wwPDB X-ray Structure Validation Summary Report (i)

Jan 5, 2022 – 09:07 pm GMT

PDB ID	:	7AB4
Title	:	Crystal structure of the Escherichia coli toxin-antitoxin system HipBST (HipT S59A)
Authors	:	Baerentsen, R.L.; Brodersen, D.E.
Deposited on	:	2020-09-06
Resolution	:	3.34 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:

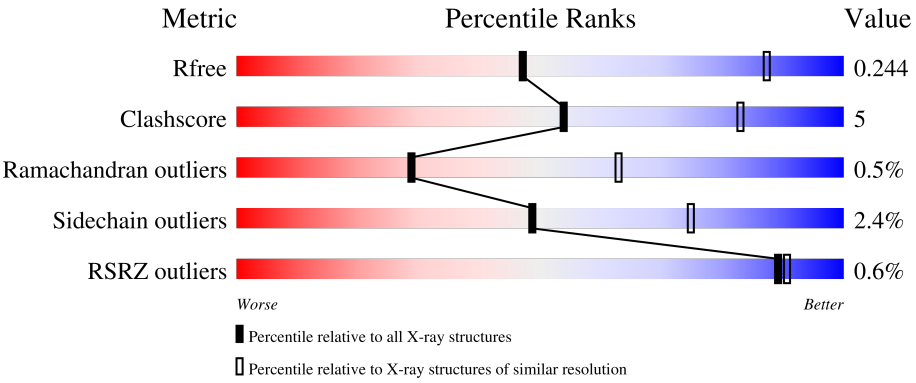
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.24
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.24

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 3.34 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}	130704	1060 (3.38-3.30)
Clashscore	141614	1111 (3.38-3.30)
Ramachandran outliers	138981	1090 (3.38-3.30)
Sidechain outliers	138945	1089 (3.38-3.30)
RSRZ outliers	127900	1028 (3.38-3.30)

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 <=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	106	59% 8% 32%
1	D	106	63% 5% 32%
2	B	102	73% 24%
2	E	102	73% 25%
3	C	340	87% 12%

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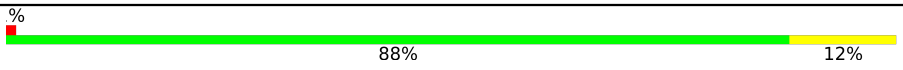
Mol	Chain	Length	Quality of chain
4	F	340	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8241 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 Predicted transcriptional regulator, XRE family.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	72	Total	C	N	O	S	0	0	0
			564	361	99	103	1			
1	D	72	Total	C	N	O	S	0	0	0
			556	356	96	103	1			

- Molecule 2 is a protein called Couple_hipA domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			811	521	145	144	1			
2	E	100	Total	C	N	O	S	0	0	0
			798	513	141	143	1			

- Molecule 3 is a protein called HipA_C domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	339	Total	C	N	O	S	0	0	0
			2745	1749	480	506	10			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	59	ALA	SER	engineered mutation	UNP B7UL96
C	336	HIS	-	expression tag	UNP B7UL96
C	337	HIS	-	expression tag	UNP B7UL96
C	338	HIS	-	expression tag	UNP B7UL96
C	339	HIS	-	expression tag	UNP B7UL96
C	340	HIS	-	expression tag	UNP B7UL96
C	341	HIS	-	expression tag	UNP B7UL96

- Molecule 4 is a protein called HipA_C domain-containing protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	F	340	Total	C	N	O	P	S	0	0	0
			2759	1755	483	510	1	10			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	59	ALA	SER	engineered mutation	UNP B7UL96
F	336	HIS	-	expression tag	UNP B7UL96
F	337	HIS	-	expression tag	UNP B7UL96
F	338	HIS	-	expression tag	UNP B7UL96
F	339	HIS	-	expression tag	UNP B7UL96
F	340	HIS	-	expression tag	UNP B7UL96
F	341	HIS	-	expression tag	UNP B7UL96

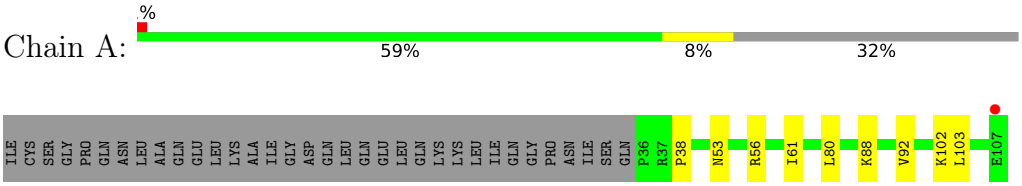
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	3	Total	O	0	0
			3	3		
5	D	3	Total	O	0	0
			3	3		
5	F	2	Total	O	0	0
			2	2		

