpdb.org/validation/2017/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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

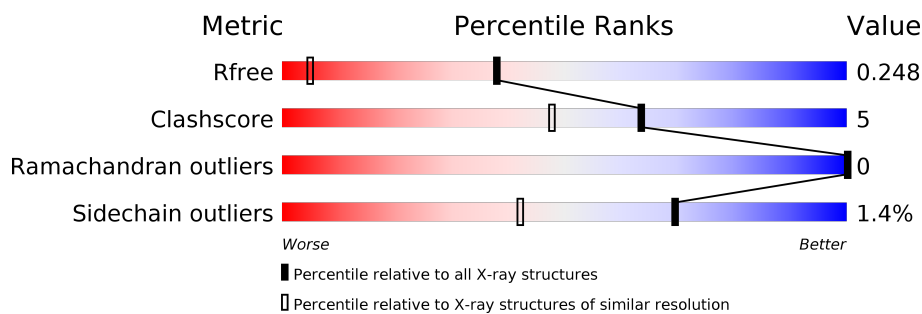
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

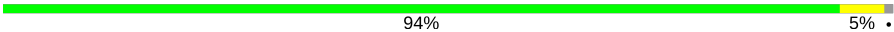

The reported resolution of this entry is 1.40 Å.

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}	111664	1450 (1.40-1.40)
Clashscore	122126	1541 (1.40-1.40)
Ramachandran outliers	120053	1500 (1.40-1.40)
Sidechain outliers	120020	1499 (1.40-1.40)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	87	 94% 5% •
1	B	87	 89% 9% •

2 Entry composition [i](#)

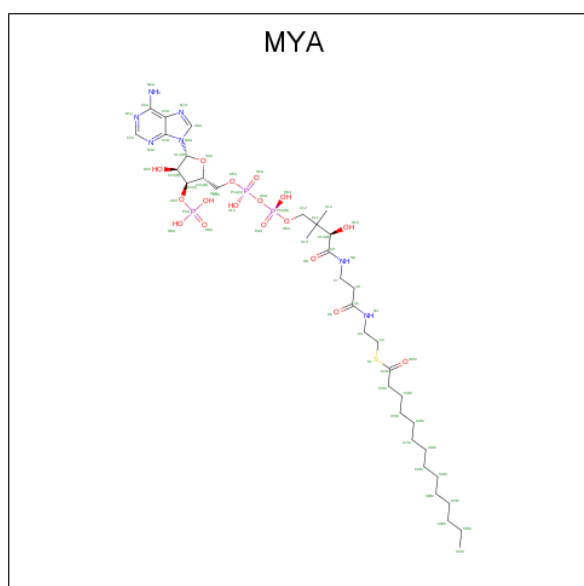
There are 6 unique types of molecules in this entry. The entry contains 1918 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ACYL-COA-BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	86	Total	C	N	O	S	0	10	0
			738	470	124	138	6			
1	B	85	Total	C	N	O	S	0	9	0
			737	469	121	142	5			

- Molecule 2 is TETRADECANOYL-COA (three-letter code: MYA) (formula: $C_{35}H_{62}N_7O_{17}P_3S$).

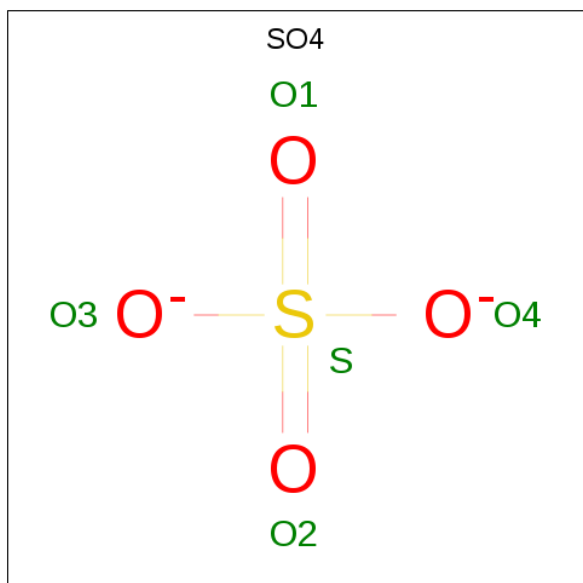


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			63	35	7	17	3		
2	B	1	Total	C	N	O	S	0	0
			19	16	1	1	1		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

