



# Full wwPDB X-ray Structure Validation Report i

Jan 5, 2022 – 09:05 pm GMT

PDB ID : 7AB5  
Title : Crystal structure of the Escherichia coli toxin-antitoxin system HipBST (HipT D233Q)  
Authors : Baerentsen, R.L.; Brodersen, D.E.  
Deposited on : 2020-09-06  
Resolution : 2.90 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](mailto: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.

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

MolProbity	:	4.02b-467
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

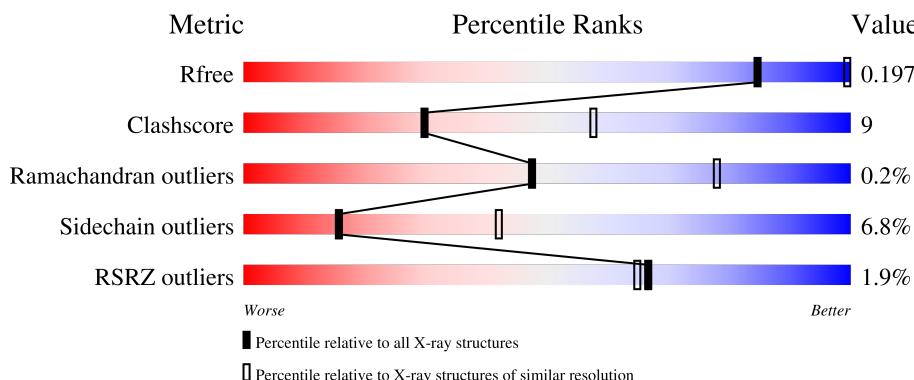
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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  $\geq 3$ , 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.



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Mol	Chain	Length	Quality of chain		
3	F	340	%	79%	19% ..

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 8204 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	70	Total	C	N	O	S	0	0
			546	350	94	101	1		

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	D	70	Total	C	N	O	S	0	0
			546	350	94	101	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
			811	521	145	144	1		

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

- Molecule 3 is a protein called HipA\_C domain-containing protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	338	Total	C	N	O	S	0	1
			2746	1749	480	507	10		

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	337	Total	C	N	O	S	0	1
			2739	1747	476	506	10		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	233	GLN	ASP	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
F	233	GLN	ASP	engineered mutation	UNP B7UL96

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Chain	Residue	Modelled	Actual	Comment	Reference
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

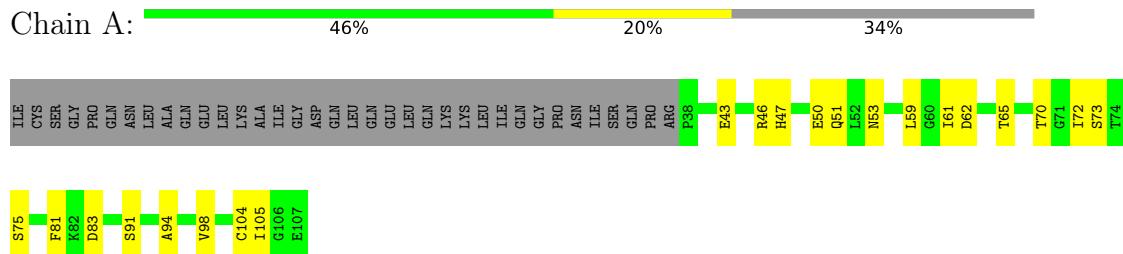
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O 1 1	0	0
4	D	1	Total O 1 1	0	0
4	F	3	Total O 3 3	0	0

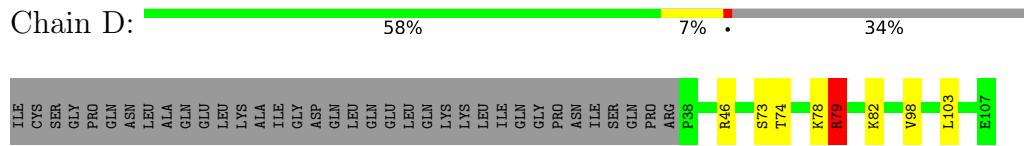
### 3 Residue-property plots [\(i\)](#)

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.

