



wwPDB X-ray Structure Validation Summary Report i

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PDB ID : 3F1V
Title : E. coli Beta Sliding Clamp, 148-153 Ala Mutant
Authors : Cody, V.
Deposited on : 2008-10-28
Resolution : 1.77 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>

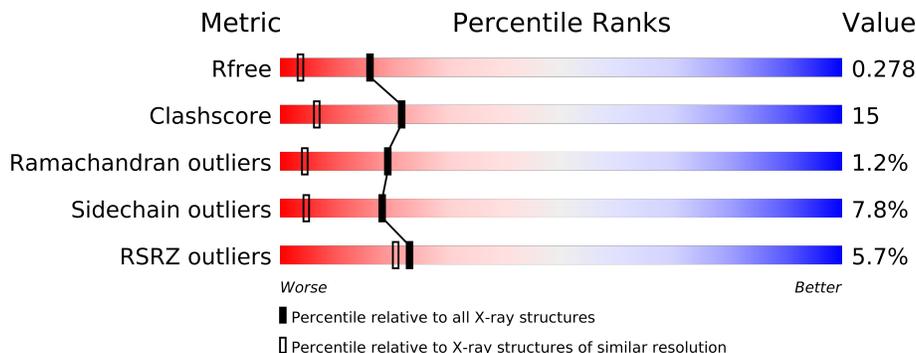
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.77 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	4987 (1.80-1.76)
Clashscore	79885	6152 (1.80-1.76)
Ramachandran outliers	78287	6074 (1.80-1.76)
Sidechain outliers	78261	6073 (1.80-1.76)
RSRZ outliers	66119	4990 (1.80-1.76)

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	366	
1	B	366	

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 6029 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 DNA polymerase III subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	366	2824	1775	492	538	19	0	4	0
1	B	366	2824	1775	492	538	19	0	3	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	148	ALA	HIS	ENGINEERED	UNP P0A988
A	149	ALA	GLN	ENGINEERED	UNP P0A988
A	150	ALA	ASP	ENGINEERED	UNP P0A988
A	151	ALA	VAL	ENGINEERED	UNP P0A988
A	152	ALA	ARG	ENGINEERED	UNP P0A988
B	148	ALA	HIS	ENGINEERED	UNP P0A988
B	149	ALA	GLN	ENGINEERED	UNP P0A988
B	150	ALA	ASP	ENGINEERED	UNP P0A988
B	151	ALA	VAL	ENGINEERED	UNP P0A988
B	152	ALA	ARG	ENGINEERED	UNP P0A988

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

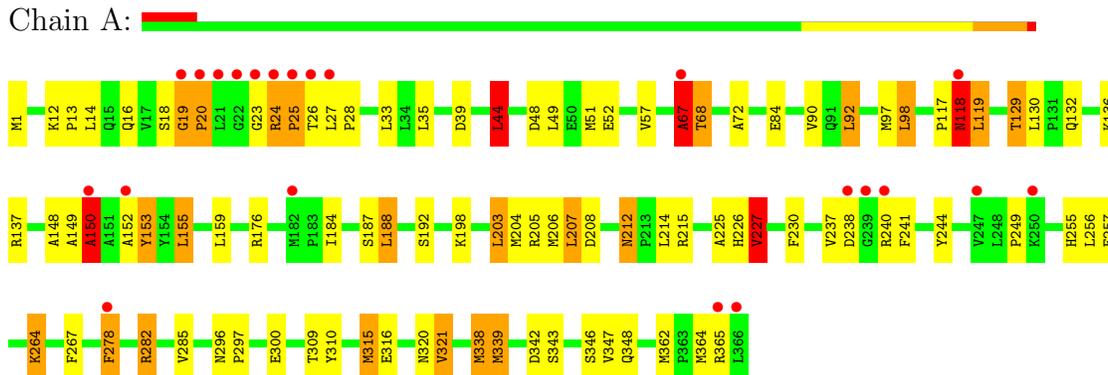
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	173	Total 173	O 173	0	0
4	B	205	Total 205	O 205	0	0

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.

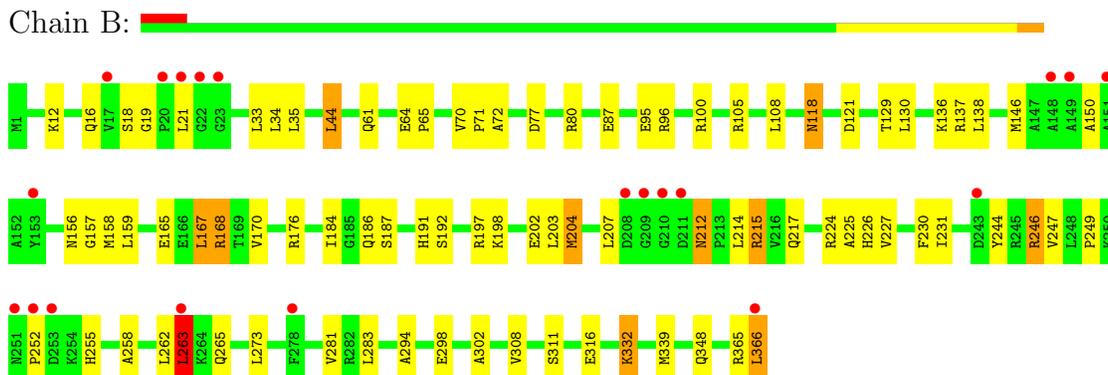
- Molecule 1: DNA polymerase III subunit beta

