wwPDB X-ray Structure Validation Summary Report (i)

Jun 17, 2024 – 03:26 AM EDT

PDB ID	:	5OCD
Title	:	structure of a CDPS from Fluoribacter dumoffii
Authors	:	Schmitt, E.; Mechulam, Y.; Bourgeois, G.
Deposited on	:	2017-06-30
Resolution	:	3.06 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

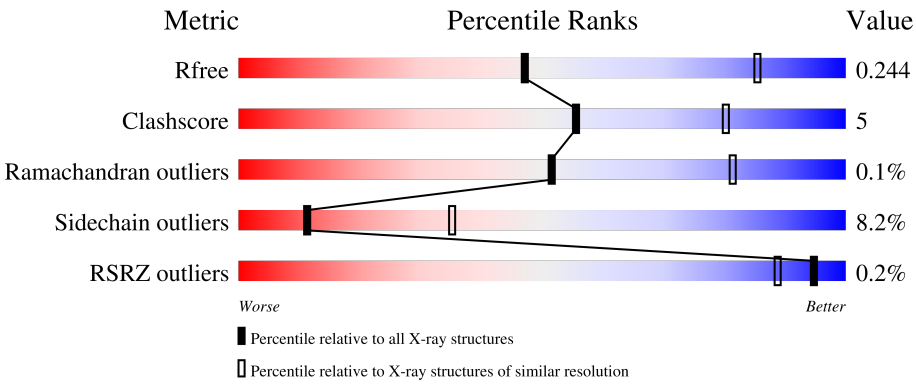
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.06 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	1754 (3.10-3.02)
Clashscore	141614	1864 (3.10-3.02)
Ramachandran outliers	138981	1794 (3.10-3.02)
Sidechain outliers	138945	1793 (3.10-3.02)
RSRZ outliers	127900	1713 (3.10-3.02)

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 >=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	266	67% 16% • 15%
1	B	266	70% 13% • 15%
1	C	266	71% 11% • 15%
1	D	266	71% 12% • 15%
1	E	266	67% 16% • 16%

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Mol	Chain	Length	Quality of chain
1	F	266	64% 16% • 17%
1	G	266	67% 14% • 17%
1	H	266	69% 15% • 15%
1	I	266	71% 11% • 16%
1	J	266	.% 69% 13% • 16%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 18821 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 Cyclodipeptide synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	226	1893	1212	329	342	10	0	0	0
1	B	226	1893	1212	329	342	10	0	0	0
1	C	226	1892	1213	328	341	10	0	0	0
1	D	225	1885	1208	327	340	10	0	0	0
1	E	224	1880	1204	327	339	10	0	0	0
1	F	220	1842	1181	319	332	10	0	0	0
1	G	221	1846	1184	317	335	10	0	0	0
1	H	226	1886	1210	325	341	10	0	0	0
1	I	224	1874	1202	323	339	10	0	0	0
1	J	224	1874	1202	323	339	10	0	0	0