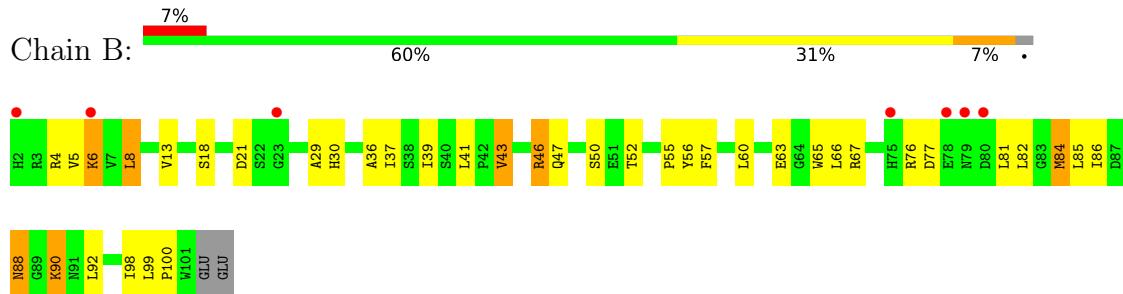
- Molecule 1: Predicted transcriptional regulator, XRE family



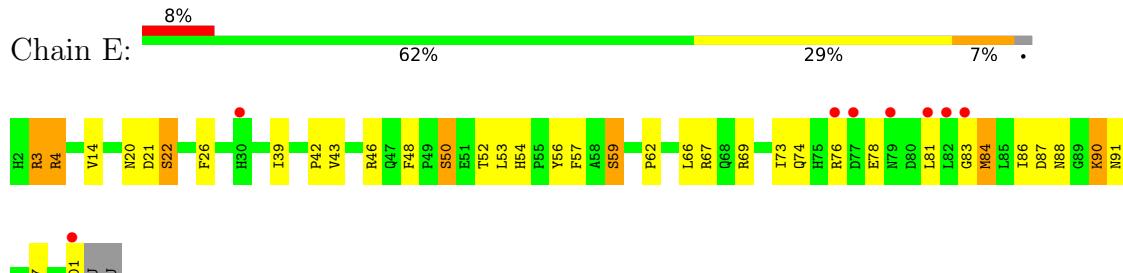
- Molecule 1: Predicted transcriptional regulator, XRE family