Chain A:



- Molecule 1: DNA polymerase III subunit beta

Chain B:



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	40.84Å 64.47Å 72.11Å 73.83° 82.72° 83.76°	Depositor
Resolution (Å)	28.86 – 1.77 28.85 – 1.77	Depositor EDS
% Data completeness (in resolution range)	91.1 (28.86-1.77) 91.1 (28.85-1.77)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 1.77Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.215 , 0.282 0.215 , 0.278	Depositor DCC
R_{free} test set	3133 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	30.4	Xtrriage
Anisotropy	0.086	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 50.8	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Outliers	0 of 62326 reflections	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6029	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.96% 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: CA, CL

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	0.93	1/2872 (0.0%)	1.02	9/3888 (0.2%)
1	B	0.86	1/2872 (0.0%)	0.96	7/3888 (0.2%)
All	All	0.89	2/5744 (0.0%)	0.99	16/7776 (0.2%)

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	1	4
1	B	0	1
All	All	1	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	84	GLU	CB-CG	6.84	1.65	1.52
1	B	96	ARG	CB-CG	-5.07	1.38	1.52

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	44	LEU	CB-CG-CD1	-8.96	95.76	111.00
1	A	67	ALA	CB-CA-C	-7.82	98.37	110.10
1	A	118	ASN	N-CA-C	7.21	130.47	111.00
1	A	227	VAL	CB-CA-C	-6.69	98.69	111.40
1	A	19	GLY	N-CA-C	6.42	129.14	113.10

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	149	ALA	CA

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	ASN	Peptide
1	A	148	ALA	Peptide
1	A	150	ALA	Peptide
1	A	67	ALA	Peptide
1	B	365	ARG	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	2824	0	2834	103	0
1	B	2824	0	2838	68	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	B	1	0	0	0	0
4	A	173	0	0	11	1
4	B	205	0	0	8	2
All	All	6029	0	5672	172	2

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 15.

The worst 5 of 172 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:118:ASN:HB3	1:A:119:LEU:CA	1.65	1.23
1:A:184:ILE:HD11	1:A:188:LEU:HD11	1.26	1.10
1:A:267:PHE:HD1	1:A:321:VAL:CG1	1.66	1.09
1:A:90:VAL:HG11	1:A:97:MET:HE1	1.16	1.09
1:A:150:ALA:HA	1:A:152:ALA:H	1.16	1.08

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:420:HOH:O	4:B:573:HOH:O[1_545]	1.74	0.46
4:B:376:HOH:O	4:B:555:HOH:O[1_455]	1.97	0.23

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	364/366 (100%)	347 (95%)	8 (2%)	9 (2%)	9 1
1	B	364/366 (100%)	352 (97%)	12 (3%)	0	100 100
All	All	728/732 (100%)	699 (96%)	20 (3%)	9 (1%)	19 4

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	20	PRO
1	A	24	ARG
1	A	68	THR
1	A	153	TYR
1	A	212	ASN

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	308/308 (100%)	278 (90%)	30 (10%)	12 2
1	B	308/308 (100%)	290 (94%)	18 (6%)	28 9
All	All	616/616 (100%)	568 (92%)	48 (8%)	18 5

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	256	LEU
1	A	321	VAL
1	B	263	LEU
1	A	264	LYS
1	A	282	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	348	GLN
1	B	156	ASN
1	B	255	HIS
1	A	335	ASN
1	B	226[A]	HIS

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 3 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	366/366 (100%)	0.38	22 (6%) 21 19	21, 33, 51, 76	1 (0%)
1	B	366/366 (100%)	0.38	20 (5%) 24 22	22, 33, 54, 63	2 (0%)
All	All	732/732 (100%)	0.38	42 (5%) 23 20	21, 33, 51, 76	3 (0%)

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	22	GLY	8.9
1	B	21	LEU	8.2
1	B	153	TYR	6.3
1	A	22	GLY	5.6
1	B	209	GLY	5.3

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

There are no carbohydrates in this entry.

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(\AA^2)	Q<0.9
3	CL	B	368	1/1	0.15	1.71	30,30,30,30	0
2	CA	A	367	1/1	0.03	-2.22	30,30,30,30	0
2	CA	B	367	1/1	0.01	-2.22	29,29,29,29	0

6.5 Other polymers

There are no such residues in this entry.