



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 24, 2023 – 03:19 PM EDT

PDB ID : 5UW3  
Title : PCY1 in Complex with Follower Peptide  
Authors : Chekan, J.R.; Nair, S.K.  
Deposited on : 2017-02-20  
Resolution : 1.96 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>.

---

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

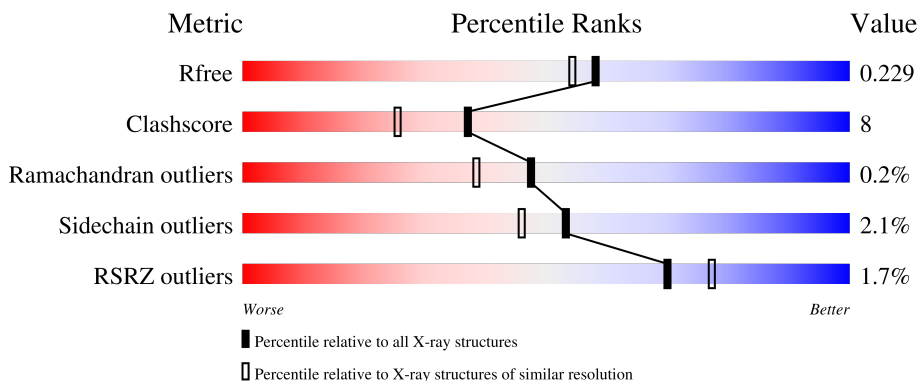
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


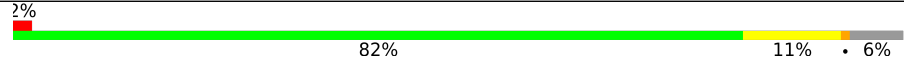
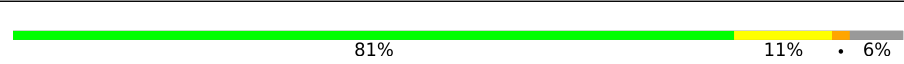

The reported resolution of this entry is 1.96 Å.

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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	750	 3% 80% 11% • 8%
1	B	750	 2% 82% 11% • 6%
1	C	750	 81% 11% • 6%
1	D	750	 % 82% 10% • 7%
2	E	19	 26% 5% 68%

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	F	19	 26% 5% 68%
2	G	19	 21% 11% 68%
2	H	19	 32% 68%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CAC	C	801	-	-	X	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 24731 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 Peptide cyclase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	693	Total 5573	C 3564	N 946	O 1038	S 25	0	0	0
1	B	707	Total 5669	C 3622	N 963	O 1058	S 26	0	0	0
1	C	702	Total 5646	C 3612	N 961	O 1048	S 25	0	0	0
1	D	698	Total 5608	C 3586	N 954	O 1043	S 25	0	0	0

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-25	MET	-	initiating methionine	UNP R4P353
A	-24	SER	-	expression tag	UNP R4P353
A	-23	TYR	-	expression tag	UNP R4P353
A	-22	TYR	-	expression tag	UNP R4P353
A	-21	HIS	-	expression tag	UNP R4P353
A	-20	HIS	-	expression tag	UNP R4P353
A	-19	HIS	-	expression tag	UNP R4P353
A	-18	HIS	-	expression tag	UNP R4P353
A	-17	HIS	-	expression tag	UNP R4P353
A	-16	HIS	-	expression tag	UNP R4P353
A	-15	LEU	-	expression tag	UNP R4P353
A	-14	GLU	-	expression tag	UNP R4P353
A	-13	SER	-	expression tag	UNP R4P353
A	-12	THR	-	expression tag	UNP R4P353
A	-11	SER	-	expression tag	UNP R4P353
A	-10	LEU	-	expression tag	UNP R4P353
A	-9	TYR	-	expression tag	UNP R4P353
A	-8	LYS	-	expression tag	UNP R4P353
A	-7	LYS	-	expression tag	UNP R4P353
A	-6	ALA	-	expression tag	UNP R4P353
A	-5	GLY	-	expression tag	UNP R4P353

