



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 1, 2021 – 09:45 PM EDT

PDB ID : 3KTH
Title : Structure of ClpP from Bacillus subtilis in orthorombic crystal form
Authors : Lee, B.-G.; Brotz-Oesterhelt, H.; Song, H.K.
Deposited on : 2009-11-25
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Xtriage (Phenix) : 1.13
EDS : 2.23.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

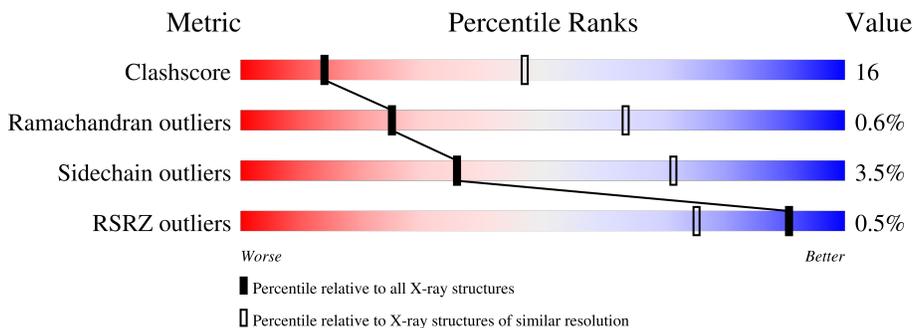
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$. 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	199	 % 61% 28% • 10%
1	B	199	 61% 29% • 9%
1	C	199	 % 60% 29% • 10%
1	D	199	 2% 61% 29% • 9%
1	E	199	 58% 30% • 9%
1	F	199	 63% 27% • 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	199	 62% 26% 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9686 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 ATP-dependent Clp protease proteolytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	180	Total 1366	C 865	N 229	O 265	S 7	0	0	0
1	B	182	Total 1374	C 870	N 231	O 266	S 7	0	0	0
1	C	180	Total 1363	C 863	N 229	O 264	S 7	0	0	0
1	D	181	Total 1368	C 866	N 230	O 265	S 7	0	0	0
1	E	181	Total 1369	C 867	N 230	O 265	S 7	0	0	0
1	F	182	Total 1373	C 869	N 231	O 266	S 7	0	0	0
1	G	181	Total 1368	C 866	N 230	O 265	S 7	0	0	0

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	192	LEU	THR	engineered mutation	UNP P80244
A	194	HIS	ASP	engineered mutation	UNP P80244
A	195	HIS	LYS	engineered mutation	UNP P80244
A	196	HIS	LYS	engineered mutation	UNP P80244
A	197	HIS	-	expression tag	UNP P80244
A	198	HIS	-	expression tag	UNP P80244
A	199	HIS	-	expression tag	UNP P80244
B	192	LEU	THR	engineered mutation	UNP P80244
B	194	HIS	ASP	engineered mutation	UNP P80244
B	195	HIS	LYS	engineered mutation	UNP P80244
B	196	HIS	LYS	engineered mutation	UNP P80244
B	197	HIS	-	expression tag	UNP P80244
B	198	HIS	-	expression tag	UNP P80244
B	199	HIS	-	expression tag	UNP P80244
C	192	LEU	THR	engineered mutation	UNP P80244

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	194	HIS	ASP	engineered mutation	UNP P80244
C	195	HIS	LYS	engineered mutation	UNP P80244
C	196	HIS	LYS	engineered mutation	UNP P80244
C	197	HIS	-	expression tag	UNP P80244
C	198	HIS	-	expression tag	UNP P80244
C	199	HIS	-	expression tag	UNP P80244
D	192	LEU	THR	engineered mutation	UNP P80244
D	194	HIS	ASP	engineered mutation	UNP P80244
D	195	HIS	LYS	engineered mutation	UNP P80244
D	196	HIS	LYS	engineered mutation	UNP P80244
D	197	HIS	-	expression tag	UNP P80244
D	198	HIS	-	expression tag	UNP P80244
D	199	HIS	-	expression tag	UNP P80244
E	192	LEU	THR	engineered mutation	UNP P80244
E	194	HIS	ASP	engineered mutation	UNP P80244
E	195	HIS	LYS	engineered mutation	UNP P80244
E	196	HIS	LYS	engineered mutation	UNP P80244
E	197	HIS	-	expression tag	UNP P80244
E	198	HIS	-	expression tag	UNP P80244
E	199	HIS	-	expression tag	UNP P80244
F	192	LEU	THR	engineered mutation	UNP P80244
F	194	HIS	ASP	engineered mutation	UNP P80244
F	195	HIS	LYS	engineered mutation	UNP P80244
F	196	HIS	LYS	engineered mutation	UNP P80244
F	197	HIS	-	expression tag	UNP P80244
F	198	HIS	-	expression tag	UNP P80244
F	199	HIS	-	expression tag	UNP P80244
G	192	LEU	THR	engineered mutation	UNP P80244
G	194	HIS	ASP	engineered mutation	UNP P80244
G	195	HIS	LYS	engineered mutation	UNP P80244
G	196	HIS	LYS	engineered mutation	UNP P80244
G	197	HIS	-	expression tag	UNP P80244
G	198	HIS	-	expression tag	UNP P80244
G	199	HIS	-	expression tag	UNP P80244

