



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 09:00 PM GMT

PDB ID : 2OX7  
Title : Crystal structure of protein EF1440 from Enterococcus faecalis  
Authors : Malashkevich, V.N.; Toro, R.; Sauder, J.M.; Schwinn, K.D.; Thompson, D.A.;  
Bain, K.T.; Adams, J.M.; Reyes, C.; Lau, C.; Gilmore, J.; Rooney, I.; Gheyi,  
T.; Wasserman, S.R.; Emtage, S.; Burley, S.K.; Almo, S.C.; New York SGX  
Research Center for Structural Genomics (NYSGXRC)  
Deposited on : 2007-02-19  
Resolution : 1.78 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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

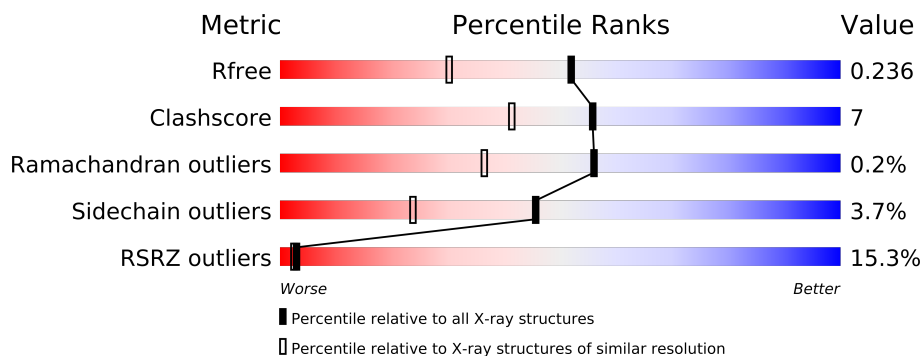
MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683



# 1 Overall quality at a glance

The reported resolution of this entry is 1.78 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))
$R_{free}$	66092	4987 (1.80-1.76)
Clashscore	79885	6152 (1.80-1.76)
Ramachandran outliers	78287	6074 (1.80-1.76)
Sidechain outliers	78261	6073 (1.80-1.76)
RSRZ outliers	66119	4990 (1.80-1.76)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	155	
1	B	155	
1	C	155	
1	D	155	



## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5377 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Hypothetical protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	144	Total	C	N	O	S	Se	0	0	0
			1183	765	185	228	1	4			
1	B	144	Total	C	N	O	S	Se	0	0	0
			1183	765	185	228	1	4			
1	C	143	Total	C	N	O	S	Se	0	0	0
			1174	760	184	225	1	4			
1	D	143	Total	C	N	O	S	Se	0	0	0
			1174	760	184	225	1	4			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	CLONING ARTIFACT	UNP Q835D7
A	2	SER	-	CLONING ARTIFACT	UNP Q835D7
A	3	LEU	-	CLONING ARTIFACT	UNP Q835D7
A	17	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
A	31	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
A	68	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
A	101	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
A	148	GLU	-	CLONING ARTIFACT	UNP Q835D7
A	149	GLY	-	CLONING ARTIFACT	UNP Q835D7
A	150	HIS	-	CLONING ARTIFACT	UNP Q835D7
A	151	HIS	-	CLONING ARTIFACT	UNP Q835D7
A	152	HIS	-	CLONING ARTIFACT	UNP Q835D7
A	153	HIS	-	CLONING ARTIFACT	UNP Q835D7
A	154	HIS	-	CLONING ARTIFACT	UNP Q835D7
A	155	HIS	-	CLONING ARTIFACT	UNP Q835D7
B	1	MET	-	CLONING ARTIFACT	UNP Q835D7
B	2	SER	-	CLONING ARTIFACT	UNP Q835D7
B	3	LEU	-	CLONING ARTIFACT	UNP Q835D7
B	17	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
B	31	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
B	68	MSE	MET	MODIFIED RESIDUE	UNP Q835D7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	101	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
B	148	GLU	-	CLONING ARTIFACT	UNP Q835D7
B	149	GLY	-	CLONING ARTIFACT	UNP Q835D7
B	150	HIS	-	CLONING ARTIFACT	UNP Q835D7
B	151	HIS	-	CLONING ARTIFACT	UNP Q835D7
B	152	HIS	-	CLONING ARTIFACT	UNP Q835D7
B	153	HIS	-	CLONING ARTIFACT	UNP Q835D7
B	154	HIS	-	CLONING ARTIFACT	UNP Q835D7
B	155	HIS	-	CLONING ARTIFACT	UNP Q835D7
C	1	MET	-	CLONING ARTIFACT	UNP Q835D7
C	2	SER	-	CLONING ARTIFACT	UNP Q835D7
C	3	LEU	-	CLONING ARTIFACT	UNP Q835D7
C	17	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
C	31	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
C	68	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
C	101	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
C	148	GLU	-	CLONING ARTIFACT	UNP Q835D7
C	149	GLY	-	CLONING ARTIFACT	UNP Q835D7
C	150	HIS	-	CLONING ARTIFACT	UNP Q835D7
C	151	HIS	-	CLONING ARTIFACT	UNP Q835D7
C	152	HIS	-	CLONING ARTIFACT	UNP Q835D7
C	153	HIS	-	CLONING ARTIFACT	UNP Q835D7
C	154	HIS	-	CLONING ARTIFACT	UNP Q835D7
C	155	HIS	-	CLONING ARTIFACT	UNP Q835D7
D	1	MET	-	CLONING ARTIFACT	UNP Q835D7
D	2	SER	-	CLONING ARTIFACT	UNP Q835D7
D	3	LEU	-	CLONING ARTIFACT	UNP Q835D7
D	17	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
D	31	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
D	68	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
D	101	MSE	MET	MODIFIED RESIDUE	UNP Q835D7
D	148	GLU	-	CLONING ARTIFACT	UNP Q835D7
D	149	GLY	-	CLONING ARTIFACT	UNP Q835D7
D	150	HIS	-	CLONING ARTIFACT	UNP Q835D7
D	151	HIS	-	CLONING ARTIFACT	UNP Q835D7
D	152	HIS	-	CLONING ARTIFACT	UNP Q835D7
D	153	HIS	-	CLONING ARTIFACT	UNP Q835D7
D	154	HIS	-	CLONING ARTIFACT	UNP Q835D7
D	155	HIS	-	CLONING ARTIFACT	UNP Q835D7