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	SER	-	expression tag	UNP R4P353
A	-3	GLU	-	expression tag	UNP R4P353
A	-2	PHE	-	expression tag	UNP R4P353
A	-1	ALA	-	expression tag	UNP R4P353
A	0	LEU	-	expression tag	UNP R4P353
B	-25	MET	-	initiating methionine	UNP R4P353
B	-24	SER	-	expression tag	UNP R4P353
B	-23	TYR	-	expression tag	UNP R4P353
B	-22	TYR	-	expression tag	UNP R4P353
B	-21	HIS	-	expression tag	UNP R4P353
B	-20	HIS	-	expression tag	UNP R4P353
B	-19	HIS	-	expression tag	UNP R4P353
B	-18	HIS	-	expression tag	UNP R4P353
B	-17	HIS	-	expression tag	UNP R4P353
B	-16	HIS	-	expression tag	UNP R4P353
B	-15	LEU	-	expression tag	UNP R4P353
B	-14	GLU	-	expression tag	UNP R4P353
B	-13	SER	-	expression tag	UNP R4P353
B	-12	THR	-	expression tag	UNP R4P353
B	-11	SER	-	expression tag	UNP R4P353
B	-10	LEU	-	expression tag	UNP R4P353
B	-9	TYR	-	expression tag	UNP R4P353
B	-8	LYS	-	expression tag	UNP R4P353
B	-7	LYS	-	expression tag	UNP R4P353
B	-6	ALA	-	expression tag	UNP R4P353
B	-5	GLY	-	expression tag	UNP R4P353
B	-4	SER	-	expression tag	UNP R4P353
B	-3	GLU	-	expression tag	UNP R4P353
B	-2	PHE	-	expression tag	UNP R4P353
B	-1	ALA	-	expression tag	UNP R4P353
B	0	LEU	-	expression tag	UNP R4P353
C	-25	MET	-	initiating methionine	UNP R4P353
C	-24	SER	-	expression tag	UNP R4P353
C	-23	TYR	-	expression tag	UNP R4P353
C	-22	TYR	-	expression tag	UNP R4P353
C	-21	HIS	-	expression tag	UNP R4P353
C	-20	HIS	-	expression tag	UNP R4P353
C	-19	HIS	-	expression tag	UNP R4P353
C	-18	HIS	-	expression tag	UNP R4P353
C	-17	HIS	-	expression tag	UNP R4P353
C	-16	HIS	-	expression tag	UNP R4P353
C	-15	LEU	-	expression tag	UNP R4P353