- Molecule 2: Couple\_ hipA domain-containing protein

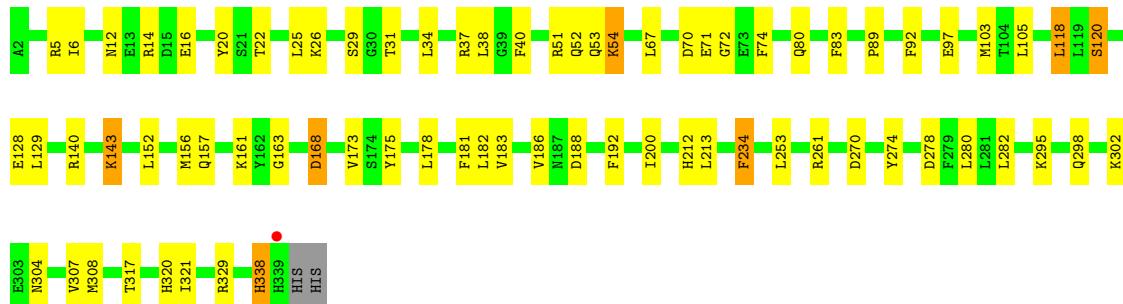


- Molecule 2: Couple\_ hipA domain-containing protein



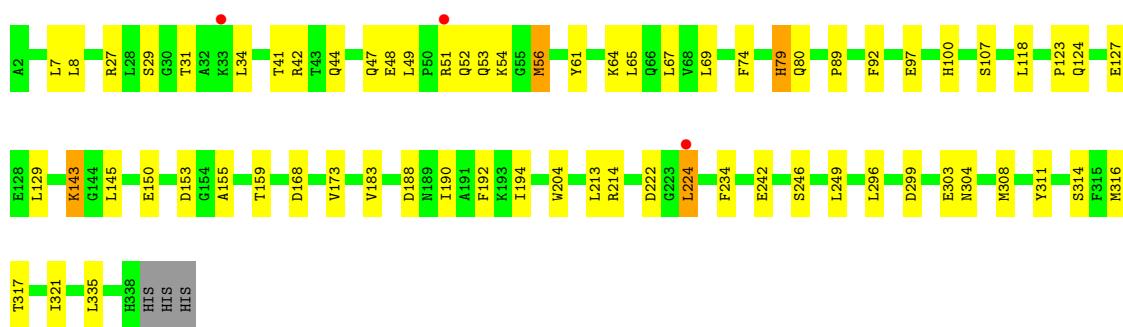
- Molecule 3: HipA\_C domain-containing protein

Chain C:



- Molecule 3: 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, $\alpha$ , $\beta$ , $\gamma$	281.66Å 106.47Å 57.75Å 90.00° 90.75° 90.00°	Depositor
Resolution (Å)	49.86 – 2.90 49.86 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.86-2.90) 99.8 (49.86-2.90)	Depositor EDS
$R_{merge}$	0.19	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) >$ <sup>1</sup>	1.21 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.19rc5_4047	Depositor
$R$ , $R_{free}$	0.193 , 0.226 0.195 , 0.197	Depositor DCC
$R_{free}$ test set	1891 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	77.9	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.49$ , $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8204	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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 [\(i\)](#)

### 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	0.26	0/553	0.49	0/745
1	D	0.26	0/553	0.59	1/745 (0.1%)
2	B	0.25	0/834	0.53	0/1133
2	E	0.30	0/834	0.60	1/1133 (0.1%)
3	C	0.26	0/2813	0.52	0/3808
3	F	0.26	0/2806	0.51	0/3799
All	All	0.26	0/8393	0.53	2/11363 (0.0%)

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	D	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	E	84	MET	CA-CB-CG	5.22	122.18	113.30
1	D	79	ARG	CG-CD-NE	-5.05	101.20	111.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	79	ARG	Sidechain

## 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	546	0	577	11	0
1	D	546	0	577	5	0
2	B	811	0	791	27	0
2	E	811	0	791	36	0
3	C	2746	0	2675	45	0
3	F	2739	0	2669	42	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
4	F	3	0	0	1	0
All	All	8204	0	8080	153	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 9.

