wwPDB X-ray Structure Validation Summary Report (i)

May 26, 2020 – 08:21 pm BST

PDB ID	:	5Z18
Title	:	The crystal structure of Ruminococcus gnavus beta-glucuronidase
Authors	:	Dashnyam, P.; Lin, H.Y.; Lin, C.H.
Deposited on	:	2017-12-25
Resolution	:	2.50 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:

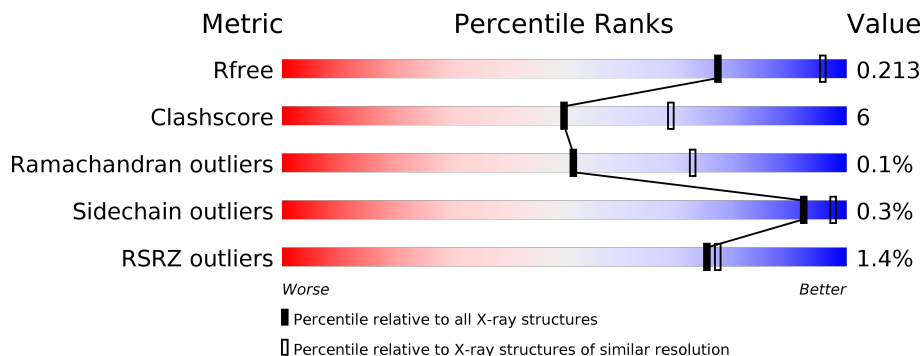|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.50 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	Percentile Ranks	Value
Rfree		0.213
Clashscore		6
Ramachandran outliers		0.1%
Sidechain outliers		0.3%
RSRZ outliers		1.4%

Worse   Better

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	A	627	82% 11% 7%
1	B	627	82% 11% 7%
1	C	627	2% 82% 11% 6%
1	D	627	2% 83% 11% 6%
1	E	627	80% 13% 7%
1	F	627	79% 14% 7%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 30433 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 Beta-glucuronidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	586	Total 4811	C 3105	N 780	O 902	S 24	0	0	0
1	B	586	Total 4811	C 3105	N 780	O 902	S 24	0	0	0
1	C	588	Total 4829	C 3117	N 784	O 904	S 24	0	0	0
1	D	591	Total 4858	C 3137	N 788	O 909	S 24	0	0	0
1	E	586	Total 4810	C 3104	N 782	O 900	S 24	0	0	0
1	F	582	Total 4773	C 3079	N 776	O 894	S 24	0	0	0