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP A0A0W0T5C6
A	1	ALA	-	expression tag	UNP A0A0W0T5C6
A	258	SER	-	expression tag	UNP A0A0W0T5C6
A	259	ARG	-	expression tag	UNP A0A0W0T5C6
A	260	HIS	-	expression tag	UNP A0A0W0T5C6
A	261	HIS	-	expression tag	UNP A0A0W0T5C6
A	262	HIS	-	expression tag	UNP A0A0W0T5C6
A	263	HIS	-	expression tag	UNP A0A0W0T5C6
A	264	HIS	-	expression tag	UNP A0A0W0T5C6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	265	HIS	-	expression tag	UNP A0A0W0T5C6
B	0	MET	-	initiating methionine	UNP A0A0W0T5C6
B	1	ALA	-	expression tag	UNP A0A0W0T5C6
B	258	SER	-	expression tag	UNP A0A0W0T5C6
B	259	ARG	-	expression tag	UNP A0A0W0T5C6
B	260	HIS	-	expression tag	UNP A0A0W0T5C6
B	261	HIS	-	expression tag	UNP A0A0W0T5C6
B	262	HIS	-	expression tag	UNP A0A0W0T5C6
B	263	HIS	-	expression tag	UNP A0A0W0T5C6
B	264	HIS	-	expression tag	UNP A0A0W0T5C6
B	265	HIS	-	expression tag	UNP A0A0W0T5C6
C	0	MET	-	initiating methionine	UNP A0A0W0T5C6
C	1	ALA	-	expression tag	UNP A0A0W0T5C6
C	258	SER	-	expression tag	UNP A0A0W0T5C6
C	259	ARG	-	expression tag	UNP A0A0W0T5C6
C	260	HIS	-	expression tag	UNP A0A0W0T5C6
C	261	HIS	-	expression tag	UNP A0A0W0T5C6
C	262	HIS	-	expression tag	UNP A0A0W0T5C6
C	263	HIS	-	expression tag	UNP A0A0W0T5C6
C	264	HIS	-	expression tag	UNP A0A0W0T5C6
C	265	HIS	-	expression tag	UNP A0A0W0T5C6
D	0	MET	-	initiating methionine	UNP A0A0W0T5C6
D	1	ALA	-	expression tag	UNP A0A0W0T5C6
D	258	SER	-	expression tag	UNP A0A0W0T5C6
D	259	ARG	-	expression tag	UNP A0A0W0T5C6
D	260	HIS	-	expression tag	UNP A0A0W0T5C6
D	261	HIS	-	expression tag	UNP A0A0W0T5C6
D	262	HIS	-	expression tag	UNP A0A0W0T5C6
D	263	HIS	-	expression tag	UNP A0A0W0T5C6
D	264	HIS	-	expression tag	UNP A0A0W0T5C6
D	265	HIS	-	expression tag	UNP A0A0W0T5C6
E	0	MET	-	initiating methionine	UNP A0A0W0T5C6
E	1	ALA	-	expression tag	UNP A0A0W0T5C6
E	258	SER	-	expression tag	UNP A0A0W0T5C6
E	259	ARG	-	expression tag	UNP A0A0W0T5C6
E	260	HIS	-	expression tag	UNP A0A0W0T5C6
E	261	HIS	-	expression tag	UNP A0A0W0T5C6
E	262	HIS	-	expression tag	UNP A0A0W0T5C6
E	263	HIS	-	expression tag	UNP A0A0W0T5C6
E	264	HIS	-	expression tag	UNP A0A0W0T5C6
E	265	HIS	-	expression tag	UNP A0A0W0T5C6
F	0	MET	-	initiating methionine	UNP A0A0W0T5C6

