



wwPDB X-ray Structure Validation Summary Report i

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PDB ID : 3H5A
Title : Crystal structure of E. coli MccB
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Deposited on : 2009-04-21
Resolution : 2.80 Å(reported)

This is a wwPDB validation summary 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>

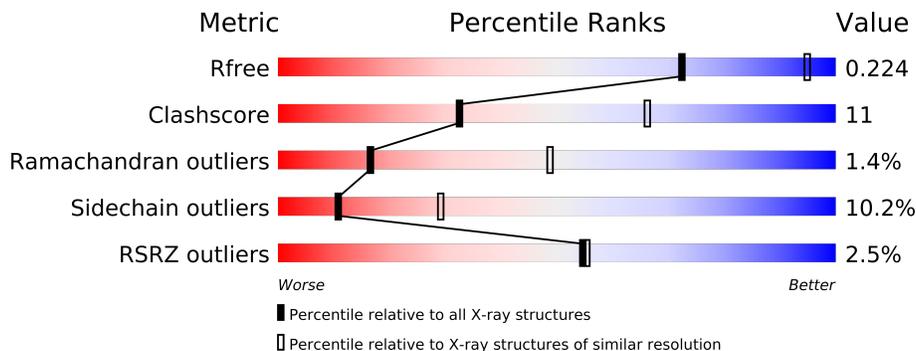
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.80 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	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)

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	358	
1	B	358	
1	C	358	
1	D	358	

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 11064 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 MccB protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	357	2770	1766	478	515	11	0	0	0
1	B	357	2768	1761	477	518	12	0	0	0
1	C	358	2786	1775	480	520	11	0	0	0
1	D	350	2736	1744	474	506	12	0	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	351	LEU	-	EXPRESSION TAG	UNP Q47506
A	352	GLU	-	EXPRESSION TAG	UNP Q47506
A	353	HIS	-	EXPRESSION TAG	UNP Q47506
A	354	HIS	-	EXPRESSION TAG	UNP Q47506
A	355	HIS	-	EXPRESSION TAG	UNP Q47506
A	356	HIS	-	EXPRESSION TAG	UNP Q47506
A	357	HIS	-	EXPRESSION TAG	UNP Q47506
A	358	HIS	-	EXPRESSION TAG	UNP Q47506
B	351	LEU	-	EXPRESSION TAG	UNP Q47506
B	352	GLU	-	EXPRESSION TAG	UNP Q47506
B	353	HIS	-	EXPRESSION TAG	UNP Q47506
B	354	HIS	-	EXPRESSION TAG	UNP Q47506
B	355	HIS	-	EXPRESSION TAG	UNP Q47506
B	356	HIS	-	EXPRESSION TAG	UNP Q47506
B	357	HIS	-	EXPRESSION TAG	UNP Q47506
B	358	HIS	-	EXPRESSION TAG	UNP Q47506
C	351	LEU	-	EXPRESSION TAG	UNP Q47506
C	352	GLU	-	EXPRESSION TAG	UNP Q47506
C	353	HIS	-	EXPRESSION TAG	UNP Q47506
C	354	HIS	-	EXPRESSION TAG	UNP Q47506
C	355	HIS	-	EXPRESSION TAG	UNP Q47506

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Chain	Residue	Modelled	Actual	Comment	Reference
C	356	HIS	-	EXPRESSION TAG	UNP Q47506
C	357	HIS	-	EXPRESSION TAG	UNP Q47506
C	358	HIS	-	EXPRESSION TAG	UNP Q47506
D	351	LEU	-	EXPRESSION TAG	UNP Q47506
D	352	GLU	-	EXPRESSION TAG	UNP Q47506
D	353	HIS	-	EXPRESSION TAG	UNP Q47506
D	354	HIS	-	EXPRESSION TAG	UNP Q47506
D	355	HIS	-	EXPRESSION TAG	UNP Q47506
D	356	HIS	-	EXPRESSION TAG	UNP Q47506
D	357	HIS	-	EXPRESSION TAG	UNP Q47506
D	358	HIS	-	EXPRESSION TAG	UNP Q47506