There are 150 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	initiating methionine	UNP Q6W7J7
A	-22	HIS	-	expression tag	UNP Q6W7J7
A	-21	HIS	-	expression tag	UNP Q6W7J7
A	-20	HIS	-	expression tag	UNP Q6W7J7
A	-19	HIS	-	expression tag	UNP Q6W7J7
A	-18	HIS	-	expression tag	UNP Q6W7J7
A	-17	HIS	-	expression tag	UNP Q6W7J7
A	-16	SER	-	expression tag	UNP Q6W7J7
A	-15	SER	-	expression tag	UNP Q6W7J7
A	-14	GLY	-	expression tag	UNP Q6W7J7
A	-13	VAL	-	expression tag	UNP Q6W7J7
A	-12	ASP	-	expression tag	UNP Q6W7J7
A	-11	LEU	-	expression tag	UNP Q6W7J7
A	-10	GLY	-	expression tag	UNP Q6W7J7
A	-9	THR	-	expression tag	UNP Q6W7J7
A	-8	GLU	-	expression tag	UNP Q6W7J7
A	-7	ASN	-	expression tag	UNP Q6W7J7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP Q6W7J7
A	-5	TYR	-	expression tag	UNP Q6W7J7
A	-4	PHE	-	expression tag	UNP Q6W7J7
A	-3	GLN	-	expression tag	UNP Q6W7J7
A	-2	SER	-	expression tag	UNP Q6W7J7
A	-1	ASN	-	expression tag	UNP Q6W7J7
A	0	GLY	-	expression tag	UNP Q6W7J7
A	1	MET	-	expression tag	UNP Q6W7J7
B	-23	MET	-	initiating methionine	UNP Q6W7J7
B	-22	HIS	-	expression tag	UNP Q6W7J7
B	-21	HIS	-	expression tag	UNP Q6W7J7
B	-20	HIS	-	expression tag	UNP Q6W7J7
B	-19	HIS	-	expression tag	UNP Q6W7J7
B	-18	HIS	-	expression tag	UNP Q6W7J7
B	-17	HIS	-	expression tag	UNP Q6W7J7
B	-16	SER	-	expression tag	UNP Q6W7J7
B	-15	SER	-	expression tag	UNP Q6W7J7
B	-14	GLY	-	expression tag	UNP Q6W7J7
B	-13	VAL	-	expression tag	UNP Q6W7J7
B	-12	ASP	-	expression tag	UNP Q6W7J7
B	-11	LEU	-	expression tag	UNP Q6W7J7
B	-10	GLY	-	expression tag	UNP Q6W7J7
B	-9	THR	-	expression tag	UNP Q6W7J7
B	-8	GLU	-	expression tag	UNP Q6W7J7
B	-7	ASN	-	expression tag	UNP Q6W7J7
B	-6	LEU	-	expression tag	UNP Q6W7J7
B	-5	TYR	-	expression tag	UNP Q6W7J7
B	-4	PHE	-	expression tag	UNP Q6W7J7
B	-3	GLN	-	expression tag	UNP Q6W7J7
B	-2	SER	-	expression tag	UNP Q6W7J7
B	-1	ASN	-	expression tag	UNP Q6W7J7
B	0	GLY	-	expression tag	UNP Q6W7J7
B	1	MET	-	expression tag	UNP Q6W7J7
C	-23	MET	-	initiating methionine	UNP Q6W7J7
C	-22	HIS	-	expression tag	UNP Q6W7J7
C	-21	HIS	-	expression tag	UNP Q6W7J7
C	-20	HIS	-	expression tag	UNP Q6W7J7
C	-19	HIS	-	expression tag	UNP Q6W7J7
C	-18	HIS	-	expression tag	UNP Q6W7J7
C	-17	HIS	-	expression tag	UNP Q6W7J7
C	-16	SER	-	expression tag	UNP Q6W7J7
C	-15	SER	-	expression tag	UNP Q6W7J7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	GLY	-	expression tag	UNP Q6W7J7
C	-13	VAL	-	expression tag	UNP Q6W7J7
C	-12	ASP	-	expression tag	UNP Q6W7J7
C	-11	LEU	-	expression tag	UNP Q6W7J7
C	-10	GLY	-	expression tag	UNP Q6W7J7
C	-9	THR	-	expression tag	UNP Q6W7J7
C	-8	GLU	-	expression tag	UNP Q6W7J7
C	-7	ASN	-	expression tag	UNP Q6W7J7
C	-6	LEU	-	expression tag	UNP Q6W7J7
C	-5	TYR	-	expression tag	UNP Q6W7J7
C	-4	PHE	-	expression tag	UNP Q6W7J7
C	-3	GLN	-	expression tag	UNP Q6W7J7
C	-2	SER	-	expression tag	UNP Q6W7J7
C	-1	ASN	-	expression tag	UNP Q6W7J7
C	0	GLY	-	expression tag	UNP Q6W7J7
C	1	MET	-	expression tag	UNP Q6W7J7