All (153) 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:E:62:PRO:HD3	2:E:88:ASN:HD21	1.43	0.84
2:E:3:ARG:HD3	2:E:4:ARG:H	1.42	0.84
3:F:173:VAL:HG11	3:F:213:LEU:HD11	1.64	0.80
3:C:71:GLU:HG2	3:C:72:GLY:H	1.47	0.80
3:F:89:PRO:HG2	3:F:92:PHE:HB2	1.64	0.79
2:E:3:ARG:NH1	2:E:4:ARG:O	2.15	0.79
2:E:59:SER:HA	3:F:214:ARG:HH21	1.47	0.78
3:C:89:PRO:HG2	3:C:92:PHE:HB2	1.67	0.76
1:A:62:ASP:OD2	1:A:65:THR:OG1	2.04	0.75
3:F:47:GLN:OE1	3:F:47:GLN:N	2.23	0.71
2:E:3:ARG:HD3	2:E:4:ARG:N	2.06	0.70
3:F:100:HIS:ND1	4:F:402:HOH:O	2.24	0.70
3:F:143:LYS:HB2	3:F:145:LEU:HD23	1.76	0.68
2:E:78:GLU:HA	2:E:84:MET:CE	2.24	0.68
2:B:57:PHE:HA	2:B:60:LEU:HD12	1.77	0.67
2:E:76:ARG:NH1	2:E:83:GLY:O	2.28	0.67
2:B:63:GLU:HA	2:B:67:ARG:HE	1.58	0.67
2:B:36:ALA:HB2	2:B:43:VAL:HG22	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:61:TYR:HD1	3:F:92:PHE:HE2	1.43	0.66
2:E:88:ASN:O	2:E:91:ASN:N	2.28	0.66
2:E:3:ARG:HH22	2:E:101:TRP:HB2	1.60	0.66
2:B:29:ALA:O	2:B:46:ARG:NH2	2.28	0.65
3:C:29:SER:HB3	3:C:34:LEU:HD22	1.82	0.62
1:A:105:ILE:HG22	1:D:103:LEU:HD12	1.79	0.62
2:B:39:ILE:HD11	3:C:181:PHE:HZ	1.65	0.61
2:B:84:MET:O	2:B:88:ASN:ND2	2.34	0.61
3:C:280:LEU:HD11	3:C:338:HIS:HB2	1.83	0.60
3:C:183:VAL:HG12	3:C:192:PHE:HE2	1.66	0.59
1:A:46:ARG:O	1:A:50:GLU:HG3	2.03	0.58
2:E:69:ARG:HD2	3:F:47:GLN:NE2	2.19	0.58
2:E:53:LEU:HB2	2:E:81:LEU:HD23	1.85	0.58
3:F:53:GLN:HG3	3:F:54:LYS:H	1.69	0.58
3:C:253:LEU:HD11	3:C:282:LEU:HD22	1.86	0.58
2:B:76:ARG:HD2	2:B:81:LEU:HD12	1.86	0.57
2:B:63:GLU:HA	2:B:67:ARG:HB2	1.87	0.56
3:C:163:GLY:HA3	3:C:173:VAL:HG12	1.88	0.56
3:F:204:TRP:HB2	3:F:249:LEU:HD21	1.86	0.56
2:E:90:LYS:NZ	2:E:97:GLN:OE1	2.38	0.56
3:C:12:ASN:OD1	3:C:14:ARG:HB2	2.06	0.56
2:B:50:SER:OG	2:B:52:THR:O	2.17	0.56
2:E:78:GLU:HA	2:E:84:MET:HE2	1.87	0.56
3:F:190:ILE:O	3:F:194:ILE:HG13	2.06	0.56
3:C:67:LEU:HB2	3:C:83:PHE:HB2	1.88	0.55
3:C:37:ARG:HH11	3:C:120:SER:HB3	1.72	0.54
2:E:62:PRO:HD3	2:E:88:ASN:ND2	2.17	0.54
2:B:6:LYS:HE2	2:B:13:VAL:HG11	1.90	0.54
2:B:77:ASP:HB3	2:B:81:LEU:H	1.73	0.54
3:C:71:GLU:N	3:C:71:GLU:OE1	2.42	0.53
2:E:20:ASN:OD1	2:E:21:ASP:N	2.42	0.53
3:C:308:MET:HE1	3:C:329:ARG:HH21	1.72	0.53
1:A:94:ALA:O	1:A:98:VAL:HG23	2.09	0.52