*Continued on next page...*

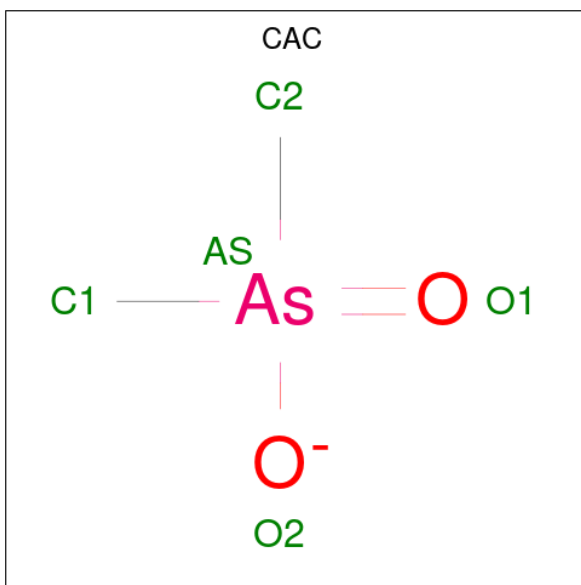
*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	GLU	-	expression tag	UNP R4P353
C	-13	SER	-	expression tag	UNP R4P353
C	-12	THR	-	expression tag	UNP R4P353
C	-11	SER	-	expression tag	UNP R4P353
C	-10	LEU	-	expression tag	UNP R4P353
C	-9	TYR	-	expression tag	UNP R4P353
C	-8	LYS	-	expression tag	UNP R4P353
C	-7	LYS	-	expression tag	UNP R4P353
C	-6	ALA	-	expression tag	UNP R4P353
C	-5	GLY	-	expression tag	UNP R4P353
C	-4	SER	-	expression tag	UNP R4P353
C	-3	GLU	-	expression tag	UNP R4P353
C	-2	PHE	-	expression tag	UNP R4P353
C	-1	ALA	-	expression tag	UNP R4P353
C	0	LEU	-	expression tag	UNP R4P353
D	-25	MET	-	initiating methionine	UNP R4P353
D	-24	SER	-	expression tag	UNP R4P353
D	-23	TYR	-	expression tag	UNP R4P353
D	-22	TYR	-	expression tag	UNP R4P353
D	-21	HIS	-	expression tag	UNP R4P353
D	-20	HIS	-	expression tag	UNP R4P353
D	-19	HIS	-	expression tag	UNP R4P353
D	-18	HIS	-	expression tag	UNP R4P353
D	-17	HIS	-	expression tag	UNP R4P353
D	-16	HIS	-	expression tag	UNP R4P353
D	-15	LEU	-	expression tag	UNP R4P353
D	-14	GLU	-	expression tag	UNP R4P353
D	-13	SER	-	expression tag	UNP R4P353
D	-12	THR	-	expression tag	UNP R4P353
D	-11	SER	-	expression tag	UNP R4P353
D	-10	LEU	-	expression tag	UNP R4P353
D	-9	TYR	-	expression tag	UNP R4P353
D	-8	LYS	-	expression tag	UNP R4P353
D	-7	LYS	-	expression tag	UNP R4P353
D	-6	ALA	-	expression tag	UNP R4P353
D	-5	GLY	-	expression tag	UNP R4P353
D	-4	SER	-	expression tag	UNP R4P353
D	-3	GLU	-	expression tag	UNP R4P353
D	-2	PHE	-	expression tag	UNP R4P353
D	-1	ALA	-	expression tag	UNP R4P353
D	0	LEU	-	expression tag	UNP R4P353

- Molecule 2 is a protein called Presegetalin A1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	6	Total	C	N	O	0	0	0
			38	23	7	8			
2	F	6	Total	C	N	O	0	0	0
			39	23	7	9			
2	G	6	Total	C	N	O	0	0	0
			38	23	7	8			
2	H	6	Total	C	N	O	0	0	0
			39	23	7	9			

- Molecule 3 is CACODYLATE ION (three-letter code: CAC) (formula: C<sub>2</sub>H<sub>6</sub>AsO<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	As	C	O	0	0
			5	1	2	2		
3	B	1	Total	As	C	O	0	0
			5	1	2	2		
3	C	1	Total	As	C	O	0	0
			5	1	2	2		
3	D	1	Total	As	C	O	0	0
			5	1	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	451	Total	O	0	0
			451	451		
4	E	6	Total	O	0	0
			6	6		

Continued on next page...