- Molecule 2 is water.



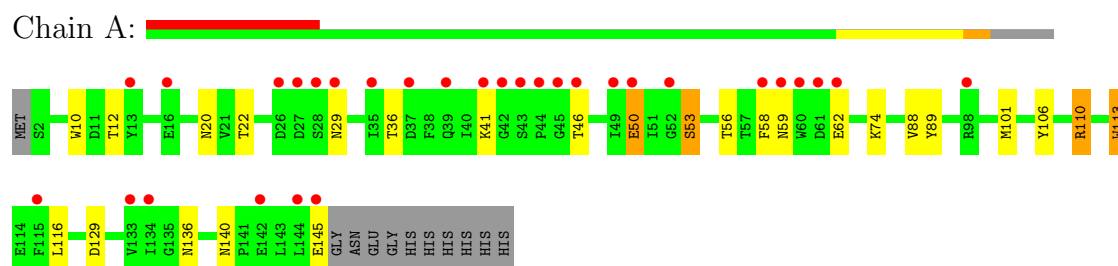
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	131	Total 131	O 131	0	0
2	B	197	Total 197	O 197	0	0
2	C	192	Total 192	O 192	0	0
2	D	143	Total 143	O 143	0	0



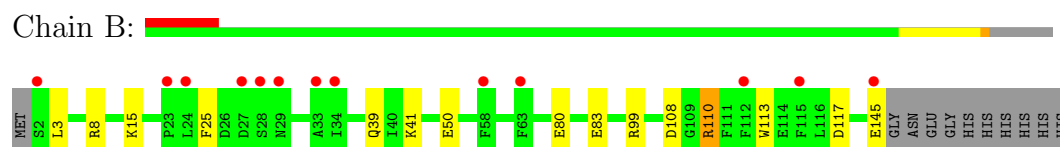
### 3 Residue-property plots

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.

