



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:54 PM GMT

PDB ID : 4JWC
Title : Crystal structure of the substrate binding domain of E.coli DnaK in complex with bovine Bac7(1-16)
Authors : Zahn, M.; Straeter, N.
Deposited on : 2013-03-27
Resolution : 1.80 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 ⓘ 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 (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

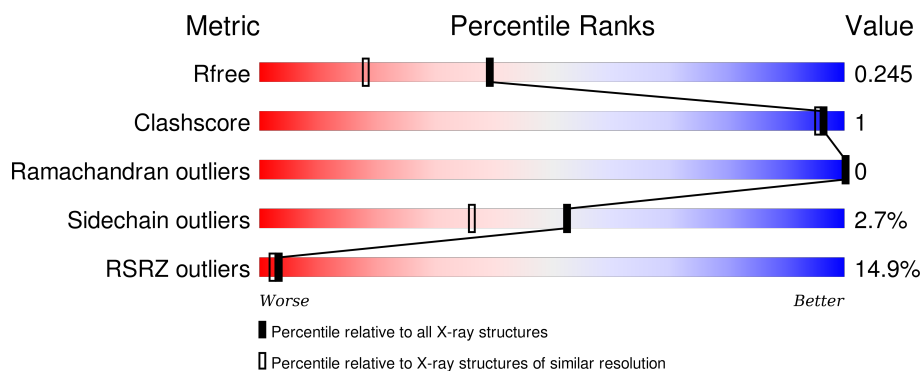
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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. 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	219	<div> <div>16%</div> <div>94%</div> <div>• •</div> </div>
1	B	219	<div> <div>12%</div> <div>91%</div> <div>5% •</div> </div>
2	C	16	<div> <div>19%</div> <div>56%</div> <div>44%</div> </div>
2	D	16	<div> <div>13%</div> <div>25%</div> <div>38%</div> <div>38%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3834 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 Chaperone protein DnaK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	213	Total	C	N	O	S	0	3	0
			1635	1006	285	338	6			
1	B	211	Total	C	N	O	S	0	8	0
			1645	1013	287	337	8			

- Molecule 2 is a protein called Cathelicidin-3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	9	Total	C	N	O	0	0	0
			80	50	21	9			
2	D	10	Total	C	N	O	0	0	0
			87	55	22	10			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

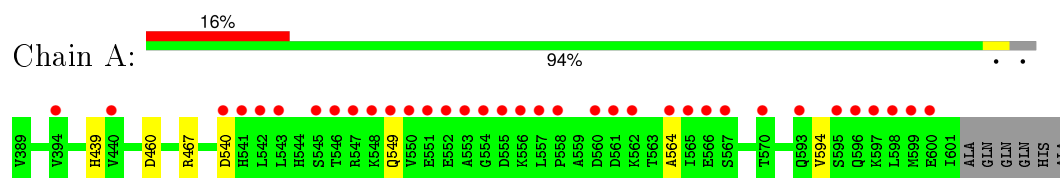
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	192	Total O 192 192	0	0
4	B	170	Total O 170 170	0	0
4	C	7	Total O 7 7	0	0
4	D	3	Total O 3 3	0	0

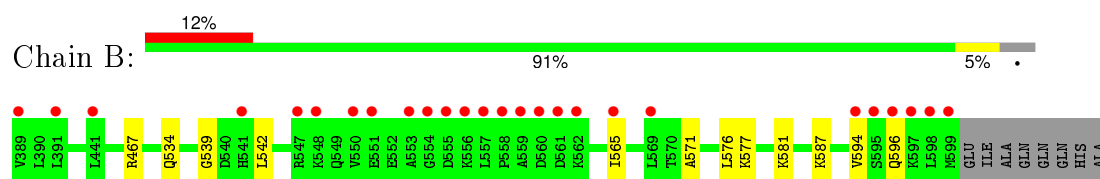
3 Residue-property plots [i](#)

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: Chaperone protein DnaK



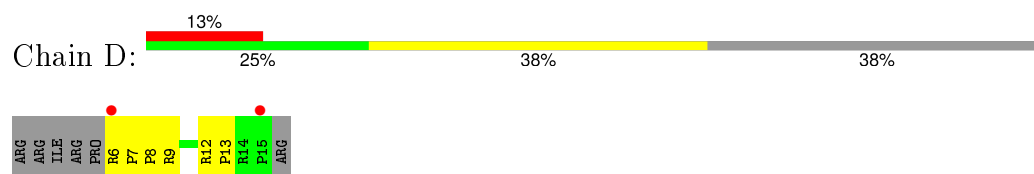
• Molecule 1: Chaperone protein DnaK



• Molecule 2: Cathelicidin-3



• Molecule 2: Cathelicidin-3



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	77.65Å 163.04Å 44.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.67 – 1.80 24.67 – 1.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (24.67-1.80) 99.5 (24.67-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 1.80Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.203 , 0.225 0.214 , 0.245	Depositor DCC
R_{free} test set	1102 reflections (2.11%)	DCC
Wilson B-factor (Å ²)	23.5	Xtriage
Anisotropy	0.592	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 53486 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3834	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% 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, 0.375 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: 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	0/1658	0.60	0/2234
1	B	0.48	0/1678	0.63	0/2262
2	C	0.44	0/83	0.63	0/112
2	D	0.41	0/91	0.56	0/124
All	All	0.48	0/3510	0.62	0/4732