*Continued from previous page...*

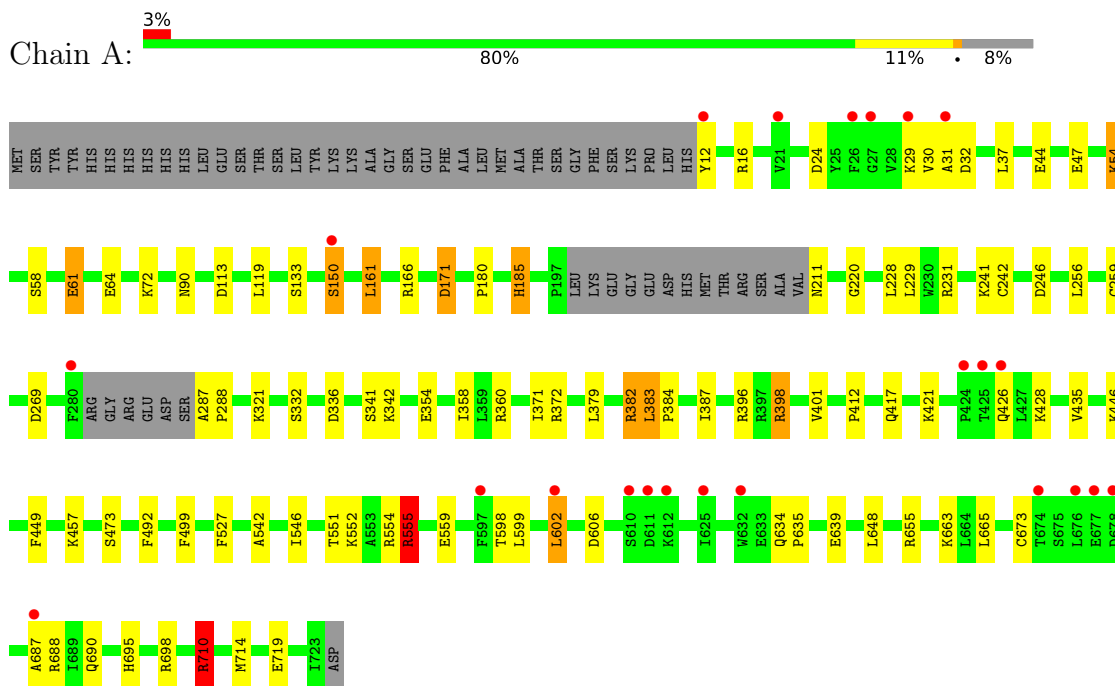
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	491	Total O 491 491	0	0
4	F	5	Total O 5 5	0	0
4	C	563	Total O 563 563	0	0
4	G	5	Total O 5 5	0	0
4	D	535	Total O 535 535	0	0
4	H	5	Total O 5 5	0	0



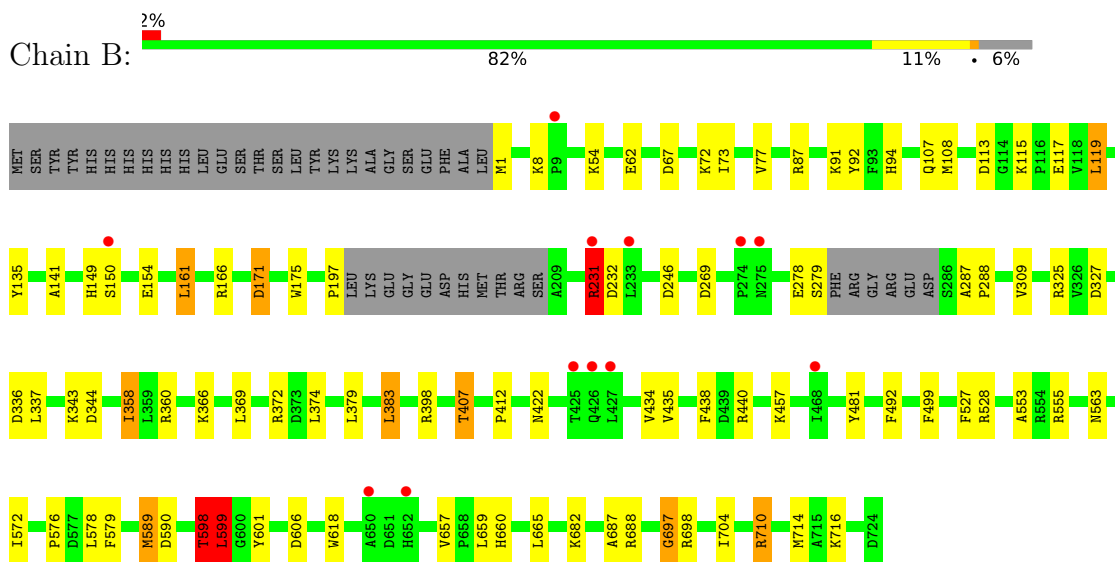
### 3 Residue-property plots [i](#)