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1	ALA	-	expression tag	UNP A0A0W0T5C6
F	258	SER	-	expression tag	UNP A0A0W0T5C6
F	259	ARG	-	expression tag	UNP A0A0W0T5C6
F	260	HIS	-	expression tag	UNP A0A0W0T5C6
F	261	HIS	-	expression tag	UNP A0A0W0T5C6
F	262	HIS	-	expression tag	UNP A0A0W0T5C6
F	263	HIS	-	expression tag	UNP A0A0W0T5C6
F	264	HIS	-	expression tag	UNP A0A0W0T5C6
F	265	HIS	-	expression tag	UNP A0A0W0T5C6
G	0	MET	-	initiating methionine	UNP A0A0W0T5C6
G	1	ALA	-	expression tag	UNP A0A0W0T5C6
G	258	SER	-	expression tag	UNP A0A0W0T5C6
G	259	ARG	-	expression tag	UNP A0A0W0T5C6
G	260	HIS	-	expression tag	UNP A0A0W0T5C6
G	261	HIS	-	expression tag	UNP A0A0W0T5C6
G	262	HIS	-	expression tag	UNP A0A0W0T5C6
G	263	HIS	-	expression tag	UNP A0A0W0T5C6
G	264	HIS	-	expression tag	UNP A0A0W0T5C6
G	265	HIS	-	expression tag	UNP A0A0W0T5C6
H	0	MET	-	initiating methionine	UNP A0A0W0T5C6
H	1	ALA	-	expression tag	UNP A0A0W0T5C6
H	258	SER	-	expression tag	UNP A0A0W0T5C6
H	259	ARG	-	expression tag	UNP A0A0W0T5C6
H	260	HIS	-	expression tag	UNP A0A0W0T5C6
H	261	HIS	-	expression tag	UNP A0A0W0T5C6
H	262	HIS	-	expression tag	UNP A0A0W0T5C6
H	263	HIS	-	expression tag	UNP A0A0W0T5C6
H	264	HIS	-	expression tag	UNP A0A0W0T5C6
H	265	HIS	-	expression tag	UNP A0A0W0T5C6
I	0	MET	-	initiating methionine	UNP A0A0W0T5C6
I	1	ALA	-	expression tag	UNP A0A0W0T5C6
I	258	SER	-	expression tag	UNP A0A0W0T5C6
I	259	ARG	-	expression tag	UNP A0A0W0T5C6
I	260	HIS	-	expression tag	UNP A0A0W0T5C6
I	261	HIS	-	expression tag	UNP A0A0W0T5C6
I	262	HIS	-	expression tag	UNP A0A0W0T5C6
I	263	HIS	-	expression tag	UNP A0A0W0T5C6
I	264	HIS	-	expression tag	UNP A0A0W0T5C6
I	265	HIS	-	expression tag	UNP A0A0W0T5C6
J	0	MET	-	initiating methionine	UNP A0A0W0T5C6
J	1	ALA	-	expression tag	UNP A0A0W0T5C6
J	258	SER	-	expression tag	UNP A0A0W0T5C6

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Chain	Residue	Modelled	Actual	Comment	Reference
J	259	ARG	-	expression tag	UNP A0A0W0T5C6
J	260	HIS	-	expression tag	UNP A0A0W0T5C6
J	261	HIS	-	expression tag	UNP A0A0W0T5C6
J	262	HIS	-	expression tag	UNP A0A0W0T5C6
J	263	HIS	-	expression tag	UNP A0A0W0T5C6
J	264	HIS	-	expression tag	UNP A0A0W0T5C6
J	265	HIS	-	expression tag	UNP A0A0W0T5C6

- Molecule 2 is water.

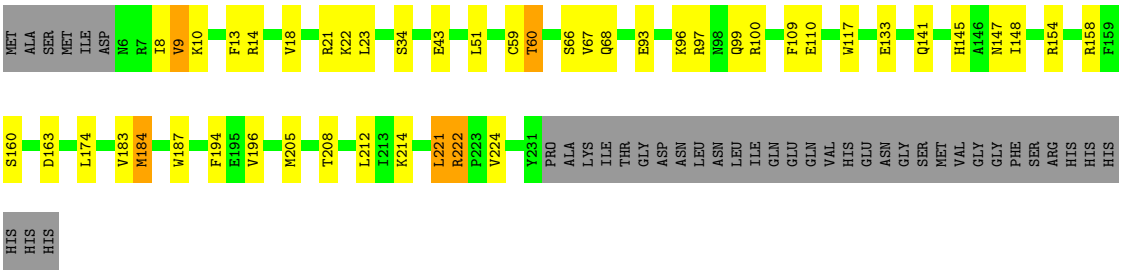
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	15	15	15	0	0
			Total	O		
2	B	8	8	8	0	0
			Total	O		
2	C	5	5	5	0	0
			Total	O		
2	D	9	9	9	0	0
			Total	O		
2	E	1	1	1	0	0
			Total	O		
2	F	1	1	1	0	0
			Total	O		
2	G	1	1	1	0	0
			Total	O		
2	H	4	4	4	0	0
			Total	O		
2	I	5	5	5	0	0
			Total	O		
2	J	7	7	7	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.