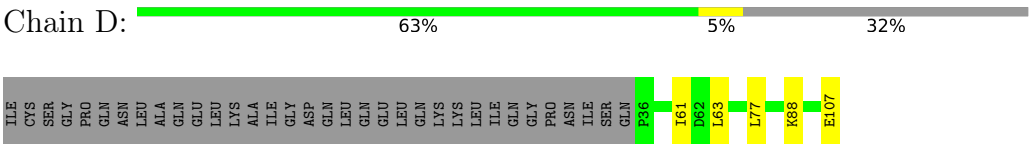
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

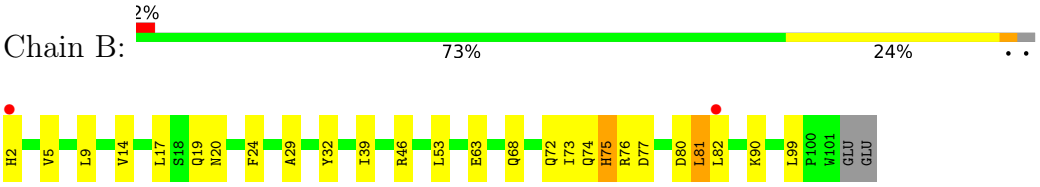
• Molecule 1: Predicted transcriptional regulator, XRE family



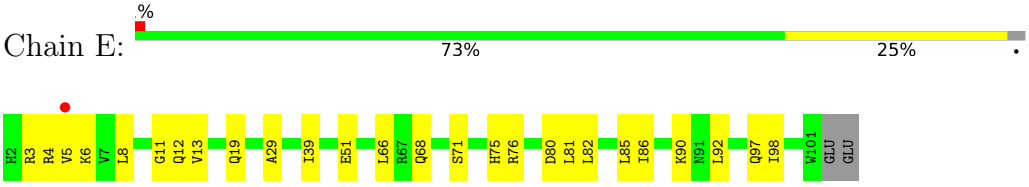
• Molecule 1: Predicted transcriptional regulator, XRE family



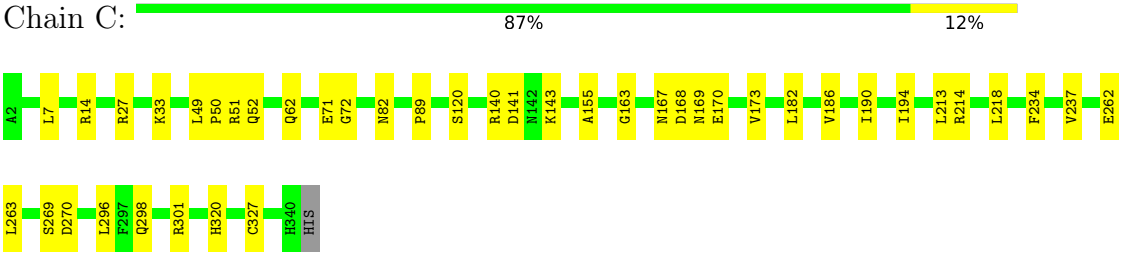
• Molecule 2: Couple_hipA domain-containing protein



• Molecule 2: Couple_hipA domain-containing protein

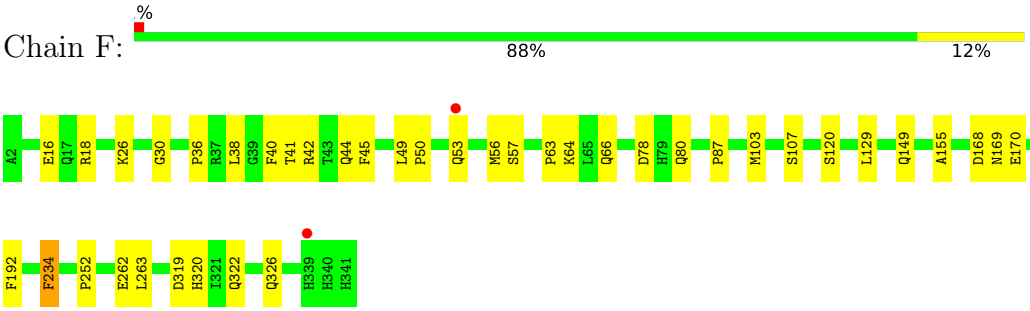


• Molecule 3: HipA_C domain-containing protein



• Molecule 4: HipA_C domain-containing protein

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	285.26Å 107.15Å 58.45Å 90.00° 90.71° 90.00°	Depositor
Resolution (Å)	50.59 – 3.34 50.59 – 3.34	Depositor EDS
% Data completeness (in resolution range)	87.6 (50.59-3.34) 87.6 (50.59-3.34)	Depositor EDS
R_{merge}	0.33	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.17 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.19rc5_4047	Depositor
R, R_{free}	0.202 , 0.243 0.201 , 0.244	Depositor DCC
R_{free} test set	1085 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å^2)	96.0	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	0.053 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8241	wwPDB-VP
Average B, all atoms (Å^2)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.79% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SEP