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: Peptide cyclase 1

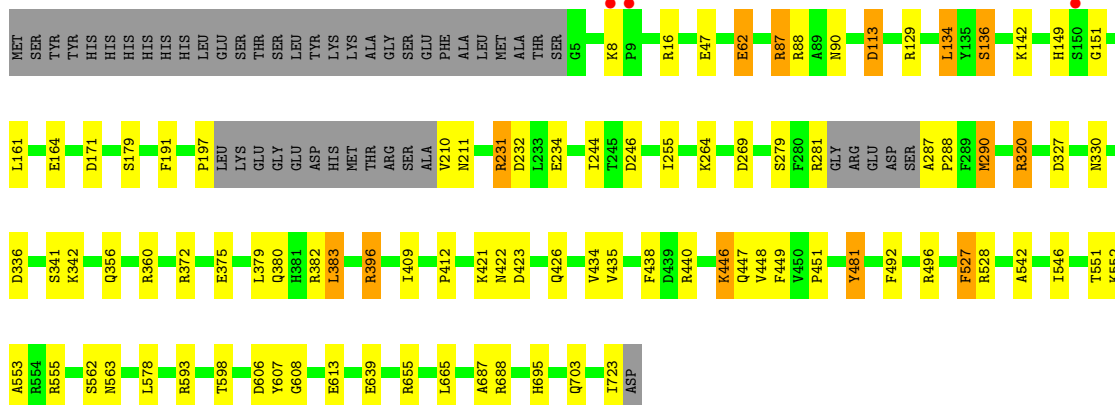


- Molecule 1: Peptide cyclase 1




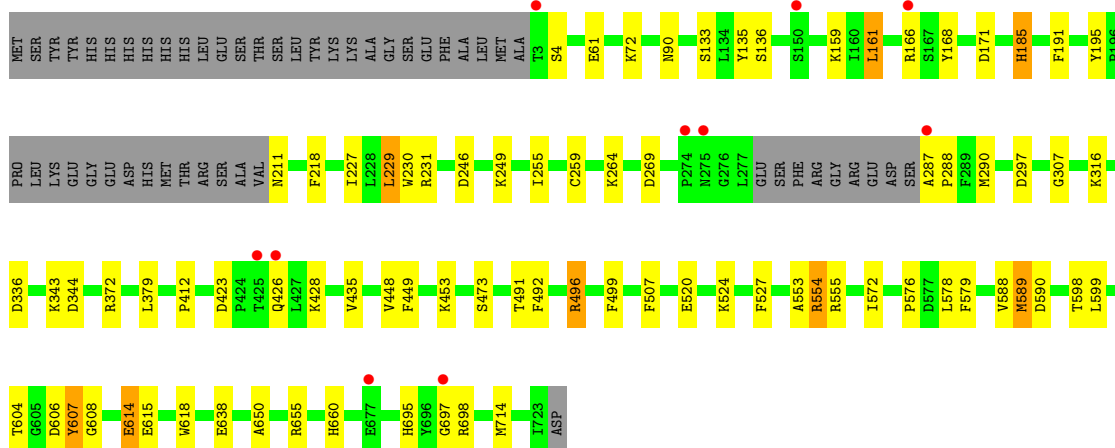
• Molecule 1: Peptide cyclase 1

Chain C:  81% 11% 6%



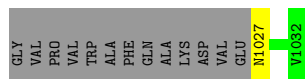
• Molecule 1: Peptide cyclase 1

Chain D:  82% 10% 7%



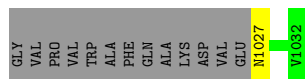
• Molecule 2: Presegetalin A1

Chain E:  26% 5% 68%



• Molecule 2: Presegetalin A1

Chain F:  26% 5% 68%



• Molecule 2: Presegetalin A1

Chain G:  21% 11% 68%

GLY	VAL	PRO	VAL	TRP	ALA	PHE	GLN	ALA	LYS	ASP	VAL	GLU	N1027	V1032
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-------	-------

