

wwPDB X-ray Structure Validation Summary Report (i)

May 22, 2020 – 01:27 am BST

PDB ID	:	4HYB
Title	:	Crystal structure of the substrate binding domain of E.coli DnaK in complex
		with pyrrhocoricin_LYZI (residues 1 to 10)
Authors	:	Zahn, M.; Straeter, N.
Deposited on	:	2012-11-13
$\operatorname{Resolution}$:	1.70 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

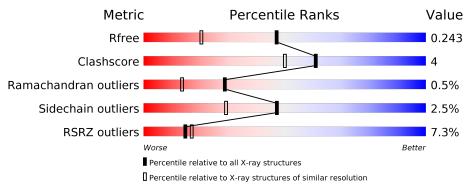
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\rm CCP4$:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695(1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 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 <=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	А	219	7% 87%		11% •		
1	В	219	7%		15% ••		
2	С	11	9%	9%	27%		
2	D	11	73%		27%		



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3747 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	А	213	Total 1637	C 1007	11	O 336	S 6	0	3	0
1	В	214	Total 1646	C 1013	N 288	O 338	S 7	0	4	0

• Molecule 2 is a protein called Pyrrhocoricin.

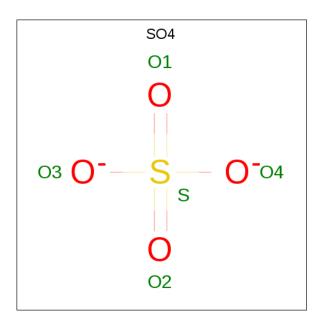
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
9	С	8	Total C N O	0	0	1
		0	65 46 11 8	0		
0	п	0	Total C N O	0	0	1
		0	65 46 11 8	0	0	1

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	4	LEU	GLY	ENGINEERED MUTATION	UNP P37362
С	5	TYR	SER	ENGINEERED MUTATION	UNP P37362
С	6	ALC	TYR	ENGINEERED MUTATION	UNP P37362
C	7	ILE	LEU	ENGINEERED MUTATION	UNP P37362
С	11	PRO	-	EXPRESSION TAG	UNP P37362
D	4	LEU	GLY	ENGINEERED MUTATION	UNP P37362
D	5	TYR	SER	ENGINEERED MUTATION	UNP P37362
D	6	ALC	TYR	ENGINEERED MUTATION	UNP P37362
D	7	ILE	LEU	ENGINEERED MUTATION	UNP P37362
D	11	PRO	-	EXPRESSION TAG	UNP P37362

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

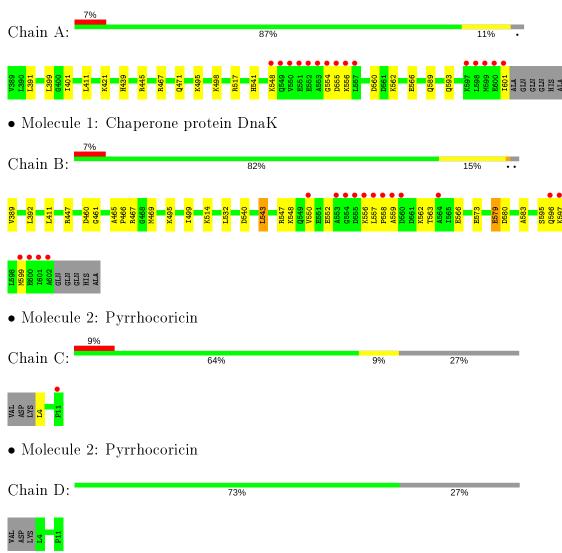
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	166	Total O 166 166	0	0
4	В	150	Total O 150 150	0	0
4	С	4	$\begin{array}{cc} \text{Total} & \text{O} \\ 4 & 4 \end{array}$	0	0
4	D	4	Total O 4 4	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 the various outlier classes 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



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	77.45Å 162.17Å 45.21Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.60 - 1.70	Depositor
Resolution (A)	24.60 - 1.70	EDS
% Data completeness	95.5 (24.60-1.70)	Depositor
(in resolution range)	95.5(24.60-1.70)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.42 (at 1.70 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
D D.	0.211 , 0.244	Depositor
R, R_{free}	0.210 , 0.243	DCC
R_{free} test set	3092 reflections $(5.08%)$	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtriage
Anisotropy	0.565	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.36, 39.8	EDS
L-test for twinning ²	$ \langle L \rangle = 0.48, \langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3747	wwPDB-VP
Average B, all atoms $(Å^2)$	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.47% of the height of the origin peak. No significant pseudotranslation is detected.

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.



