



# wwPDB X-ray Structure Validation Summary Report

Mar 6, 2026 – 10:54 AM UTC

PDB ID : 3WTW / pdb\_00003wtw  
Title : Crystal structure of the complex comprised of ETS1(K167A), RUNX1, CBF-BETA, and the tcralpha gene enhancer DNA  
Authors : Shiina, M.; Hamada, K.; Ogata, K.  
Deposited on : 2014-04-21  
Resolution : 2.90 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](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  symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

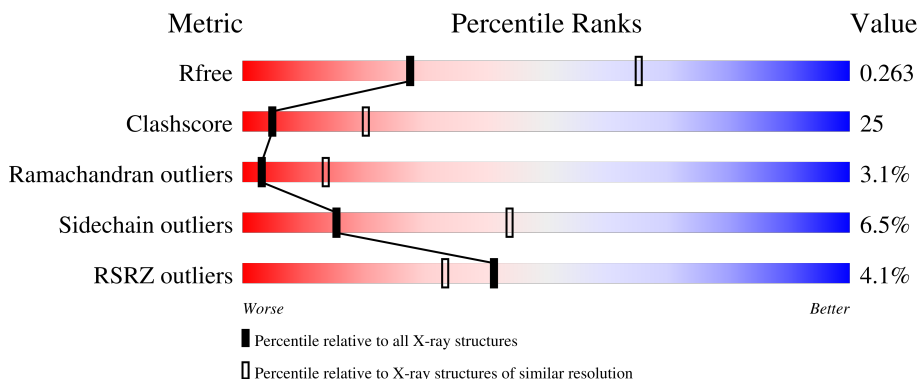
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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.




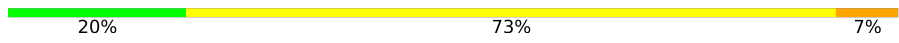
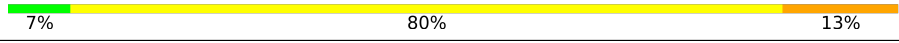

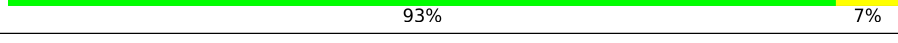
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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.

Mol	Chain	Length	Quality of chain
1	A	204	
1	F	204	
2	B	142	
2	G	142	
3	C	166	

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Mol	Chain	Length	Quality of chain
3	H	166	 13% 21% 31% 9% 39%
4	D	15	 20% 73% 7%
4	I	15	 7% 80% 13%
5	E	15	 87% 13%
5	J	15	 93% 7%

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7014 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 Runt-related transcription factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	118	910	571	168	167	4	0	0	0
1	F	119	921	577	172	168	4	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	94	LYS	LEU	engineered mutation	UNP Q03347
A	167	ALA	LYS	engineered mutation	UNP Q03347
F	94	LYS	LEU	engineered mutation	UNP Q03347
F	167	ALA	LYS	engineered mutation	UNP Q03347

- Molecule 2 is a protein called Core-binding factor subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	130	1071	671	195	199	6	0	0	0
2	G	129	1062	666	193	197	6	0	0	0

- Molecule 3 is a protein called Protein C-ets-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	118	967	627	165	171	4	0	0	0
3	H	101	853	553	147	149	4	0	0	0

- Molecule 4 is a DNA chain called DNA (5'-D(\*GP\*AP\*AP\*GP\*CP\*CP\*AP\*CP\*AP\*TP\*CP\*CP\*TP\*CP\*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	15	Total	C	N	O	P	0	0	0
			299	144	54	87	14			
4	I	15	Total	C	N	O	P	0	0	0
			299	144	54	87	14			

- Molecule 5 is a DNA chain called DNA (5'-D(\*AP\*GP\*AP\*GP\*GP\*AP\*TP\*GP\*TP\*GP\*GP\*CP\*TP\*TP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	15	Total	C	N	O	P	0	0	0
			310	148	59	89	14			
5	J	15	Total	C	N	O	P	0	0	0
			310	148	59	89	14			