- Molecule 2: Presegetalin A1

Chain H:  32% 68%

GLY	VAL	PRO	VAL	TRP	ALA	PHE	GLN	ALA	LYS	ASP	VAL	GLU	N1027	V1032
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-------	-------

## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.50Å 85.59Å 137.72Å 87.41° 78.28° 89.33°	Depositor
Resolution (Å)	44.90 – 1.96 44.91 – 1.96	Depositor EDS
% Data completeness (in resolution range)	95.8 (44.90-1.96) 95.8 (44.91-1.96)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.13	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.16 (at 1.97Å)	Xtrriage
Refinement program	REFMAC 5.8.0073	Depositor
R, $R_{free}$	0.189 , 0.224 0.195 , 0.229	Depositor DCC
$R_{free}$ test set	9945 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.5	Xtrriage
Anisotropy	0.234	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 52.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.086 for h,-k,h-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	24731	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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

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

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	0.83	0/5717	0.86	13/7743 (0.2%)
1	B	0.83	2/5815 (0.0%)	0.89	18/7876 (0.2%)
1	C	0.87	3/5793 (0.1%)	0.90	22/7845 (0.3%)
1	D	0.87	4/5753 (0.1%)	0.92	13/7791 (0.2%)
2	E	0.99	0/38	0.72	0/52
2	F	0.98	0/39	0.68	0/52
2	G	0.99	0/38	0.74	0/52
2	H	0.89	0/39	0.75	0/52
All	All	0.85	9/23232 (0.0%)	0.89	66/31463 (0.2%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	608	GLY	N-CA	10.86	1.62	1.46
1	C	608	GLY	N-CA	10.67	1.62	1.46
1	B	618	TRP	CB-CG	-7.13	1.37	1.50
1	D	496	ARG	CD-NE	-6.31	1.35	1.46
1	C	136	SER	CB-OG	-5.75	1.34	1.42

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	496	ARG	NE-CZ-NH2	-14.50	113.05	120.30
1	D	607	TYR	C-N-CA	-12.52	96.01	122.30
1	C	607	TYR	C-N-CA	-12.06	96.97	122.30
1	D	496	ARG	NE-CZ-NH1	11.56	126.08	120.30
1	A	382	ARG	NE-CZ-NH2	-7.94	116.33	120.30

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	5573	0	5417	113	1
1	B	5669	0	5515	80	0
1	C	5646	0	5494	70	0
1	D	5608	0	5457	87	1
2	E	38	0	36	1	0
2	F	39	0	36	1	0
2	G	38	0	36	2	0
2	H	39	0	36	0	0
3	A	5	0	0	0	0
3	B	5	0	0	3	0
3	C	5	0	0	4	0
3	D	5	0	0	1	0
4	A	451	0	0	58	0
4	B	491	0	0	43	0
4	C	563	0	0	27	0
4	D	535	0	0	46	0
4	E	6	0	0	1	0
4	F	5	0	0	1	0
4	G	5	0	0	1	0
4	H	5	0	0	0	0
All	All	24731	0	22027	350	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 8.