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: SO4, $\rm ALC$

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	Bo	nd lengths	Bond angles		
	Cham	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	1.04	1/1658~(0.1%)	1.02	4/2234~(0.2%)	
1	В	0.96	1/1670~(0.1%)	1.04	7/2251~(0.3%)	
2	С	1.18	1/55~(1.8%)	0.93	0/74	
2	D	0.92	0/55	0.89	0/74	
All	All	1.00	3/3438~(0.1%)	1.03	11/4633~(0.2%)	

All (3) bond length outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
2	С	4	LEU	N-CA	6.22	1.58	1.46
1	В	579	GLU	CG-CD	5.36	1.59	1.51
1	А	445	ARG	CZ-NH1	5.05	1.39	1.33

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	447	ARG	NE-CZ-NH1	8.56	124.58	120.30
1	В	467	ARG	NE-CZ-NH1	6.82	123.71	120.30
1	А	411	LEU	CA-CB-CG	-6.15	101.14	115.30
1	В	411	LEU	CA-CB-CG	-6.06	101.37	115.30
1	В	447	ARG	NE-CZ-NH2	-5.96	117.32	120.30

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	1637	0	1654	10	0
1	В	1646	0	1664	21	0
2	С	65	0	71	0	0
2	D	65	0	71	0	0
3	В	10	0	0	0	0
4	А	166	0	0	4	0
4	В	150	0	0	4	0
4	С	4	0	0	0	0
4	D	4	0	0	0	0
All	All	3747	0	3460	31	0

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.

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 4.

The worst 5 of 31 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:465:ALA:HB1	1:B:469[B]:MET:CE	1.72	1.18
1:B:465:ALA:HB1	1:B:469[B]:MET:HE2	1.05	1.04
1:B:465:ALA:CB	1:B:469[B]:MET:CE	2.42	0.98
1:B:465:ALA:CB	1:B:469[B]:MET:HE2	1.93	0.97
1:A:589:GLN:HE21	1:A:593:GLN:HE21	1.24	0.85

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	А	214/219~(98%)	212~(99%)	1 (0%)	1 (0%)	29 13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	В	216/219~(99%)	212~(98%)	3~(1%)	1 (0%)	29	13
2	С	5/11~(46%)	5(100%)	0	0	100	100
2	D	5/11~(46%)	5~(100%)	0	0	100	100
All	All	440/460~(96%)	434~(99%)	4 (1%)	2(0%)	29	13

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All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	554	GLY
1	В	559	ALA

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	Perce	ntiles
1	А	180/181~(99%)	177~(98%)	3 (2%)	60	46
1	В	$181/181 \ (100\%)$	175~(97%)	6 (3%)	38	19
2	С	6/10~(60%)	6~(100%)	0	100	100
2	D	6/10~(60%)	6 (100%)	0	100	100
All	All	373/382~(98%)	364 (98%)	9 (2%)	47	31

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	548	LYS
1	В	597	LYS
1	В	556	LYS
1	А	560	ASP
1	В	552	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:



Mol	Chain	Res	Type
1	А	593	GLN
1	В	589	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

2 non-standard protein/DNA/RNA residues 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	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Dec	Timle	B	ond leng	gths	В	ond ang	les
	Type	Chain	\mathbf{Res}	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2									
2	ALC	D	6	2	$9,\!11,\!12$	1.07	0	$10,\!13,\!15$	1.46	1 (10%)									
2	ALC	С	6	2	$9,\!11,\!12$	1.05	0	10, 13, 15	1.52	2 (20%)									

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	\mathbf{Res}	Link	Chirals	Torsions	Rings
2	ALC	D	6	2	-	1/5/14/16	0/1/1/1
2	ALC	С	6	2	-	1/5/14/16	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	D	6	ALC	CB-CG-CD2	-3.35	104.45	111.73
2	С	6	ALC	CE2-CD2-CG	-3.21	106.09	112.15
2	С	6	ALC	CB-CG-CD2	-2.18	107.01	111.73

There are no chirality outliers.



Mol	Chain	Res	Type	Atoms
2	D	6	ALC	N-CA-CB-CG
2	С	6	ALC	N-CA-CB-CG

All (2) torsion outliers are listed below:

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 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	Chain	Chain Res	s Link	Bond lengths			Bond angles		
IVIOI		Unam			Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	SO4	В	701	-	4,4,4	0.57	0	6,6,6	0.59	0
3	SO4	В	702	-	4,4,4	0.60	0	6,6,6	0.56	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 (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, 95^{th} 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	А	213/219~(97%)	0.31	15 (7%) 16 18	11, 19, 58, 85	0
1	В	214/219 (97%)	0.43	16 (7%) 14 16	12, 22, 75, 94	0
2	С	7/11~(63%)	0.62	1 (14%) 2 2	17, 24, 30, 40	0
2	D	7/11~(63%)	0.16	0 100 100	17, 22, 26, 32	0
All	All	441/460 (95%)	0.37	32 (7%) 15 17	11, 20, 65, 94	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	553	ALA	6.3
1	В	555	ASP	5.7
1	В	556	LYS	5.2
1	В	559	ALA	5.1
1	В	554	GLY	5.0

6.2 Non-standard residues in protein, DNA, RNA chains (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. The B-factors column lists the minimum, median, 95^{th} 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	\mathbf{Res}	Atoms	RSCC	\mathbf{RSR}	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	$Q{<}0.9$
2	ALC	D	6	11/12	0.94	0.09	$16,\!17,\!20,\!21$	0
2	ALC	С	6	11/12	0.97	0.07	$13,\!14,\!18,\!18$	0

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. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
3	SO4	В	701	5/5	0.85	0.31	$43,\!50,\!58,\!59$	0
3	SO4	В	702	5/5	0.94	0.22	$41,\!42,\!53,\!57$	0

6.5 Other polymers (i)

There are no such residues in this entry.