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	1635	0	1653	2	0
1	B	1645	0	1671	6	0
2	C	80	0	90	0	0
2	D	87	0	97	5	0
3	A	5	0	0	0	0
3	B	10	0	0	0	0
4	A	192	0	0	1	0
4	B	170	0	0	0	0
4	C	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	3	0	0	0	0
All	All	3834	0	3511	10	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 (10) 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:B:467:ARG:HH11	2:D:9:ARG:HH12	1.48	0.62
1:B:467:ARG:NH1	2:D:9:ARG:HH12	2.04	0.54
1:B:565:ILE:HD13	1:B:594:VAL:HG23	1.90	0.53
1:A:439:HIS:HE1	4:A:946:HOH:O	1.91	0.52
1:B:467:ARG:HH11	2:D:9:ARG:NH1	2.11	0.45
1:B:571:ALA:HB1	1:B:587:LYS:HD2	1.98	0.45
1:B:539:GLY:HA3	1:B:576:LEU:HD21	2.01	0.43
2:D:7:PRO:HA	2:D:8:PRO:HD3	1.93	0.43
2:D:12:ARG:HG2	2:D:13:PRO:HD2	2.01	0.42
1:A:564:ALA:HB1	1:A:594:VAL:HG11	2.02	0.41

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	214/219 (98%)	212 (99%)	2 (1%)	0	100	100
1	B	217/219 (99%)	212 (98%)	5 (2%)	0	100	100
2	C	7/16 (44%)	7 (100%)	0	0	100	100
2	D	8/16 (50%)	8 (100%)	0	0	100	100
All	All	446/470 (95%)	439 (98%)	7 (2%)	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	180/181 (99%)	175 (97%)	5 (3%)	51	35
1	B	183/181 (101%)	178 (97%)	5 (3%)	52	36
2	C	9/16 (56%)	9 (100%)	0	100	100
2	D	10/16 (62%)	9 (90%)	1 (10%)	9	2
All	All	382/394 (97%)	371 (97%)	11 (3%)	52	34

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	460[A]	ASP
1	A	460[B]	ASP
1	A	467	ARG
1	A	540	ASP
1	A	549	GLN
1	B	534	GLN
1	B	542	LEU
1	B	577	LYS
1	B	581	LYS
1	B	596	GLN
2	D	6	ARG

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	485	HIS

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 ⓘ

3 ligands are modelled in this entry.

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	$\# Z > 2$
3	SO4	A	701	-	4,4,4	0.58	0	6,6,6	0.21	0
3	SO4	B	701	-	4,4,4	0.19	0	6,6,6	0.22	0
3	SO4	B	702	-	4,4,4	0.18	0	6,6,6	0.09	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
3	SO4	A	701	-	-	0/0/0/0	0/0/0/0
3	SO4	B	701	-	-	0/0/0/0	0/0/0/0
3	SO4	B	702	-	-	0/0/0/0	0/0/0/0

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

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	213/219 (97%)	0.63	35 (16%) 2 2	16, 28, 90, 110	0
1	B	211/219 (96%)	0.66	26 (12%) 5 4	18, 31, 87, 114	0
2	C	9/16 (56%)	1.43	3 (33%) 0 0	26, 33, 68, 68	0
2	D	10/16 (62%)	1.49	2 (20%) 1 1	26, 41, 66, 75	0
All	All	443/470 (94%)	0.68	66 (14%) 3 2	16, 30, 87, 114	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	15	PRO	7.5
1	B	558	PRO	7.3
1	B	553	ALA	7.1
1	B	557	LEU	6.8
1	B	569	LEU	6.5
1	A	562	LYS	6.2
1	A	557	LEU	6.0
1	B	550	VAL	5.8
1	A	553	ALA	5.6
1	A	552	GLU	5.6
1	B	560	ASP	5.5
1	B	559	ALA	5.3
1	A	551	GLU	5.3
1	B	556	LYS	4.9
1	B	555	ASP	4.6
1	A	556	LYS	4.6
1	B	596	GLN	4.5
1	A	555	ASP	4.3
1	B	548	LYS	4.2
1	B	554	GLY	4.2
1	A	599	MET	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	554	GLY	4.1
1	B	597	LYS	4.1
1	A	561	ASP	4.1
1	A	560	ASP	3.8
1	B	599	MET	3.8
1	B	561	ASP	3.7
1	A	596	GLN	3.7
1	A	549	GLN	3.6
1	A	558	PRO	3.5
1	B	595	SER	3.5
1	A	600	GLU	3.4
1	B	541[A]	HIS	3.3
1	A	595	SER	3.3
1	A	564	ALA	3.2
1	A	548	LYS	3.1
1	A	542	LEU	3.1
1	B	598	LEU	3.1
1	A	565	ILE	3.1
1	A	550	VAL	3.1
1	B	565	ILE	3.1
2	C	6	ARG	3.0
2	C	12	ARG	3.0
1	A	541	HIS	2.9
1	A	540	ASP	2.8
2	C	13	PRO	2.5
1	B	594	VAL	2.5
1	A	598	LEU	2.5
1	B	562	LYS	2.5
1	A	597	LYS	2.4
1	B	441	LEU	2.4
1	A	394	VAL	2.4
1	A	567	SER	2.4
1	B	551	GLU	2.4
1	A	545	SER	2.4
1	A	543	LEU	2.4
1	A	546	THR	2.3
1	A	570	THR	2.3
1	A	547	ARG	2.3
2	D	6	ARG	2.2
1	B	389	VAL	2.2
1	B	391	LEU	2.1
1	B	547	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	566	GLU	2.1
1	A	593	GLN	2.1
1	A	440	VAL	2.0

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(\AA^2)	Q<0.9
3	SO4	A	701	5/5	0.94	0.13	0.44	40,42,46,48	0
3	SO4	B	702	5/5	0.95	0.11	-0.85	71,76,76,77	0
3	SO4	B	701	5/5	0.79	0.27	-	69,73,74,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.