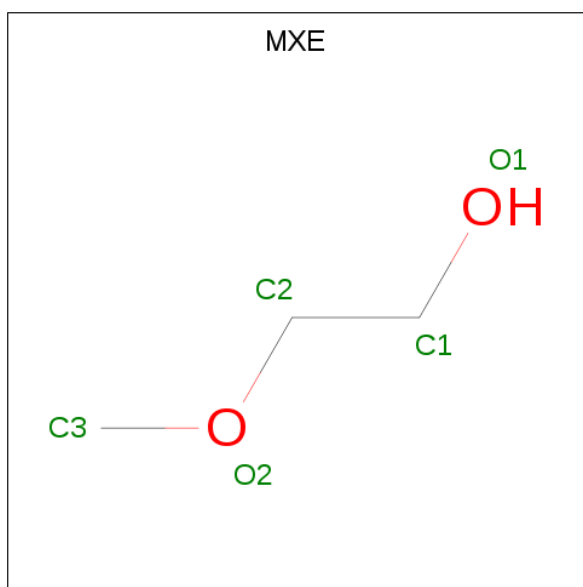
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Zn	0	0
			2	2		
3	A	6	Total	Zn	0	0
			6	6		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 5 is 2-METHOXYETHANOL (three-letter code: MXE) (formula: C₃H₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			5	3	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	155	Total	O	0	0
			155	155		
6	B	134	Total	O	0	0
			134	134		

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.

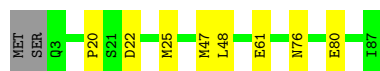
- Molecule 1: ACYL-COA-BINDING PROTEIN

Chain A: 



- Molecule 1: ACYL-COA-BINDING PROTEIN

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	118.49Å 118.49Å 118.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	18.29 – 1.40 18.28 – 1.35	Depositor EDS
% Data completeness (in resolution range)	100.0 (18.29-1.40) 99.8 (18.28-1.35)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 1.35Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.171 , 0.194 0.230 , 0.248	Depositor DCC
R_{free} test set	1152 reflections (1.90%)	wwPDB-VP
Wilson B-factor (Å ²)	18.1	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 62.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	1918	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: MYA, ZN, MXE, 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	0.49	0/797	0.69	0/1059
1	B	0.56	0/786	0.68	0/1047
All	All	0.53	0/1583	0.68	0/2106

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	738	0	737	5	0
1	B	737	0	726	8	0
2	A	54	0	22	1	0
2	B	82	0	89	2	0
3	A	6	0	0	0	0
3	B	2	0	0	0	0
4	A	5	0	0	0	0
5	B	5	0	8	0	0
6	A	155	0	0	3	0
6	B	134	0	0	6	0
All	All	1918	0	1582	15	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 5.

All (15) 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)
2:A:1088:MYA:P3X	6:A:2146:HOH:O	2.30	0.88
1:B:22:ASP:OD2	6:B:2047:HOH:O	2.01	0.79
2:B:1088:MYA:O10	6:B:2128:HOH:O	2.04	0.74
1:A:14[B]:ARG:NH2	6:A:2025:HOH:O	2.16	0.62
1:B:76[B]:ASN:ND2	6:B:2107:HOH:O	2.32	0.61
1:B:80[B]:GLU:HG2	6:B:2114:HOH:O	1.99	0.60
1:A:61:GLU:HG3	6:B:2061:HOH:O	2.08	0.54
1:B:61[A]:GLU:HG3	6:B:2090:HOH:O	2.17	0.44
1:A:40:ILE:HA	1:A:59:TRP:CZ2	2.53	0.44
1:A:61:GLU:OE1	6:A:2115:HOH:O	2.21	0.42
1:B:20:PRO:HG2	1:B:25[A]:MET:HE1	2.03	0.41
1:A:14[B]:ARG:CD	2:B:1088:MYA:HDMA	2.52	0.40

There are no symmetry-related clashes.

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	94/87 (108%)	93 (99%)	1 (1%)	0	100	100
1	B	91/87 (105%)	91 (100%)	0	0	100	100
All	All	185/174 (106%)	184 (100%)	1 (0%)	0	100	100

There are no Ramachandran outliers to report.