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	0.26	0/572	0.52	0/771
1	D	0.24	0/563	0.47	0/760
2	B	0.25	0/834	0.49	0/1133
2	E	0.26	0/821	0.51	0/1117
3	C	0.25	0/2813	0.49	0/3809
4	F	0.26	0/2817	0.50	0/3813
All	All	0.25	0/8420	0.49	0/11403

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

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	564	0	597	5	0
1	D	556	0	580	5	0
2	B	811	0	791	17	0
2	E	798	0	765	24	0
3	C	2745	0	2671	23	1
4	F	2759	0	2676	24	0
5	C	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	3	0	0	0	0
5	F	2	0	0	0	0
All	All	8241	0	8080	87	1

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 5.

The worst 5 of 87 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)
2:B:19:GLN:NE2	2:B:20:ASN:O	2.11	0.84
1:A:53:ASN:OD1	1:A:56:ARG:NH1	2.20	0.73
2:E:4:ARG:NH2	2:E:19:GLN:O	2.21	0.73
2:E:8:LEU:HD23	2:E:97:GLN:O	1.89	0.72
2:E:71:SER:HA	2:E:76:ARG:H	1.56	0.70

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:14:ARG:NH1	3:C:269:SER:O[1_556]	2.08	0.12

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	70/106 (66%)	67 (96%)	2 (3%)	1 (1%)	11 41
1	D	70/106 (66%)	68 (97%)	2 (3%)	0	100 100
2	B	98/102 (96%)	92 (94%)	4 (4%)	2 (2%)	7 34
2	E	98/102 (96%)	93 (95%)	4 (4%)	1 (1%)	15 49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	C	337/340 (99%)	322 (96%)	15 (4%)	0	100 100
4	F	337/340 (99%)	324 (96%)	12 (4%)	1 (0%)	41 72
All	All	1010/1096 (92%)	966 (96%)	39 (4%)	5 (0%)	29 63

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	F	40	PHE
1	A	38	PRO
2	B	81	LEU
2	E	29	ALA
2	B	75	HIS

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	63/92 (68%)	62 (98%)	1 (2%)	62 81
1	D	61/92 (66%)	61 (100%)	0	100 100
2	B	86/88 (98%)	84 (98%)	2 (2%)	50 75
2	E	83/88 (94%)	83 (100%)	0	100 100
3	C	292/293 (100%)	283 (97%)	9 (3%)	40 69
4	F	292/292 (100%)	283 (97%)	9 (3%)	40 69
All	All	877/945 (93%)	856 (98%)	21 (2%)	49 75

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	F	42	ARG
4	F	149	GLN
4	F	320	HIS
4	F	192	PHE
4	F	120	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	52	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)

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
4	SEP	F	57	4	8,9,10	1.58	1 (12%)	8,12,14	1.30	1 (12%)

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
4	SEP	F	57	4	-	1/5/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	57	SEP	P-O1P	3.41	1.61	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	F	57	SEP	P-OG-CB	-2.57	111.22	118.30

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	57	SEP	CB-OG-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

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

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, 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	A	72/106 (67%)	-0.39	1 (1%) 75 75	61, 78, 113, 147	0
1	D	72/106 (67%)	-0.55	0 100 100	61, 79, 115, 136	0
2	B	100/102 (98%)	-0.10	2 (2%) 65 64	89, 126, 221, 261	0
2	E	100/102 (98%)	-0.08	1 (1%) 82 83	94, 153, 241, 289	0
3	C	339/340 (99%)	-0.34	0 100 100	59, 85, 133, 168	3 (0%)
4	F	339/340 (99%)	-0.35	2 (0%) 89 90	54, 91, 155, 258	3 (0%)
All	All	1022/1096 (93%)	-0.31	6 (0%) 89 90	54, 92, 173, 289	6 (0%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	2	HIS	3.8
1	A	107	GLU	2.9
4	F	339	HIS	2.9
2	E	5	VAL	2.2
2	B	82	LEU	2.2

6.2 Non-standard residues in protein, DNA, RNA chains

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	B-factors(Å^2)	Q<0.9
4	SEP	F	57	10/11	0.88	0.28	98,118,139,141	10

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.