3:C:103:MET:HE2	3:C:234:PHE:HB2	1.91	0.52
3:C:274:TYR:HA	3:C:278:ASP:OD2	2.08	0.52
3:F:29:SER:HB3	3:F:34:LEU:HD22	1.90	0.52
1:D:98:VAL:HG22	3:F:190:ILE:HB	1.91	0.52
2:E:20:ASN:OD1	2:E:22:SER:N	2.42	0.52
2:E:54:HIS:HB2	2:E:57:PHE:HD2	1.75	0.52
2:E:74:GLN:OE1	2:E:87:ASP:OD2	2.28	0.52
3:C:5:ARG:HH11	3:C:118:LEU:HD23	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:76:ARG:HH12	2:E:86:ILE:HD11	1.74	0.51
1:D:46:ARG:HG3	1:D:82:LYS:O	2.11	0.51
3:F:67:LEU:HD23	3:F:74:PHE:CD1	2.45	0.51
3:F:183:VAL:HG12	3:F:192:PHE:HE2	1.76	0.51
2:B:56:TYR:CE2	2:B:60:LEU:HD11	2.46	0.50
3:C:308:MET:HE1	3:C:329:ARG:NH2	2.26	0.50
3:C:182:LEU:O	3:C:186:VAL:HG22	2.11	0.50
3:F:56:MET:HE3	3:F:61:TYR:CE2	2.47	0.50
2:E:50:SER:OG	2:E:52:THR:O	2.29	0.50
3:C:97:GLU:HG3	3:C:118:LEU:HD21	1.93	0.50
2:E:91:ASN:OD1	3:F:79:HIS:HA	2.12	0.50
3:F:56:MET:HE3	3:F:61:TYR:HE2	1.77	0.50
3:C:71:GLU:HG2	3:C:72:GLY:N	2.23	0.49
3:F:61:TYR:CD1	3:F:92:PHE:HE2	2.26	0.49
3:F:314:SER:OG	3:F:316:MET:HG3	2.13	0.49
3:C:152:LEU:O	3:C:156:MET:HG3	2.13	0.49
3:F:304:ASN:O	3:F:308:MET:HG2	2.13	0.48
3:C:38:LEU:HD22	3:C:40:PHE:CZ	2.49	0.48
2:E:88:ASN:OD1	2:E:88:ASN:N	2.45	0.48
3:C:20:TYR:HB3	3:C:25:LEU:HD13	1.96	0.48
2:E:4:ARG:O	2:E:4:ARG:HG2	2.13	0.48
3:C:188:ASP:OD1	3:C:188:ASP:N	2.35	0.48
3:F:29:SER:OG	3:F:31:THR:O	2.31	0.48
3:F:41:THR:HG23	3:F:44:GLN:HB2	1.95	0.48
2:B:65:TRP:HE3	2:B:66:LEU:HD23	1.77	0.47
3:C:161:LYS:HE3	3:C:212:HIS:CE1	2.48	0.47
1:A:70:THR:OG1	1:A:72:ILE:HD12	2.13	0.47
3:F:299:ASP:O	3:F:303:GLU:HG3	2.14	0.47
2:E:26:PHE:HB3	2:E:48:PHE:HB2	1.97	0.47
3:C:51:ARG:NH2	3:C:54:LYS:HD3	2.30	0.47
1:A:46:ARG:HB2	1:A:83:ASP:OD1	2.15	0.47
3:F:42:ARG:NH2	3:F:48:GLU:OE1	2.48	0.46
2:B:57:PHE:HA	2:B:60:LEU:CD1	2.44	0.46
3:F:8:LEU:HD22	3:F:314:SER:HA	1.96	0.46
2:E:42:PRO:HD2	2:E:48:PHE:HZ	1.80	0.46
2:B:8:LEU:HB3	2:B:13:VAL:HA	1.99	0.45
2:B:86:ILE:HD12	2:B:86:ILE:H	1.80	0.45
3:F:311:TYR:O	3:F:321:ILE:HD13	2.16	0.45
2:B:76:ARG:HD2	2:B:81:LEU:CD1	2.45	0.45
2:E:21:ASP:N	2:E:21:ASP:OD2	2.42	0.45
3:F:224:LEU:H	3:F:224:LEU:HG	1.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:ASN:HB2	1:A:81:PHE:HB3	1.98	0.45
1:D:74:THR:O	1:D:78:LYS:HG3	2.17	0.45