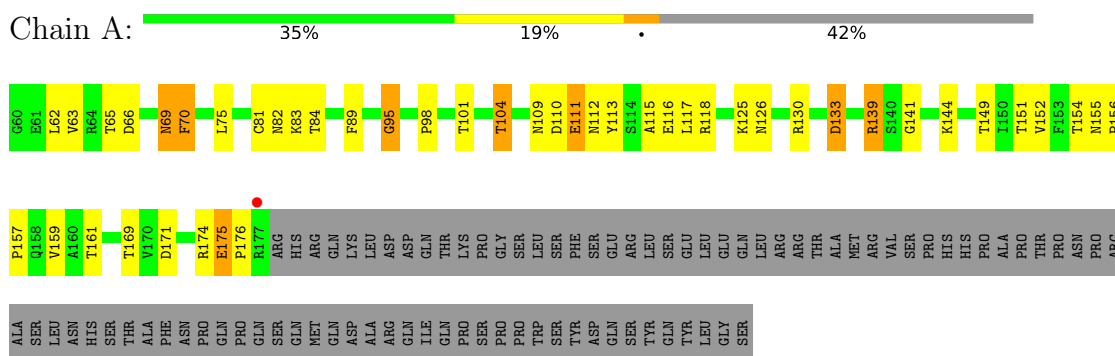
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	O	0	0
			1	1		
6	B	1	Total	O	0	0
			1	1		
6	C	3	Total	O	0	0
			3	3		
6	F	5	Total	O	0	0
			5	5		
6	G	1	Total	O	0	0
			1	1		
6	E	1	Total	O	0	0
			1	1		

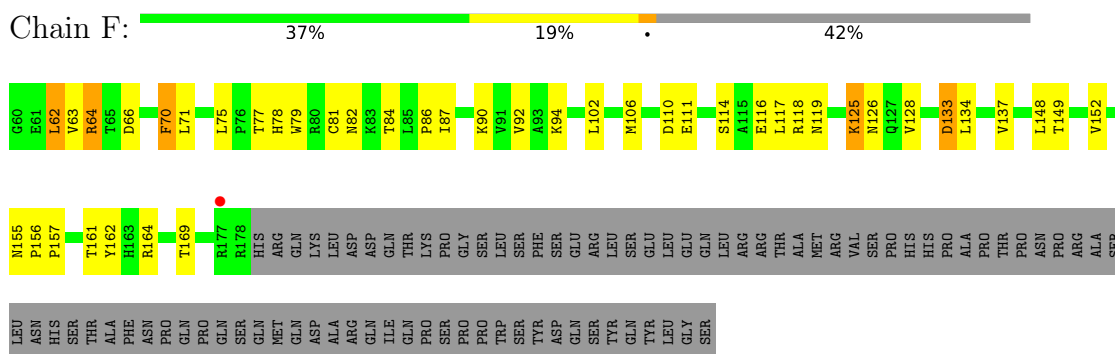
### 3 Residue-property plots [i](#)

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.

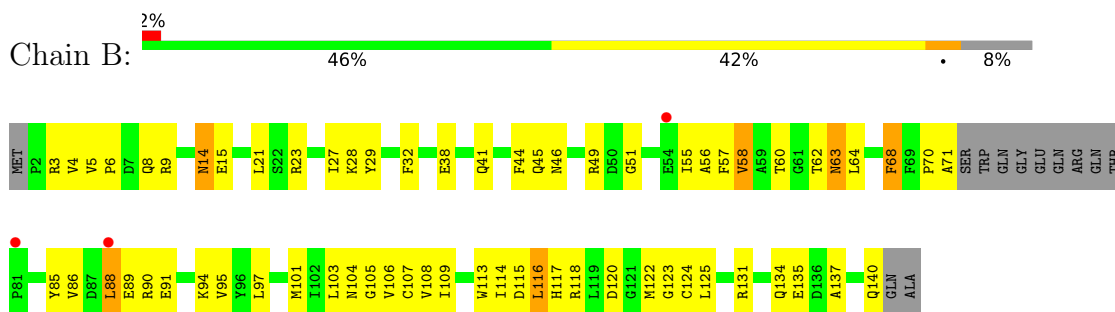
- Molecule 1: Runt-related transcription factor 1



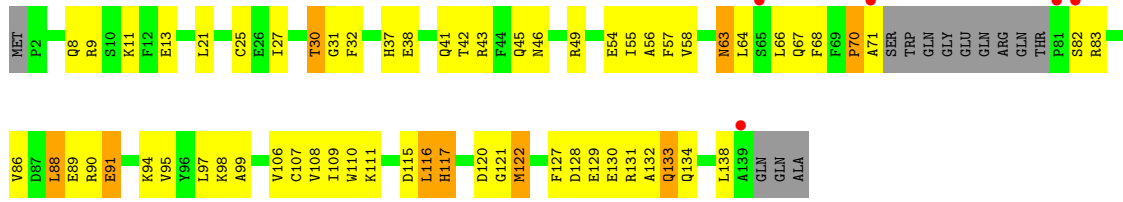
- Molecule 1: Runt-related transcription factor 1