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	82/73 (112%)	82 (100%)	0	100	100
1	B	80/73 (110%)	77 (96%)	3 (4%)	36	7
All	All	162/146 (111%)	159 (98%)	3 (2%)	69	26

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	47[A]	MET
1	B	47[B]	MET
1	B	48	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 for Mogul analysis.

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	MYA	A	1088	3	26,29,65	1.43	1 (3%)	30,45,91	2.04	7 (23%)
2	MYA	A	1094	3	26,29,65	1.47	2 (7%)	30,45,91	1.88	5 (16%)
4	SO4	A	1095	3	4,4,4	0.13	0	6,6,6	0.93	0
2	MYA	B	1088	3	54,65,65	2.39	6 (11%)	66,91,91	2.14	12 (18%)
2	MYA	B	1089	-	15,18,65	0.94	1 (6%)	16,18,91	0.70	0
5	MXE	B	1092	-	4,4,4	0.56	0	2,3,3	0.58	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	MYA	A	1088	3	-	0/11/31/80	0/3/3/3
2	MYA	A	1094	3	-	0/11/31/80	0/3/3/3
4	SO4	A	1095	3	-	0/0/0/0	0/0/0/0
2	MYA	B	1088	3	-	0/59/80/80	0/3/3/3
2	MYA	B	1089	-	-	0/16/17/80	0/0/0/3
5	MXE	B	1092	-	-	0/2/2/2	0/0/0/0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1089	MYA	C2-S1	-3.54	1.76	1.81
2	B	1088	MYA	C2-S1	-3.27	1.77	1.81
2	A	1094	MYA	P1A-O1A	-2.12	1.46	1.54
2	B	1088	MYA	C5-N4	5.38	1.45	1.33
2	A	1088	MYA	C4A-N3A	5.61	1.43	1.35
2	B	1088	MYA	C9-N8	5.82	1.45	1.33
2	B	1088	MYA	C4A-N3A	6.03	1.44	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1094	MYA	C4A-N3A	6.05	1.44	1.35
2	B	1088	MYA	O9-C9	9.31	1.42	1.23
2	B	1088	MYA	O5-C5	9.43	1.42	1.23

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1088	MYA	N3A-C2A-N1A	-8.07	121.96	128.86
2	A	1094	MYA	N3A-C2A-N1A	-8.06	121.97	128.86
2	A	1088	MYA	N3A-C2A-N1A	-7.77	122.21	128.86
2	B	1088	MYA	O5-C5-C6	-6.88	109.24	122.00
2	B	1088	MYA	O9-C9-N8	-6.57	110.43	123.05
2	B	1088	MYA	O5-C5-N4	-5.72	112.27	123.02
2	B	1088	MYA	C7-C6-C5	-4.56	104.82	112.31
2	A	1088	MYA	C4A-C5A-N7A	-3.53	106.00	109.41
2	B	1088	MYA	O9-C9-C10	-3.13	110.81	120.78
2	B	1088	MYA	C7-N8-C9	-2.83	117.40	122.59
2	B	1088	MYA	C4A-C5A-N7A	-2.71	106.79	109.41
2	A	1088	MYA	O7A-P3X-O3X	-2.62	94.23	105.99
2	A	1094	MYA	C4A-C5A-N7A	-2.49	107.00	109.41
2	A	1094	MYA	O3A-P1A-O5X	-2.38	100.40	106.73
2	B	1088	MYA	P2A-O3A-P1A	-2.26	125.03	132.63
2	B	1088	MYA	C10-C9-N8	-2.19	112.07	116.58
2	A	1088	MYA	O4X-C4X-C5X	-2.13	102.30	109.39
2	B	1088	MYA	C2A-N1A-C6A	2.02	122.17	118.75
2	A	1094	MYA	C4X-O4X-C1X	2.13	112.05	109.83
2	A	1094	MYA	O7A-P3X-O8A	2.31	116.74	107.59
2	A	1088	MYA	O8A-P3X-O3X	2.38	116.68	105.99
2	B	1088	MYA	C2-S1-C2M	2.88	105.13	100.21
2	A	1088	MYA	O1A-P1A-O2A	2.92	121.97	110.60
2	A	1088	MYA	O8A-P3X-O9A	3.05	122.50	110.60

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1088	MYA	1	0
2	B	1088	MYA	2	0

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

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.