D	-23	MET	-	initiating methionine	UNP Q6W7J7
D	-22	HIS	-	expression tag	UNP Q6W7J7
D	-21	HIS	-	expression tag	UNP Q6W7J7
D	-20	HIS	-	expression tag	UNP Q6W7J7
D	-19	HIS	-	expression tag	UNP Q6W7J7
D	-18	HIS	-	expression tag	UNP Q6W7J7
D	-17	HIS	-	expression tag	UNP Q6W7J7
D	-16	SER	-	expression tag	UNP Q6W7J7
D	-15	SER	-	expression tag	UNP Q6W7J7
D	-14	GLY	-	expression tag	UNP Q6W7J7
D	-13	VAL	-	expression tag	UNP Q6W7J7
D	-12	ASP	-	expression tag	UNP Q6W7J7
D	-11	LEU	-	expression tag	UNP Q6W7J7
D	-10	GLY	-	expression tag	UNP Q6W7J7
D	-9	THR	-	expression tag	UNP Q6W7J7
D	-8	GLU	-	expression tag	UNP Q6W7J7
D	-7	ASN	-	expression tag	UNP Q6W7J7
D	-6	LEU	-	expression tag	UNP Q6W7J7
D	-5	TYR	-	expression tag	UNP Q6W7J7
D	-4	PHE	-	expression tag	UNP Q6W7J7
D	-3	GLN	-	expression tag	UNP Q6W7J7
D	-2	SER	-	expression tag	UNP Q6W7J7
D	-1	ASN	-	expression tag	UNP Q6W7J7
D	0	GLY	-	expression tag	UNP Q6W7J7
D	1	MET	-	expression tag	UNP Q6W7J7
E	-23	MET	-	initiating methionine	UNP Q6W7J7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-22	HIS	-	expression tag	UNP Q6W7J7
E	-21	HIS	-	expression tag	UNP Q6W7J7
E	-20	HIS	-	expression tag	UNP Q6W7J7
E	-19	HIS	-	expression tag	UNP Q6W7J7
E	-18	HIS	-	expression tag	UNP Q6W7J7
E	-17	HIS	-	expression tag	UNP Q6W7J7
E	-16	SER	-	expression tag	UNP Q6W7J7
E	-15	SER	-	expression tag	UNP Q6W7J7
E	-14	GLY	-	expression tag	UNP Q6W7J7
E	-13	VAL	-	expression tag	UNP Q6W7J7
E	-12	ASP	-	expression tag	UNP Q6W7J7
E	-11	LEU	-	expression tag	UNP Q6W7J7
E	-10	GLY	-	expression tag	UNP Q6W7J7
E	-9	THR	-	expression tag	UNP Q6W7J7
E	-8	GLU	-	expression tag	UNP Q6W7J7
E	-7	ASN	-	expression tag	UNP Q6W7J7
E	-6	LEU	-	expression tag	UNP Q6W7J7
E	-5	TYR	-	expression tag	UNP Q6W7J7
E	-4	PHE	-	expression tag	UNP Q6W7J7
E	-3	GLN	-	expression tag	UNP Q6W7J7
E	-2	SER	-	expression tag	UNP Q6W7J7
E	-1	ASN	-	expression tag	UNP Q6W7J7
E	0	GLY	-	expression tag	UNP Q6W7J7
E	1	MET	-	expression tag	UNP Q6W7J7
F	-23	MET	-	initiating methionine	UNP Q6W7J7
F	-22	HIS	-	expression tag	UNP Q6W7J7
F	-21	HIS	-	expression tag	UNP Q6W7J7
F	-20	HIS	-	expression tag	UNP Q6W7J7
F	-19	HIS	-	expression tag	UNP Q6W7J7
F	-18	HIS	-	expression tag	UNP Q6W7J7
F	-17	HIS	-	expression tag	UNP Q6W7J7
F	-16	SER	-	expression tag	UNP Q6W7J7
F	-15	SER	-	expression tag	UNP Q6W7J7
F	-14	GLY	-	expression tag	UNP Q6W7J7
F	-13	VAL	-	expression tag	UNP Q6W7J7
F	-12	ASP	-	expression tag	UNP Q6W7J7
F	-11	LEU	-	expression tag	UNP Q6W7J7
F	-10	GLY	-	expression tag	UNP Q6W7J7
F	-9	THR	-	expression tag	UNP Q6W7J7
F	-8	GLU	-	expression tag	UNP Q6W7J7
F	-7	ASN	-	expression tag	UNP Q6W7J7
F	-6	LEU	-	expression tag	UNP Q6W7J7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-5	TYR	-	expression tag	UNP Q6W7J7
F	-4	PHE	-	expression tag	UNP Q6W7J7
F	-3	GLN	-	expression tag	UNP Q6W7J7
F	-2	SER	-	expression tag	UNP Q6W7J7
F	-1	ASN	-	expression tag	UNP Q6W7J7
F	0	GLY	-	expression tag	UNP Q6W7J7
F	1	MET	-	expression tag	UNP Q6W7J7