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

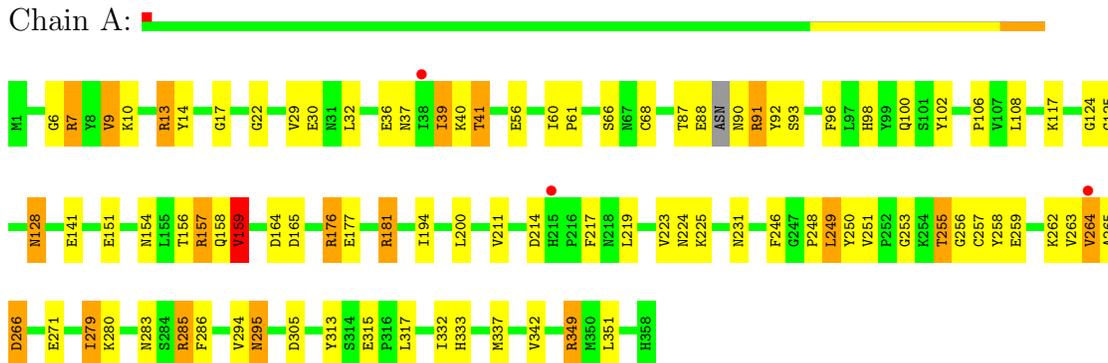
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total 1	Zn 1	0	0
2	A	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0

3 Residue-property plots

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.

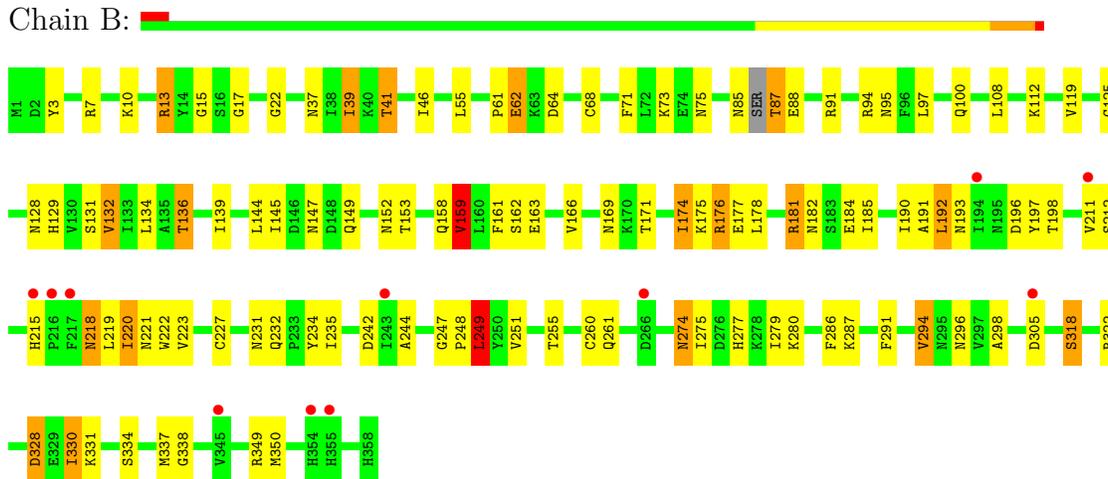
- Molecule 1: MccB protein

Chain A:



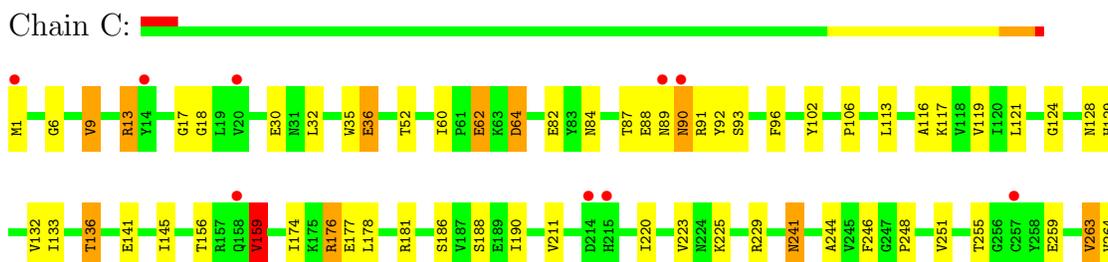
- Molecule 1: MccB protein

Chain B:



- Molecule 1: MccB protein

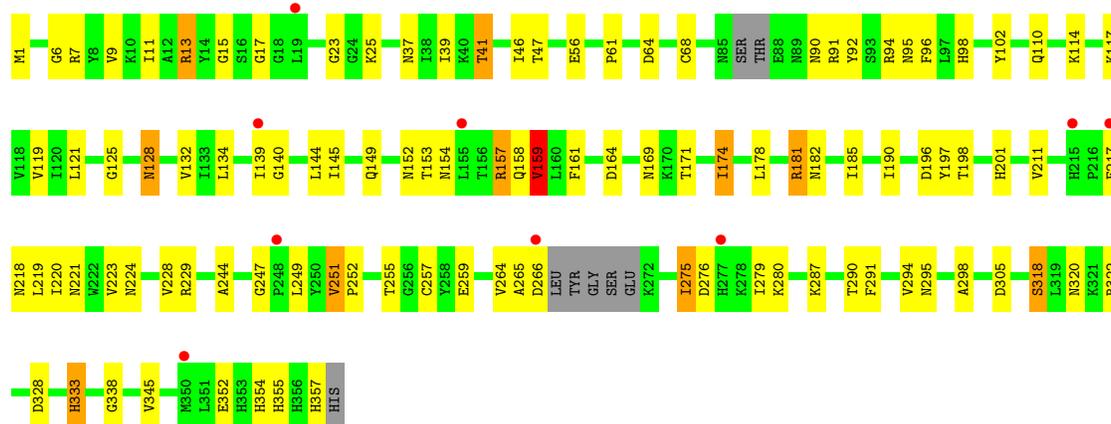
Chain C:





● Molecule 1: MccB protein

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	144.65Å 145.03Å 158.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.69 – 2.80 49.69 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.8 (49.69-2.80) 98.0 (49.69-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.223 , 0.255 0.211 , 0.224	Depositor DCC
R_{free} test set	4120 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	57.0	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 14.8	EDS
Estimated twinning fraction	0.460 for k,h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 81821 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11064	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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:
ZN

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	0.62	0/2831	0.71	0/3845
1	B	0.60	0/2828	0.71	1/3839 (0.0%)
1	C	0.61	0/2848	0.68	0/3868
1	D	0.62	0/2795	0.72	0/3791
All	All	0.61	0/11302	0.71	1/15343 (0.0%)

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	249	LEU	CA-CB-CG	5.19	127.24	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	253	GLY	Peptide

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	2770	0	2694	71	0
1	B	2768	0	2685	73	0
1	C	2786	0	2714	60	0
1	D	2736	0	2679	69	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	11064	0	10772	247	0

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 11.

The worst 5 of 247 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:248:PRO:HD3	1:C:337:MET:HE1	1.17	1.14
1:C:156:THR:HG21	1:D:95:ASN:HD21	1.19	1.04
1:A:248:PRO:HG3	1:A:337:MET:HE1	1.39	1.04
1:C:248:PRO:CD	1:C:337:MET:HE1	2.02	0.89
1:D:305:ASP:OD2	1:D:318:SER:HB2	1.73	0.89

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	353/358 (99%)	325 (92%)	22 (6%)	6 (2%)	14	42
1	B	353/358 (99%)	316 (90%)	34 (10%)	3 (1%)	27	65
1	C	356/358 (99%)	324 (91%)	24 (7%)	8 (2%)	10	32
1	D	344/358 (96%)	310 (90%)	32 (9%)	2 (1%)	33	72
All	All	1406/1432 (98%)	1275 (91%)	112 (8%)	19 (1%)	16	49

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	ASP
1	B	159	VAL
1	C	90	ASN
1	C	347	GLY
1	D	159	VAL

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	295/310 (95%)	265 (90%)	30 (10%)	11	29
1	B	295/310 (95%)	262 (89%)	33 (11%)	9	25
1	C	298/310 (96%)	269 (90%)	29 (10%)	12	32
1	D	294/310 (95%)	265 (90%)	29 (10%)	11	31
All	All	1182/1240 (95%)	1061 (90%)	121 (10%)	11	29

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	242	ASP
1	C	36	GLU
1	D	217	PHE
1	B	274	ASN
1	B	328	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	128	ASN
1	C	221	ASN
1	D	333	HIS
1	C	129	HIS
1	C	152	ASN

5.3.3 RNA [i](#)

There are no RNA chains 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 4 ligands modelled in this entry, 4 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 [i](#)

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 [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	357/358 (99%)	0.55	3 (0%) 83 83	33, 49, 76, 85	0
1	B	357/358 (99%)	0.61	11 (3%) 47 47	34, 53, 82, 97	0
1	C	358/358 (100%)	0.62	13 (3%) 41 41	33, 50, 76, 85	0
1	D	350/358 (97%)	0.62	9 (2%) 53 54	34, 54, 73, 87	0
All	All	1422/1432 (99%)	0.60	36 (2%) 54 55	33, 52, 77, 97	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	217	PHE	4.9
1	D	155	LEU	3.5
1	A	215	HIS	3.4
1	C	265	ALA	3.4
1	D	215	HIS	3.3

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ZN	B	360	1/1	0.13	-1.09	81,81,81,81	0
2	ZN	D	360	1/1	0.17	-1.29	76,76,76,76	0
2	ZN	C	360	1/1	0.16	-2.00	68,68,68,68	0
2	ZN	A	360	1/1	0.15	-2.16	68,68,68,68	0

6.5 Other polymers

There are no such residues in this entry.