2:B:5:VAL:HG21	2:B:98:ILE:HG23	1.99	0.45
2:B:37:ILE:HD11	2:B:41:LEU:HD12	1.97	0.44
2:B:55:PRO:HB2	3:C:157:GLN:HA	1.99	0.44
2:E:90:LYS:HE3	2:E:90:LYS:HB3	1.57	0.44
1:A:59:LEU:HB2	1:A:61:ILE:HD12	1.99	0.44
2:E:56:TYR:HE1	3:F:150:GLU:HG3	1.83	0.44
2:B:8:LEU:HD21	2:B:99:LEU:HD12	2.00	0.44
2:B:90:LYS:HE2	2:B:90:LYS:HB3	1.70	0.44
2:E:39:ILE:HD11	3:F:155:ALA:HB1	2.00	0.44
1:A:43:GLU:HG2	1:A:47:HIS:ND1	2.33	0.44
2:E:43:VAL:O	2:E:46:ARG:HG2	2.18	0.44
3:F:97:GLU:HG3	3:F:118:LEU:HD11	1.99	0.44
3:C:103:MET:CE	3:C:234:PHE:HB2	2.48	0.44
3:F:69:LEU:HD12	3:F:69:LEU:HA	1.90	0.43
3:C:143:LYS:HB2	3:C:143:LYS:HE2	1.72	0.43
2:E:69:ARG:HH11	3:F:47:GLN:NE2	2.17	0.43
3:C:80:GLN:HB3	3:C:140:ARG:NH2	2.33	0.43
3:C:317:THR:O	3:C:321:ILE:HG13	2.17	0.43
3:C:54:LYS:HE2	3:C:54:LYS:HB2	1.28	0.43
3:C:280:LEU:CD1	3:C:338:HIS:HB2	2.49	0.43
1:A:72:ILE:HG12	1:A:91:SER:OG	2.19	0.43
3:C:173:VAL:HG11	3:C:213:LEU:HD11	2.00	0.43
2:E:59:SER:HB2	3:F:153:ASP:OD2	2.18	0.43
1:A:47:HIS:O	1:A:51:GLN:HG2	2.19	0.43
1:D:79:ARG:HD3	1:D:79:ARG:HA	1.30	0.43
3:F:49:LEU:HD12	3:F:52:GLN:HG3	2.00	0.43
3:F:123:PRO:HG3	3:F:129:LEU:HD21	2.01	0.43
2:E:86:ILE:HD12	2:E:87:ASP:OD1	2.19	0.43
3:F:7:LEU:HD21	3:F:27:ARG:HD2	2.01	0.43
3:C:70:ASP:HB3	3:C:71:GLU:OE1	2.19	0.42
3:F:65:LEU:HD23	3:F:65:LEU:HA	1.90	0.42
3:F:124:GLN:HB2	3:F:127:GLU:OE1	2.20	0.42
2:B:39:ILE:HD11	3:C:181:PHE:CZ	2.50	0.42
2:B:43:VAL:O	2:B:46:ARG:HD2	2.19	0.42
3:C:34:LEU:HD11	3:C:74:PHE:CE2	2.54	0.42
3:C:298:GLN:O	3:C:302:LYS:HG3	2.20	0.42
3:C:38:LEU:HD12	3:C:120:SER:O	2.20	0.42
2:B:57:PHE:O	2:B:85:LEU:HD21	2.19	0.42
3:C:105:LEU:HD21	3:C:307:VAL:HG13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:175:TYR:HB3	3:C:200:ILE:HD13	2.02	0.41
3:C:168:ASP:N	3:C:168:ASP:OD1	2.52	0.41
3:F:242:GLU:CD	3:F:242:GLU:H	2.23	0.41
3:C:6:ILE:HD12	3:C:25:LEU:HD12	2.02	0.41
3:F:335:LEU:HD23	3:F:335:LEU:HA	1.93	0.41
2:B:84:MET:SD	2:B:84:MET:N	2.93	0.41
2:B:92:LEU:O	3:C:80:GLN:NE2	2.48	0.41
2:E:66:LEU:H	2:E:66:LEU:HD12	1.85	0.41
2:E:78:GLU:HA	2:E:84:MET:HE3	2.01	0.41
3:C:129:LEU:HD23	3:C:129:LEU:HA	1.89	0.40
2:E:42:PRO:HD2	2:E:48:PHE:CZ	2.56	0.40
3:F:296:LEU:HD23	3:F:296:LEU:HA	1.90	0.40