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	265	Total 265	O 265	0	0
2	B	240	Total 240	O 240	0	0
2	C	268	Total 268	O 268	0	0
2	D	224	Total 224	O 224	0	0
2	E	250	Total 250	O 250	0	0
2	F	294	Total 294	O 294	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 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.
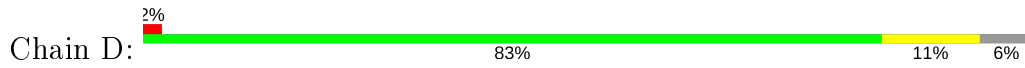
- Molecule 1: Beta-glucuronidase
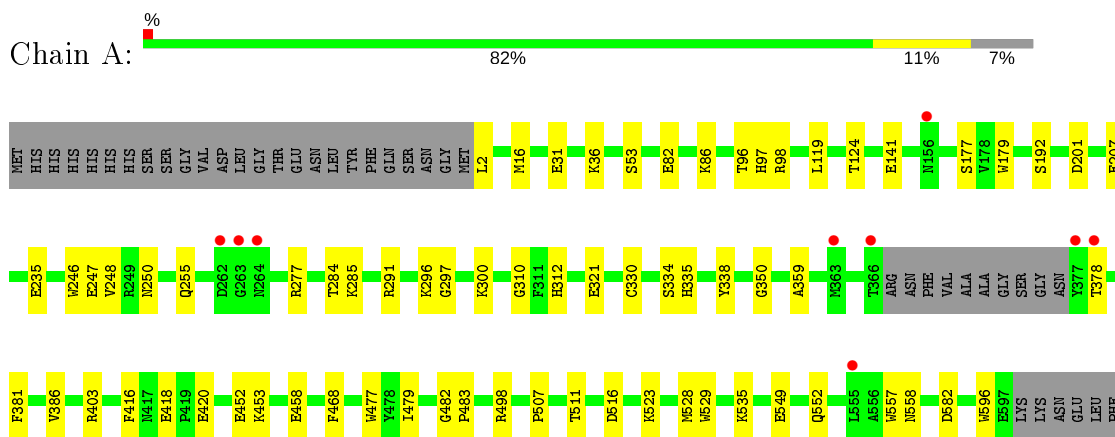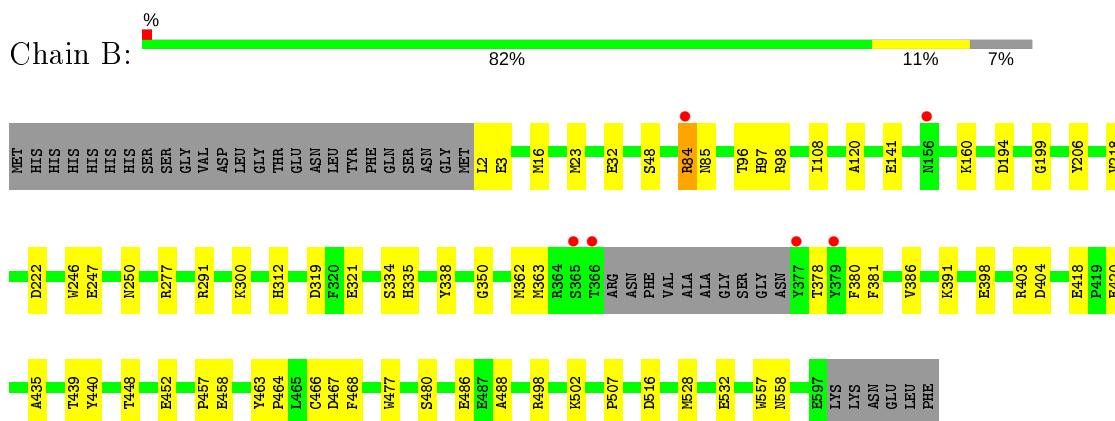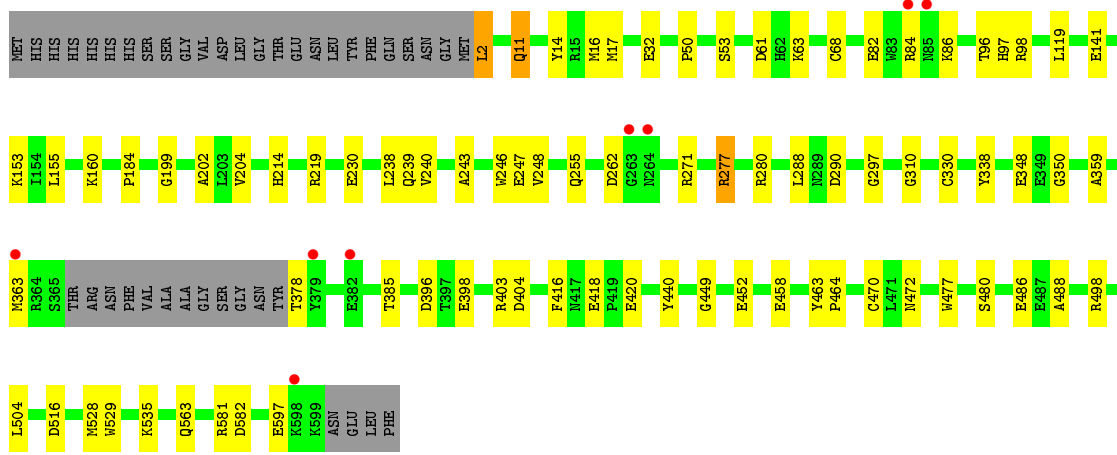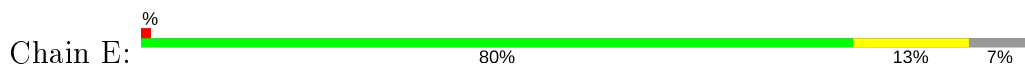