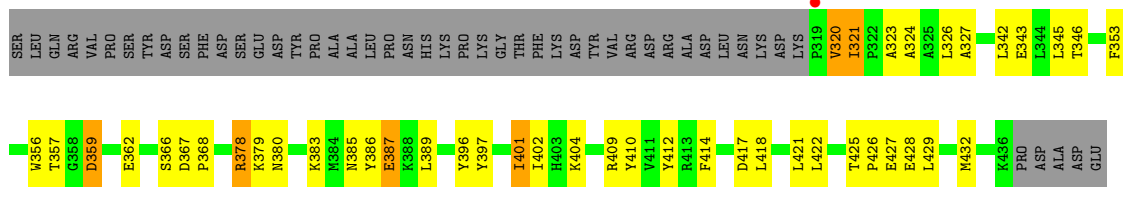
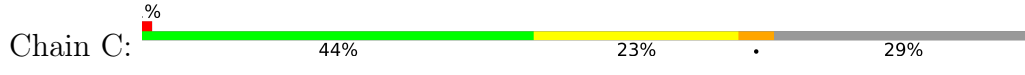
- Molecule 2: Core-binding factor subunit beta



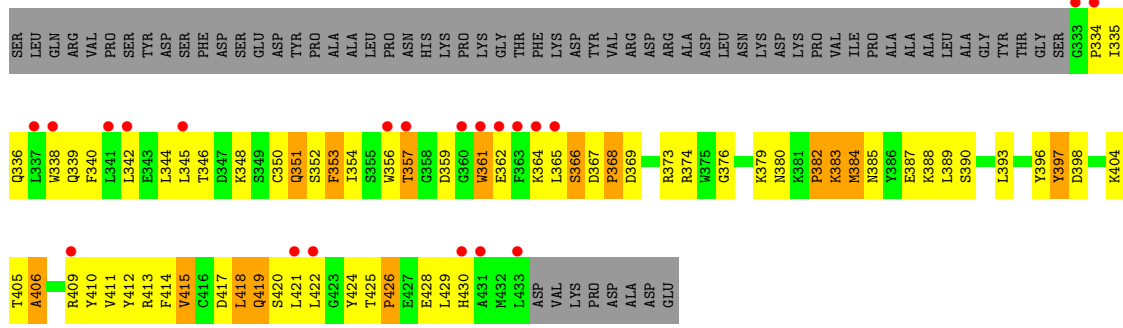
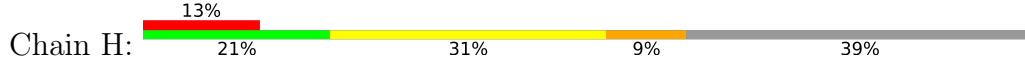
- Molecule 2: Core-binding factor subunit beta



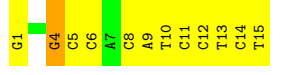
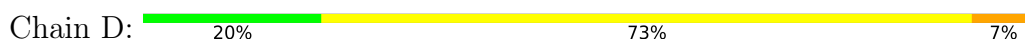
• Molecule 3: Protein C-ets-1



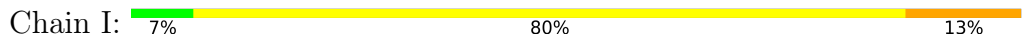
• Molecule 3: Protein C-ets-1



• Molecule 4: DNA (5'-D(\*GP\*AP\*AP\*GP\*CP\*CP\*AP\*CP\*AP\*TP\*CP\*CP\*TP\*CP\*T)-3')



• Molecule 4: DNA (5'-D(\*GP\*AP\*AP\*GP\*CP\*CP\*AP\*CP\*AP\*TP\*CP\*CP\*TP\*CP\*T)-3')



- Molecule 5: DNA (5'-D(\*AP\*GP\*AP\*GP\*GP\*AP\*TP\*GP\*TP\*GP\*GP\*CP\*TP\*TP\*C)-3')

Chain E:  87% 13%



- Molecule 5: DNA (5'-D(\*AP\*GP\*AP\*GP\*GP\*AP\*TP\*GP\*TP\*GP\*GP\*CP\*TP\*TP\*C)-3')

Chain J:  93% 7%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.50Å 100.61Å 194.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.36 – 2.90 42.36 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.9 (42.36-2.90) 97.9 (42.36-2.90)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.60 (at 2.90Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.219 , 0.264 0.218 , 0.263	Depositor DCC
$R_{free}$ test set	3414 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	77.0	Xtrriage
Anisotropy	0.301	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 52.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7014	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	88.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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	0.68	0/929	1.02	3/1264 (0.2%)
1	F	0.73	0/940	1.09	2/1278 (0.2%)
2	B	0.49	0/1093	0.80	1/1466 (0.1%)
2	G	0.59	1/1084 (0.1%)	0.86	0/1454
3	C	0.66	0/994	1.03	1/1342 (0.1%)
3	H	0.47	0/877	0.82	3/1181 (0.3%)
4	D	0.45	0/334	0.98	1/512 (0.2%)
4	I	0.47	0/334	0.99	1/512 (0.2%)
5	E	0.47	0/348	0.80	0/537
5	J	0.44	0/348	0.85	0/537
All	All	0.59	1/7281 (0.0%)	0.93	12/10083 (0.1%)