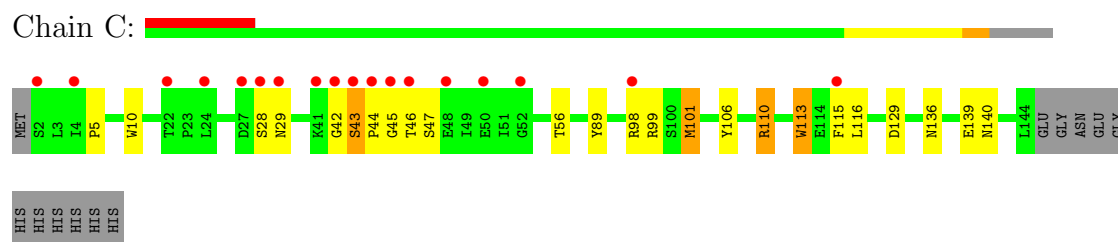
- Molecule 1: Hypothetical protein



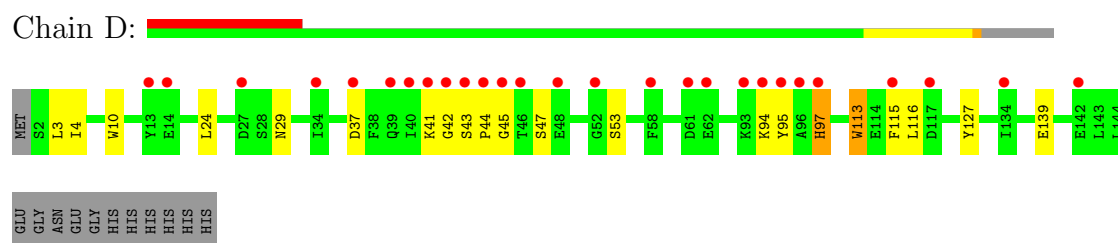
- Molecule 1: Hypothetical protein



- Molecule 1: Hypothetical protein



- Molecule 1: Hypothetical protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.35Å 70.38Å 150.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.63 – 1.78 25.29 – 1.78	Depositor EDS
% Data completeness (in resolution range)	(Not available) (19.63-1.78) 99.5 (25.29-1.78)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.13 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.3.0028	Depositor
R, $R_{free}$	0.190 , 0.235 0.193 , 0.236	Depositor DCC
$R_{free}$ test set	3368 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.0	Xtriage
Anisotropy	0.328	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 55.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 66362 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5377	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% of the height of the origin peak. No significant pseudotranslation is detected.*

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



## 5 Model quality

### 5.1 Standard geometry

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	0.70	0/1211	0.74	1/1635 (0.1%)
1	B	0.85	2/1211 (0.2%)	0.83	2/1635 (0.1%)
1	C	0.88	1/1202 (0.1%)	0.86	2/1623 (0.1%)
1	D	0.68	0/1202	0.73	0/1623
All	All	0.78	3/4826 (0.1%)	0.79	5/6516 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	101	MSE	SE-CE	-7.68	1.50	1.95
1	B	83	GLU	CB-CG	5.49	1.62	1.52
1	B	83	GLU	CD-OE2	5.12	1.31	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	110	ARG	NE-CZ-NH2	-7.33	116.63	120.30
1	B	8	ARG	NE-CZ-NH1	-6.25	117.18	120.30
1	A	110	ARG	NE-CZ-NH2	-6.07	117.27	120.30
1	C	101	MSE	CG-SE-CE	-6.06	85.56	98.90
1	C	110	ARG	NE-CZ-NH2	-5.42	117.59	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the



chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1183	0	1123	16	0
1	B	1183	0	1123	10	0
1	C	1174	0	1117	22	0
1	D	1174	0	1117	22	0
2	A	131	0	0	2	0
2	B	197	0	0	8	0
2	C	192	0	0	0	0
2	D	143	0	0	2	0
All	All	5377	0	4480	61	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (61) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:36:THR:OG1	1:A:53:SER:HB3	1.68	0.92
1:D:42:GLY:HA3	1:D:47:SER:HA	1.53	0.91
1:B:110:ARG:NH2	2:B:348:HOH:O	2.03	0.91
1:A:74:LYS:HE3	2:A:180:HOH:O	1.72	0.88
2:A:283:HOH:O	1:B:117:ASP:HB3	1.73	0.87
1:D:42:GLY:CA	1:D:47:SER:HA	2.14	0.77
1:B:80:GLU:HG2	2:B:253:HOH:O	1.87	0.72
1:A:136:ASN:H	1:A:140:ASN:HD22	1.37	0.71
1:C:136:ASN:H	1:C:140:ASN:HD22	1.39	0.70
1:A:29:ASN:HB3	1:D:4:ILE:HD13	1.72	0.70
1:D:94:LYS:O	1:D:97:HIS:CE1	2.46	0.69
1:A:110:ARG:HD3	2:D:284:HOH:O	1.94	0.65
1:B:110:ARG:CZ	2:B:348:HOH:O	2.43	0.65
1:A:41:LYS:HE3	1:A:50:GLU:OE2	1.96	0.65
1:D:94:LYS:HB2	1:D:97:HIS:HE1	1.60	0.65
1:C:45:GLY:N	1:C:46:THR:HA	2.13	0.63
1:A:88:VAL:CG1	1:A:101:MSE:HG2	2.29	0.62
1:C:10:TRP:CZ3	1:C:139:GLU:HG2	2.37	0.59
1:C:98:ARG:HD2	1:C:99:ARG:N	2.18	0.59
1:B:15:LYS:HE2	2:B:290:HOH:O	2.03	0.58
1:B:3:LEU:HB2	1:C:106:TYR:CD2	2.39	0.57
1:D:44:PRO:HD2	1:D:45:GLY:H	1.70	0.57
1:D:37:ASP:HB3	1:D:53:SER:HB3	1.87	0.57
1:D:94:LYS:HB2	1:D:97:HIS:CE1	2.40	0.56
1:C:115:PHE:HD1	1:D:115:PHE:HD1	1.54	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:224:HOH:O	1:C:110:ARG:HD2	2.07	0.54
2:B:224:HOH:O	1:C:110:ARG:CD	2.56	0.53
1:A:22:THR:HG21	1:D:24:LEU:HD23	1.91	0.52
1:C:28:SER:O	1:C:29:ASN:HB2	2.11	0.51
1:A:36:THR:HG1	1:A:53:SER:HB3	1.75	0.49
1:A:88:VAL:HG12	1:A:101:MSE:HG2	1.94	0.49
1:A:89:TYR:CZ	1:A:129:ASP:HB2	2.48	0.49
1:C:43:SER:N	1:C:44:PRO:HA	2.28	0.48
1:C:45:GLY:N	1:C:46:THR:CA	2.76	0.48
1:A:10:TRP:CD1	1:A:12:THR:HG22	2.48	0.47
1:D:127:TYR:HD2	2:D:314:HOH:O	1.97	0.47
1:C:115:PHE:CD1	1:D:115:PHE:HD1	2.32	0.46
1:D:113:TRP:CE2	1:D:116:LEU:HD23	2.50	0.46
1:C:28:SER:O	1:C:28:SER:OG	2.31	0.46
1:C:43:SER:N	1:C:44:PRO:CA	2.79	0.46
1:A:106:TYR:CD2	1:D:3:LEU:HB2	2.51	0.45
1:A:22:THR:HG21	1:D:24:LEU:CD2	2.46	0.45
1:D:44:PRO:CD	1:D:45:GLY:H	2.30	0.45
1:C:98:ARG:HD2	1:C:99:ARG:H	1.82	0.44
1:C:89:TYR:CZ	1:C:129:ASP:HB2	2.52	0.44
1:D:42:GLY:HA3	1:D:47:SER:CA	2.35	0.44
1:A:113:TRP:CD2	1:A:116:LEU:HD23	2.53	0.43
1:A:59:ASN:ND2	1:D:47:SER:OG	2.51	0.43
1:D:10:TRP:CZ3	1:D:139:GLU:HG3	2.54	0.43
1:B:108:ASP:HA	2:B:156:HOH:O	2.19	0.43
1:C:113:TRP:CE2	1:C:116:LEU:HD23	2.54	0.42
1:C:101:MSE:HB2	1:C:101:MSE:HE2	1.78	0.42
2:B:224:HOH:O	1:C:110:ARG:HD3	2.19	0.42
1:B:39:GLN:NE2	1:B:50:GLU:OE1	2.53	0.42
1:D:113:TRP:CD2	1:D:116:LEU:HD23	2.55	0.42
1:D:10:TRP:CZ3	1:D:139:GLU:CG	3.04	0.41
1:B:25:PHE:CZ	1:C:5:PRO:HD2	2.55	0.41
1:C:42:GLY:HA3	1:C:47:SER:HA	2.01	0.41
1:D:94:LYS:O	1:D:95:TYR:C	2.60	0.40
1:B:41:LYS:HD3	1:B:41:LYS:HA	1.88	0.40
1:C:10:TRP:HZ3	1:C:139:GLU:HG2	1.83	0.40

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	142/155 (92%)	137 (96%)	5 (4%)	0	100	100
1	B	142/155 (92%)	138 (97%)	4 (3%)	0	100	100
1	C	141/155 (91%)	135 (96%)	5 (4%)	1 (1%)	30	12
1	D	141/155 (91%)	132 (94%)	9 (6%)	0	100	100
All	All	566/620 (91%)	542 (96%)	23 (4%)	1 (0%)	56	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	43	SER