- Molecule 1: Beta-glucuronidase

- Molecule 1: Beta-glucuronidase

• Molecule 1: Beta-glucuronidase

Chain D:

• Molecule 1: Beta-glucuronidase

Chain E:

• Molecule 1: Beta-glucuronidase

Chain F:
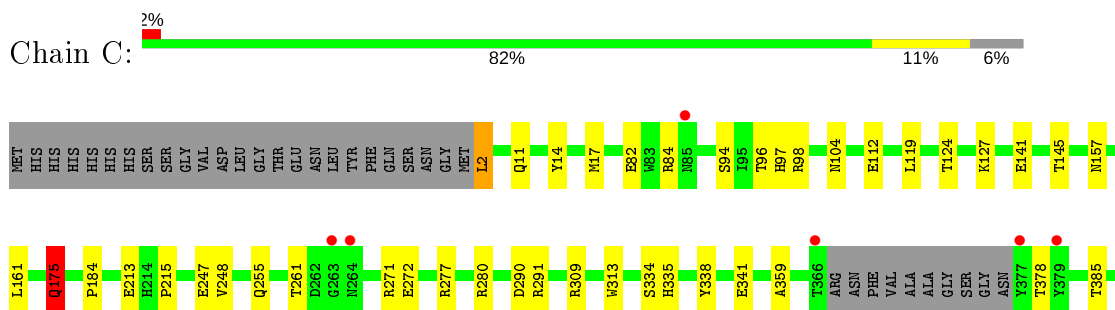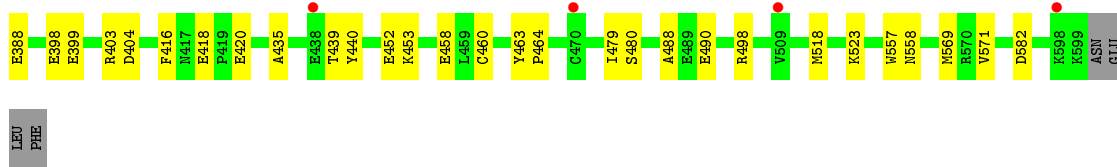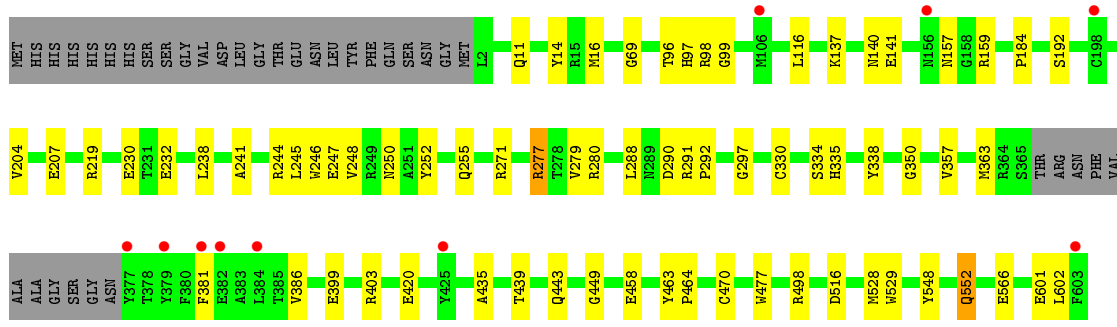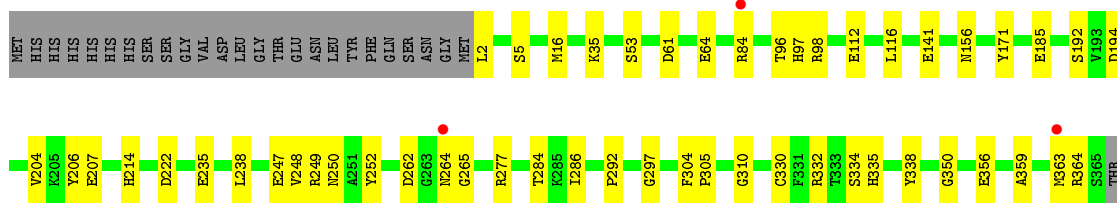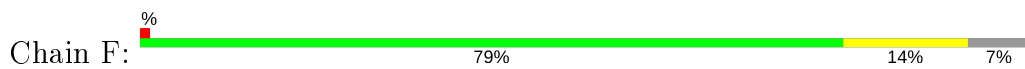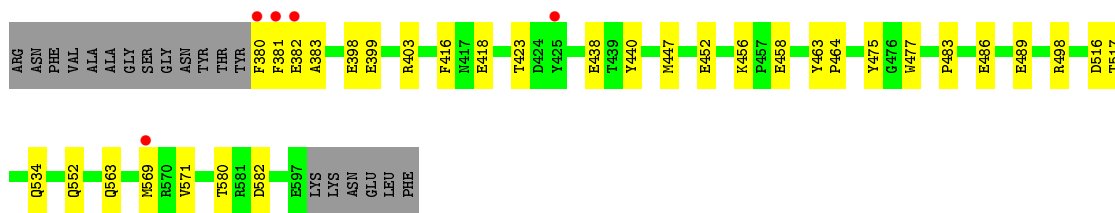
4   Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	181.87Å 118.18Å 210.35Å 90.00° 93.45° 90.00°	Depositor
Resolution (Å)	29.03 – 2.50	Depositor
	29.03 – 2.50	EDS
% Data completeness	94.3 (29.03-2.50)	Depositor
(in resolution range)	94.0 (29.03-2.50)	EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.45 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.167 , 0.209	Depositor
	0.175 , 0.213	DCC
R_{free} test set	2000 reflections (1.32%)	wwPDB-VP
Wilson B-factor (Å^2)	35.6	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 40.6	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	30433	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.38% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (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	0.47	0/4949	0.61	1/6711 (0.0%)
1	B	0.46	0/4949	0.61	1/6711 (0.0%)
1	C	0.47	0/4967	0.61	3/6733 (0.0%)
1	D	0.45	0/4997	0.58	0/6773
1	E	0.47	0/4947	0.61	2/6705 (0.0%)
1	F	0.48	0/4909	0.62	0/6655
All	All	0.47	0/29718	0.61	7/40288 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	2	LEU	CA-CB-CG	6.37	129.96	115.30
1	A	119	LEU	CA-CB-CG	-5.76	102.05	115.30
1	C	2	LEU	CA-CB-CG	5.69	128.39	115.30
1	B	2	LEU	CA-CB-CG	5.69	128.38	115.30
1	C	119	LEU	CA-CB-CG	-5.37	102.95	115.30