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
4	D	0	3
4	I	0	2
5	E	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	122	MET	SD-CE	5.82	1.94	1.79

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	4	DG	N9-C1'-C2'	-6.85	103.23	113.50
1	F	70	PHE	N-CA-C	6.41	119.16	109.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	111	GLU	N-CA-C	-6.40	107.32	114.62
1	F	133	ASP	N-CA-C	6.40	120.22	111.39
4	I	4	DG	N9-C1'-C2'	-6.25	104.12	113.50

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	4	DG	Sidechain
4	D	5	DC	Sidechain
4	D	6	DC	Sidechain
5	E	13	DT	Sidechain
4	I	4	DG	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	910	0	914	38	0
1	F	921	0	927	38	0
2	B	1071	0	1034	71	0
2	G	1062	0	1026	56	0
3	C	967	0	966	36	0
3	H	853	0	847	82	0
4	D	299	0	170	14	0
4	I	299	0	170	17	0
5	E	310	0	171	1	0
5	J	310	0	171	1	0
6	A	1	0	0	0	0
6	B	1	0	0	1	0
6	C	3	0	0	0	0
6	E	1	0	0	0	0
6	F	5	0	0	1	0
6	G	1	0	0	0	0
All	All	7014	0	6396	339	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 25.

The worst 5 of 339 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)
3:C:385:ASN:HD21	3:C:387:GLU:HB2	1.22	1.01
1:A:82:ASN:HD21	1:A:118:ARG:HH11	1.04	0.89
2:B:8:GLN:HE21	2:B:107:CYS:H	1.16	0.88
1:A:161:THR:H	2:B:104:ASN:HD21	1.20	0.87
1:A:109:ASN:HD21	1:A:111:GLU:HB2	1.39	0.86

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	116/204 (57%)	108 (93%)	6 (5%)	2 (2%)	7	26
1	F	117/204 (57%)	109 (93%)	7 (6%)	1 (1%)	14	41
2	B	126/142 (89%)	99 (79%)	24 (19%)	3 (2%)	4	18
2	G	125/142 (88%)	107 (86%)	13 (10%)	5 (4%)	2	9
3	C	116/166 (70%)	109 (94%)	6 (5%)	1 (1%)	14	41
3	H	99/166 (60%)	68 (69%)	21 (21%)	10 (10%)	0	1
All	All	699/1024 (68%)	600 (86%)	77 (11%)	22 (3%)	3	14

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	320	VAL
3	H	366	SER
3	H	382	PRO
2	B	15	GLU
2	B	116	LEU

### 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	99/178 (56%)	93 (94%)	6 (6%)	17	46
1	F	100/178 (56%)	92 (92%)	8 (8%)	11	34
2	B	113/123 (92%)	107 (95%)	6 (5%)	20	52
2	G	112/123 (91%)	104 (93%)	8 (7%)	13	40
3	C	102/145 (70%)	96 (94%)	6 (6%)	18	48
3	H	91/145 (63%)	85 (93%)	6 (7%)	15	43
All	All	617/892 (69%)	577 (94%)	40 (6%)	15	44

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	86	VAL
3	H	353	PHE
2	G	88	LEU
2	G	120	ASP
3	H	384	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	385	ASN
3	H	380	ASN
1	F	112	ASN
2	G	134	GLN
1	F	82	ASN

### 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 oligosaccharides 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	118/204 (57%)	-0.00	1 (0%) 82 77	57, 77, 94, 111	0
1	F	119/204 (58%)	-0.18	1 (0%) 82 77	51, 66, 86, 132	0
2	B	130/142 (91%)	0.61	3 (2%) 61 52	80, 105, 131, 136	0
2	G	129/142 (90%)	0.41	5 (3%) 43 35	68, 89, 117, 122	0
3	C	118/166 (71%)	-0.13	1 (0%) 82 77	52, 72, 104, 115	0
3	H	101/166 (60%)	1.25	21 (20%) 2 2	77, 131, 172, 180	0
4	D	15/15 (100%)	-0.46	0 100 100	59, 67, 79, 80	0
4	I	15/15 (100%)	-0.32	0 100 100	61, 72, 90, 92	0
5	E	15/15 (100%)	-0.64	0 100 100	55, 67, 81, 85	0
5	J	15/15 (100%)	-0.23	0 100 100	59, 69, 92, 98	0
All	All	775/1084 (71%)	0.25	32 (4%) 41 33	51, 82, 143, 180	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	81	PRO	6.0
2	G	139	ALA	4.5
3	H	360	GLY	4.0
2	B	81	PRO	4.0
3	H	422	LEU	3.8

### 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 oligosaccharides 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.