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	12	Total O 12 12	0	0
2	B	13	Total O 13 13	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	12	Total O 12 12	0	0
2	D	20	Total O 20 20	0	0
2	E	9	Total O 9 9	0	0
2	F	23	Total O 23 23	0	0
2	G	16	Total O 16 16	0	0



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain E: 58% 30% 9%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain F: 63% 27% 9%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain G: 62% 26% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	96.29Å 108.12Å 152.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.00 48.15 – 3.00	Depositor EDS
% Data completeness (in resolution range)	80.6 (50.00-3.00) 80.6 (48.15-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 3.01Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.248 , 0.275 0.235 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	58.0	Xtrriage
Anisotropy	1.048	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9686	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.44	0/1382	0.59	0/1863
1	B	0.43	0/1390	0.59	0/1874
1	C	0.41	0/1379	0.60	0/1859
1	D	0.42	0/1384	0.58	0/1866
1	E	0.42	0/1385	0.62	0/1867
1	F	0.42	0/1389	0.60	0/1873
1	G	0.41	0/1384	0.59	0/1866
All	All	0.42	0/9693	0.60	0/13068

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 [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	1366	0	1393	43	0
1	B	1374	0	1392	48	0
1	C	1363	0	1386	44	0
1	D	1368	0	1388	44	0
1	E	1369	0	1390	49	0
1	F	1373	0	1390	44	0
1	G	1368	0	1388	44	0
2	A	12	0	0	1	0
2	B	13	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	12	0	0	3	0
2	D	20	0	0	1	0
2	E	9	0	0	1	0
2	F	23	0	0	2	0
2	G	16	0	0	3	0
All	All	9686	0	9727	305	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 16.

The worst 5 of 305 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:84:LYS:HD2	1:B:193:GLU:HA	1.59	0.84
1:A:40:ALA:HA	1:A:76:ILE:HD11	1.66	0.78
1:F:40:ALA:HA	1:F:76:ILE:HD11	1.66	0.77
1:C:40:ALA:HA	1:C:76:ILE:HD11	1.67	0.76
1:B:40:ALA:HA	1:B:76:ILE:HD11	1.68	0.76

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	176/199 (88%)	163 (93%)	12 (7%)	1 (1%)	25 64
1	B	178/199 (89%)	164 (92%)	13 (7%)	1 (1%)	25 64
1	C	176/199 (88%)	162 (92%)	13 (7%)	1 (1%)	25 64
1	D	177/199 (89%)	161 (91%)	16 (9%)	0	100 100
1	E	177/199 (89%)	163 (92%)	11 (6%)	3 (2%)	9 39

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	F	178/199 (89%)	163 (92%)	14 (8%)	1 (1%)	25 64
1	G	177/199 (89%)	164 (93%)	12 (7%)	1 (1%)	25 64
All	All	1239/1393 (89%)	1140 (92%)	91 (7%)	8 (1%)	25 64

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ASP
1	B	6	VAL
1	C	5	THR
1	E	189	LEU
1	E	190	THR

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	144/165 (87%)	138 (96%)	6 (4%)	30 66
1	B	143/165 (87%)	138 (96%)	5 (4%)	36 71
1	C	143/165 (87%)	138 (96%)	5 (4%)	36 71
1	D	143/165 (87%)	138 (96%)	5 (4%)	36 71
1	E	143/165 (87%)	139 (97%)	4 (3%)	43 77
1	F	143/165 (87%)	139 (97%)	4 (3%)	43 77
1	G	143/165 (87%)	137 (96%)	6 (4%)	30 66
All	All	1002/1155 (87%)	967 (96%)	35 (4%)	36 71

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	172	ASN
1	G	19	ILE
1	G	122	HIS
1	C	108	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	92	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	41	ASN
1	E	172	ASN
1	G	150	ASN
1	E	150	ASN
1	F	116	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	180/199 (90%)	-0.14	1 (0%) 89 72	55, 65, 84, 95	0
1	B	182/199 (91%)	-0.24	0 100 100	55, 66, 89, 107	0
1	C	180/199 (90%)	-0.19	1 (0%) 89 72	55, 65, 83, 98	0
1	D	181/199 (90%)	-0.12	4 (2%) 62 33	53, 64, 87, 114	0
1	E	181/199 (90%)	-0.17	0 100 100	52, 64, 84, 96	0
1	F	182/199 (91%)	-0.18	0 100 100	53, 64, 84, 95	0
1	G	181/199 (90%)	-0.15	0 100 100	55, 64, 83, 94	0
All	All	1267/1393 (90%)	-0.17	6 (0%) 91 75	52, 65, 86, 114	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	193	GLU	3.7
1	C	17	TYR	3.0
1	D	26	ASP	2.9
1	A	25	LYS	2.4
1	D	22	ARG	2.4

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 monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.