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 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	4811	0	4589	53	0
1	B	4811	0	4589	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4829	0	4615	55	0
1	D	4858	0	4640	46	1
1	E	4810	0	4599	63	1
1	F	4773	0	4557	70	0
2	A	265	0	0	14	2
2	B	240	0	0	12	4
2	C	268	0	0	14	0
2	D	224	0	0	8	0
2	E	250	0	0	20	0
2	F	294	0	0	23	2
All	All	30433	0	27589	325	5

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 6.

The worst 5 of 325 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:C:2:LEU:N	2:C:702:HOH:O	1.82	1.12
1:F:563:GLN:NE2	2:F:702:HOH:O	1.87	1.06
1:C:213:GLU:OE2	2:C:701:HOH:O	1.82	0.98
1:F:552:GLN:NE2	2:F:704:HOH:O	1.99	0.95
1:F:262:ASP:OD1	2:F:701:HOH:O	1.85	0.94

All (5) 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)
2:B:705:HOH:O	2:F:731:HOH:O[4_1413]	1.89	0.31
2:B:777:HOH:O	2:F:887:HOH:O[4_1413]	2.00	0.20
2:A:962:HOH:O	2:B:939:HOH:O[4_1413]	2.05	0.15
1:D:159:ARG:NH2	1:E:486:GLU:OE2[3_445]	2.18	0.02
2:A:760:HOH:O	2:B:907:HOH:O[4_1413]	2.19	0.01

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	582/627 (93%)	563 (97%)	19 (3%)	0	100	100
1	B	582/627 (93%)	566 (97%)	15 (3%)	1 (0%)	47	68
1	C	584/627 (93%)	565 (97%)	18 (3%)	1 (0%)	47	68
1	D	587/627 (94%)	570 (97%)	17 (3%)	0	100	100
1	E	582/627 (93%)	561 (96%)	20 (3%)	1 (0%)	47	68
1	F	578/627 (92%)	559 (97%)	19 (3%)	0	100	100
All	All	3495/3762 (93%)	3384 (97%)	108 (3%)	3 (0%)	51	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	84	ARG
1	E	84	ARG
1	C	84	ARG

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	512/546 (94%)	511 (100%)	1 (0%)	93	98
1	B	512/546 (94%)	510 (100%)	2 (0%)	91	97
1	C	514/546 (94%)	513 (100%)	1 (0%)	93	98
1	D	517/546 (95%)	513 (99%)	4 (1%)	81	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	512/546 (94%)	510 (100%)	2 (0%)	91	97
1	F	508/546 (93%)	508 (100%)	0	100	100
All	All	3075/3276 (94%)	3065 (100%)	10 (0%)	92	97

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	277	ARG
1	D	357	VAL
1	D	602	LEU
1	C	175	GLN
1	D	552	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	255	GLN
1	F	534	GLN
1	E	11	GLN
1	C	175	GLN
1	E	239	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 carbohydrates 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, 95th 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	586/627 (93%)	-0.24	9 (1%)	73	75	25, 33, 49, 76	0
1	B	586/627 (93%)	-0.28	6 (1%)	82	84	26, 34, 52, 73	0
1	C	588/627 (93%)	-0.26	10 (1%)	70	72	26, 33, 50, 74	0
1	D	591/627 (94%)	-0.24	10 (1%)	70	72	27, 36, 55, 76	0
1	E	586/627 (93%)	-0.27	8 (1%)	75	77	27, 35, 53, 79	0
1	F	582/627 (92%)	-0.30	8 (1%)	75	77	25, 33, 51, 84	0
All	All	3519/3762 (93%)	-0.26	51 (1%)	75	77	25, 34, 52, 84	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	381	PHE	6.8
1	D	377	TYR	6.4
1	D	379	TYR	5.8
1	B	366	THR	5.7
1	C	264	ASN	5.5

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 carbohydrates 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.