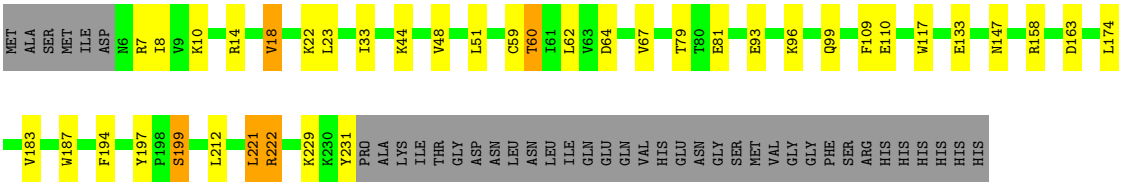
• Molecule 1: Cyclodipeptide synthase

Chain A:



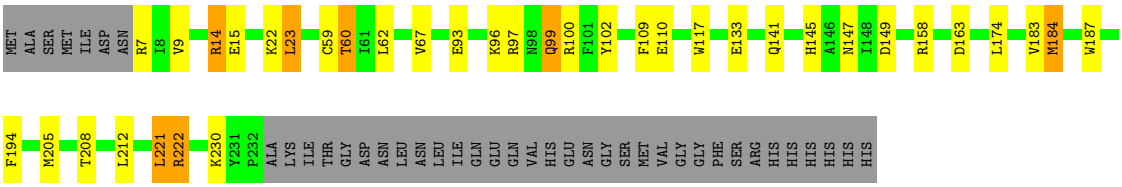
• Molecule 1: Cyclodipeptide synthase

Chain B:



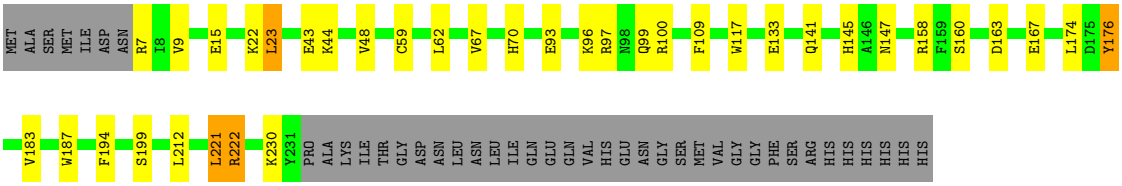
• Molecule 1: Cyclodipeptide synthase

Chain C:



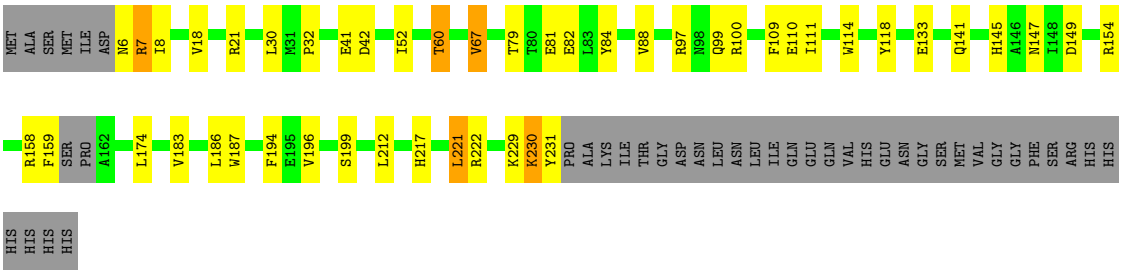
• Molecule 1: Cyclodipeptide synthase

Chain D:



- Molecule 1: Cyclodipeptide synthase

Chain E:

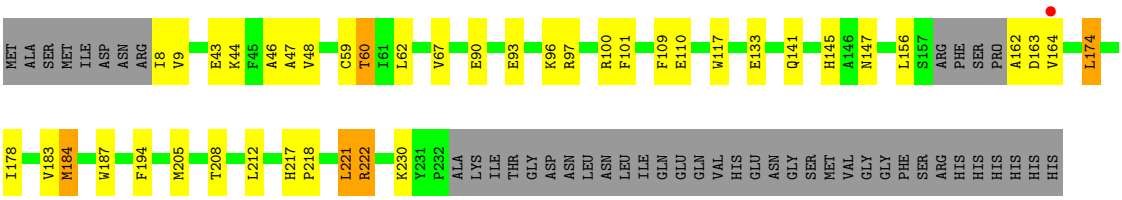


- Molecule 1: Cyclodipeptide synthase

Chain F:

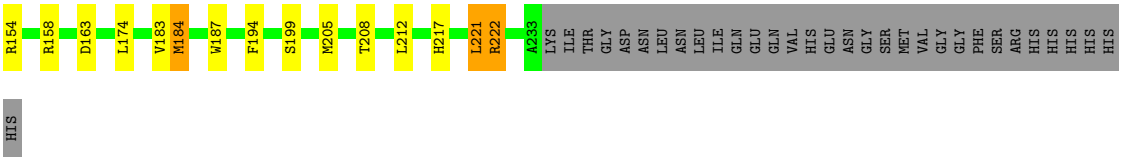
- Molecule 1: Cyclodipeptide synthase

Chain G:



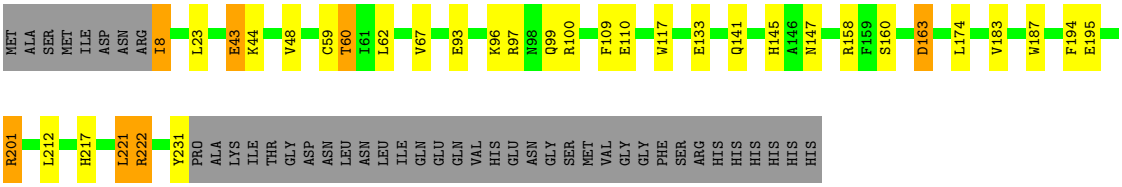
- Molecule 1: Cyclodipeptide synthase

Chain H:



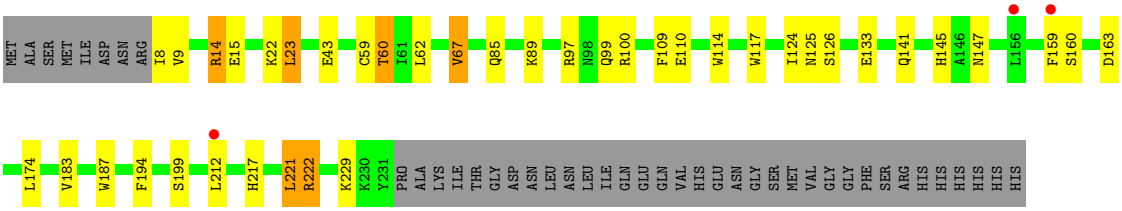
- Molecule 1: Cyclodipeptide synthase

Chain I:



- Molecule 1: Cyclodipeptide synthase

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	185.03Å 97.80Å 211.28Å 90.00° 115.58° 90.00°	Depositor
Resolution (Å)	48.16 – 3.06 48.16 – 3.06	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.16-3.06) 99.3 (48.16-3.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.33 (at 3.07Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.210 , 0.249 0.217 , 0.244	Depositor DCC
R_{free} test set	3223 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	76.6	Xtriage
Anisotropy	0.894	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 61.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	18821	wwPDB-VP
Average B, all atoms (Å^2)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 26.56 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.5771e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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	0.58	0/1943	0.73	0/2629
1	B	0.56	0/1943	0.74	0/2629
1	C	0.51	0/1943	0.70	0/2630
1	D	0.53	0/1935	0.70	0/2618
1	E	0.54	0/1928	0.71	0/2606
1	F	0.50	0/1890	0.71	0/2555
1	G	0.49	0/1894	0.72	0/2563
1	H	0.49	0/1937	0.71	0/2623
1	I	0.49	0/1924	0.70	0/2604
1	J	0.52	0/1924	0.72	0/2604
All	All	0.52	0/19261	0.71	0/26061

There are no bond length outliers.

There are no bond angle outliers.