### 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	129/134 (96%)	120 (93%)	9 (7%)	21	6
1	B	129/134 (96%)	126 (98%)	3 (2%)	63	43
1	C	128/134 (96%)	126 (98%)	2 (2%)	75	61
1	D	128/134 (96%)	123 (96%)	5 (4%)	43	21
All	All	514/536 (96%)	495 (96%)	19 (4%)	45	24

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	46	THR

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Mol	Chain	Res	Type
1	A	50	GLU
1	A	53	SER
1	A	56	THR
1	A	58	PHE
1	A	62	GLU
1	A	113	TRP
1	A	145	GLU
1	B	99	ARG
1	B	113	TRP
1	B	145	GLU
1	C	56	THR
1	C	113	TRP
1	D	29	ASN
1	D	41	LYS
1	D	43	SER
1	D	97	HIS
1	D	113	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	ASN
1	B	29	ASN
1	C	29	ASN
1	C	77	ASN
1	C	140	ASN
1	D	39	GLN
1	D	97	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no ligands in this entry.

## 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, 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	144/155 (92%)	1.16	30 (20%) 1 1	17, 34, 59, 67	0
1	B	144/155 (92%)	0.60	13 (9%) 10 9	18, 27, 41, 47	0
1	C	143/155 (92%)	0.71	18 (12%) 4 4	16, 24, 46, 64	0
1	D	143/155 (92%)	1.24	27 (18%) 2 1	18, 34, 61, 75	0
All	All	574/620 (92%)	0.93	88 (15%) 3 2	16, 28, 56, 75	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	45	GLY	12.5
1	D	95	TYR	12.3
1	C	43	SER	9.8
1	D	44	PRO	9.4
1	C	44	PRO	9.4
1	D	45	GLY	9.1
1	C	46	THR	9.1
1	D	46	THR	7.8
1	A	59	ASN	7.6
1	A	58	PHE	7.5
1	A	115	PHE	6.9
1	A	45	GLY	6.7
1	D	41	LYS	6.3
1	A	43	SER	6.3
1	B	27	ASP	6.3
1	D	43	SER	6.1
1	D	96	ALA	5.8
1	A	61	ASP	5.7
1	A	13	TYR	5.6
1	A	46	THR	5.6
1	A	42	GLY	5.5

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Mol	Chain	Res	Type	RSRZ
1	D	115	PHE	5.4
1	C	42	GLY	5.4
1	D	42	GLY	5.4
1	A	44	PRO	5.3
1	D	97	HIS	5.2
1	D	40	ILE	4.8
1	B	145	GLU	4.7
1	B	58	PHE	4.3
1	D	94	LYS	4.3
1	D	58	PHE	4.1
1	A	41	LYS	3.9
1	A	62	GLU	3.9
1	A	60	TRP	3.8
1	D	61	ASP	3.6
1	C	28	SER	3.5
1	D	117	ASP	3.3
1	C	29	ASN	3.1
1	D	142	GLU	3.1
1	C	115	PHE	3.1
1	B	28	SER	3.1
1	D	62	GLU	3.1
1	A	37	ASP	3.0
1	A	145	GLU	2.9
1	B	24	LEU	2.8
1	B	115	PHE	2.8
1	B	33	ALA	2.8
1	D	93	LYS	2.8
1	A	28	SER	2.8
1	B	112	PHE	2.7
1	D	52	GLY	2.7
1	C	24	LEU	2.7
1	A	35	ILE	2.7
1	A	98	ARG	2.6
1	C	41	LYS	2.5
1	D	48	GLU	2.5
1	A	39	GLN	2.5
1	B	63	PHE	2.5
1	C	50	GLU	2.5
1	B	29	ASN	2.4
1	C	22	THR	2.4
1	A	27	ASP	2.4
1	D	37	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	27	ASP	2.4
1	C	98	ARG	2.4
1	D	39	GLN	2.3
1	B	34	ILE	2.3
1	C	4	ILE	2.3
1	B	2	SER	2.3
1	C	48	GLU	2.3
1	A	16	GLU	2.3
1	C	27	ASP	2.3
1	A	52	GLY	2.3
1	A	133	VAL	2.3
1	A	29	ASN	2.2
1	A	134	ILE	2.2
1	C	52	GLY	2.2
1	A	50	GLU	2.2
1	B	23	PRO	2.2
1	A	142	GLU	2.2
1	D	14	GLU	2.2
1	C	2	SER	2.2
1	D	134	ILE	2.1
1	A	144	LEU	2.1
1	D	13	TYR	2.1
1	A	49	ILE	2.1
1	D	34	ILE	2.0
1	A	26	ASP	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates 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.