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	68/106 (64%)	66 (97%)	2 (3%)	0	100 100
1	D	68/106 (64%)	66 (97%)	2 (3%)	0	100 100
2	B	98/102 (96%)	94 (96%)	4 (4%)	0	100 100
2	E	98/102 (96%)	91 (93%)	7 (7%)	0	100 100
3	C	337/340 (99%)	321 (95%)	15 (4%)	1 (0%)	41 71
3	F	336/340 (99%)	318 (95%)	17 (5%)	1 (0%)	41 71
All	All	1005/1096 (92%)	956 (95%)	47 (5%)	2 (0%)	47 78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	53	GLN

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Mol	Chain	Res	Type
3	F	80	GLN

### 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	61/92 (66%)	58 (95%)	3 (5%)	25 57
1	D	61/92 (66%)	60 (98%)	1 (2%)	62 86
2	B	86/88 (98%)	72 (84%)	14 (16%)	2 7
2	E	86/88 (98%)	77 (90%)	9 (10%)	7 21
3	C	293/294 (100%)	274 (94%)	19 (6%)	17 45
3	F	292/294 (99%)	278 (95%)	14 (5%)	25 58
All	All	879/948 (93%)	819 (93%)	60 (7%)	16 42

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	SER
1	A	75	SER
1	A	104	CYS
2	B	4	ARG
2	B	6	LYS
2	B	8	LEU
2	B	18	SER
2	B	21	ASP
2	B	30	HIS
2	B	43	VAL
2	B	46	ARG
2	B	47	GLN
2	B	82	LEU
2	B	84	MET
2	B	88	ASN
2	B	90	LYS
2	B	100	PRO

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Mol	Chain	Res	Type
3	C	16	GLU
3	C	22	THR
3	C	26	LYS
3	C	31	THR
3	C	52	GLN
3	C	54	LYS
3	C	118	LEU
3	C	120	SER
3	C	128	GLU
3	C	143	LYS
3	C	168	ASP
3	C	178	LEU
3	C	234	PHE
3	C	261	ARG
3	C	270	ASP
3	C	295	LYS
3	C	304	ASN
3	C	320	HIS
3	C	338	HIS
1	D	73	SER
2	E	3	ARG
2	E	4	ARG
2	E	14	VAL
2	E	22	SER
2	E	50	SER
2	E	59	SER
2	E	67	ARG
2	E	73	ILE
2	E	90	LYS
3	F	51	ARG
3	F	56	MET
3	F	64	LYS
3	F	79	HIS
3	F	107	SER
3	F	143	LYS
3	F	159	THR
3	F	168	ASP
3	F	188	ASP
3	F	222	ASP
3	F	224	LEU
3	F	234	PHE
3	F	246	SER

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Mol	Chain	Res	Type
3	F	317	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	68	GLN
2	B	88	ASN
3	C	17	GLN
3	C	338	HIS
2	E	74	GLN

### 5.3.3 RNA [\(i\)](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	70/106 (66%)	-0.33	0 [100] [100]	56, 68, 93, 140	0
1	D	70/106 (66%)	-0.40	0 [100] [100]	50, 67, 95, 121	0
2	B	100/102 (98%)	0.35	7 (7%) [16] [12]	80, 110, 170, 210	0
2	E	100/102 (98%)	0.61	8 (8%) [12] [9]	83, 142, 226, 262	0
3	C	338/340 (99%)	-0.21	1 (0%) [94] [94]	51, 74, 129, 193	0
3	F	337/340 (99%)	-0.24	3 (0%) [84] [84]	46, 74, 135, 180	0
All	All	1015/1096 (92%)	-0.11	19 (1%) [66] [65]	46, 78, 161, 262	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	82	LEU	4.6
2	E	81	LEU	4.5
2	B	80	ASP	4.5
2	E	79	ASN	3.7
2	E	77	ASP	3.6
3	F	224	LEU	3.1
3	F	33	LYS	2.9
3	F	51	ARG	2.8
2	B	78	GLU	2.6
2	B	79	ASN	2.5
2	B	75	HIS	2.5
2	B	2	HIS	2.4
2	B	23	GLY	2.3
2	E	76	ARG	2.3
2	E	83	GLY	2.2
3	C	339	HIS	2.2
2	B	6	LYS	2.2
2	E	30	HIS	2.1
2	E	101	TRP	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 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.