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	1893	0	1848	21	0
1	B	1893	0	1848	18	0
1	C	1892	0	1849	19	0
1	D	1885	0	1842	14	0
1	E	1880	0	1835	20	0
1	F	1842	0	1801	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1846	0	1801	23	0
1	H	1886	0	1841	20	0
1	I	1874	0	1829	16	0
1	J	1874	0	1829	17	0
2	A	15	0	0	0	0
2	B	8	0	0	0	0
2	C	5	0	0	0	0
2	D	9	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	1	0
2	H	4	0	0	0	0
2	I	5	0	0	0	0
2	J	7	0	0	0	0
All	All	18821	0	18323	189	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 5.

The worst 5 of 189 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:222:ARG:HH21	1:C:222:ARG:HG3	1.24	1.03
1:D:222:ARG:HH21	1:D:222:ARG:HG3	1.24	1.02
1:G:222:ARG:HH21	1:G:222:ARG:HG3	1.26	1.01
1:J:222:ARG:HG3	1:J:222:ARG:HH21	1.25	1.01
1:F:222:ARG:HG3	1:F:222:ARG:HH21	1.26	1.00

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	224/266 (84%)	216 (96%)	8 (4%)	0	100	100
1	B	224/266 (84%)	218 (97%)	6 (3%)	0	100	100
1	C	224/266 (84%)	216 (96%)	8 (4%)	0	100	100
1	D	223/266 (84%)	216 (97%)	7 (3%)	0	100	100
1	E	220/266 (83%)	210 (96%)	9 (4%)	1 (0%)	29	60
1	F	216/266 (81%)	208 (96%)	7 (3%)	1 (0%)	29	60
1	G	217/266 (82%)	205 (94%)	12 (6%)	0	100	100
1	H	224/266 (84%)	215 (96%)	9 (4%)	0	100	100
1	I	222/266 (84%)	214 (96%)	8 (4%)	0	100	100
1	J	222/266 (84%)	215 (97%)	7 (3%)	0	100	100
All	All	2216/2660 (83%)	2133 (96%)	81 (4%)	2 (0%)	51	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	42	ASP
1	E	42	ASP

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	206/240 (86%)	185 (90%)	21 (10%)	7	24
1	B	206/240 (86%)	190 (92%)	16 (8%)	12	37
1	C	206/240 (86%)	191 (93%)	15 (7%)	14	40
1	D	205/240 (85%)	188 (92%)	17 (8%)	11	35
1	E	204/240 (85%)	187 (92%)	17 (8%)	11	35
1	F	201/240 (84%)	181 (90%)	20 (10%)	7	25
1	G	201/240 (84%)	190 (94%)	11 (6%)	21	50
1	H	205/240 (85%)	189 (92%)	16 (8%)	12	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	204/240 (85%)	189 (93%)	15 (7%)	13	39
1	J	204/240 (85%)	185 (91%)	19 (9%)	9	29
All	All	2042/2400 (85%)	1875 (92%)	167 (8%)	11	35

5 of 167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	221	LEU
1	I	174	LEU
1	H	62	LEU
1	H	217	HIS
1	J	23	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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, 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	226/266 (84%)	-0.16	0	100	100	52, 70, 98, 126	0
1	B	226/266 (84%)	-0.16	0	100	100	49, 69, 102, 135	0
1	C	226/266 (84%)	-0.07	0	100	100	64, 91, 126, 153	0
1	D	225/266 (84%)	-0.10	0	100	100	60, 89, 120, 149	0
1	E	224/266 (84%)	-0.18	0	100	100	65, 95, 130, 160	0
1	F	220/266 (82%)	-0.09	0	100	100	66, 103, 144, 173	0
1	G	221/266 (83%)	-0.06	1 (0%)	91	79	70, 103, 144, 164	0
1	H	226/266 (84%)	-0.10	0	100	100	73, 97, 122, 139	0
1	I	224/266 (84%)	-0.06	0	100	100	76, 100, 123, 129	0
1	J	224/266 (84%)	-0.11	3 (1%)	77	56	60, 98, 139, 150	0
All	All	2242/2660 (84%)	-0.11	4 (0%)	95	89	49, 93, 130, 173	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	159	PHE	3.4
1	J	156	LEU	2.3
1	G	164	VAL	2.1
1	J	212	LEU	2.1

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.