The worst 5 of 350 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:A:321:LYS:HE3	4:A:905:HOH:O	1.31	1.30
1:B:714:MET:SD	4:B:1318:HOH:O	1.99	1.18
1:D:714:MET:SD	4:D:1365:HOH:O	1.95	1.18
1:C:422:ASN:CG	4:C:902:HOH:O	1.81	1.16
1:D:588:VAL:C	1:D:589:MET:HE2	1.69	1.12

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:554:ARG:NH2	1:D:638:GLU:OE1[1_456]	2.12	0.08

## 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	687/750 (92%)	666 (97%)	20 (3%)	1 (0%)	51	43
1	B	701/750 (94%)	676 (96%)	23 (3%)	2 (0%)	41	30
1	C	696/750 (93%)	673 (97%)	21 (3%)	2 (0%)	41	30
1	D	692/750 (92%)	671 (97%)	20 (3%)	1 (0%)	51	43
2	E	4/19 (21%)	4 (100%)	0	0	100	100
2	F	4/19 (21%)	4 (100%)	0	0	100	100
2	G	4/19 (21%)	4 (100%)	0	0	100	100
2	H	4/19 (21%)	4 (100%)	0	0	100	100
All	All	2792/3076 (91%)	2702 (97%)	84 (3%)	6 (0%)	47	38

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	598	THR
1	C	279	SER
1	C	598	THR
1	A	598	THR
1	D	598	THR

### 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	603/652 (92%)	586 (97%)	17 (3%)	43	33
1	B	614/652 (94%)	601 (98%)	13 (2%)	53	46
1	C	611/652 (94%)	601 (98%)	10 (2%)	62	58
1	D	607/652 (93%)	596 (98%)	11 (2%)	59	53
2	E	4/14 (29%)	4 (100%)	0	100	100
2	F	4/14 (29%)	4 (100%)	0	100	100
2	G	4/14 (29%)	4 (100%)	0	100	100
2	H	4/14 (29%)	4 (100%)	0	100	100
All	All	2451/2664 (92%)	2400 (98%)	51 (2%)	53	46

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	599	LEU
1	C	396	ARG
1	D	554	ARG
1	B	606	ASP
1	C	231	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	185	HIS
1	C	652	HIS
1	D	185	HIS
1	C	670	HIS
1	B	149	HIS

### 5.3.3 RNA ⓘ

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](#)

4 ligands are 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	$\# Z  > 2$
3	CAC	A	801	-	0,4,4	-	-	0,6,6	-	-
3	CAC	B	801	-	0,4,4	-	-	0,6,6	-	-
3	CAC	D	801	-	0,4,4	-	-	0,6,6	-	-
3	CAC	C	801	-	0,4,4	-	-	0,6,6	-	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	801	CAC	3	0
3	D	801	CAC	1	0
3	C	801	CAC	4	0

## 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	693/750 (92%)	0.19	23 (3%) 46 56	8, 20, 41, 58	0
1	B	707/750 (94%)	-0.05	12 (1%) 70 77	8, 17, 39, 59	0
1	C	702/750 (93%)	-0.14	3 (0%) 92 95	6, 15, 34, 63	0
1	D	698/750 (93%)	-0.12	10 (1%) 75 82	7, 16, 34, 74	0
2	E	6/19 (31%)	-0.23	0 100 100	13, 14, 16, 18	0
2	F	6/19 (31%)	-0.36	0 100 100	12, 14, 17, 19	0
2	G	6/19 (31%)	-0.10	0 100 100	15, 16, 20, 20	0
2	H	6/19 (31%)	-0.33	0 100 100	13, 14, 18, 19	0
All	All	2824/3076 (91%)	-0.03	48 (1%) 70 77	6, 17, 37, 74	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	3	THR	7.9
1	D	425	THR	4.3
1	A	150	SER	3.8
1	A	625	ILE	3.7
1	A	677	GLU	3.7

### 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](#)

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	CAC	A	801	5/5	0.99	0.06	24,25,28,28	0
3	CAC	B	801	5/5	0.99	0.10	17,21,25,25	0
3	CAC	C	801	5/5	0.99	0.08	14,17,18,20	0
3	CAC	D	801	5/5	1.00	0.05	15,16,17,17	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.