wwPDB X-ray Structure Validation Summary Report (i)

Jun 23, 2024 – 03:02 AM EDT

PDB ID	:	5LEL
Title	:	Crystal structure of DARPin-DARPin rigid fusion, variant DD_Off7_10_3G124 in complex with Maltose-binding Protein and Green Fluorescent Protein
Authors	:	Batyuk, A.; Wu, Y.; Mittl, P.R.; Plueckthun, A.
Deposited on	:	2016-06-30
Resolution	:	3.10 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 (i)) were used in the production of this report:

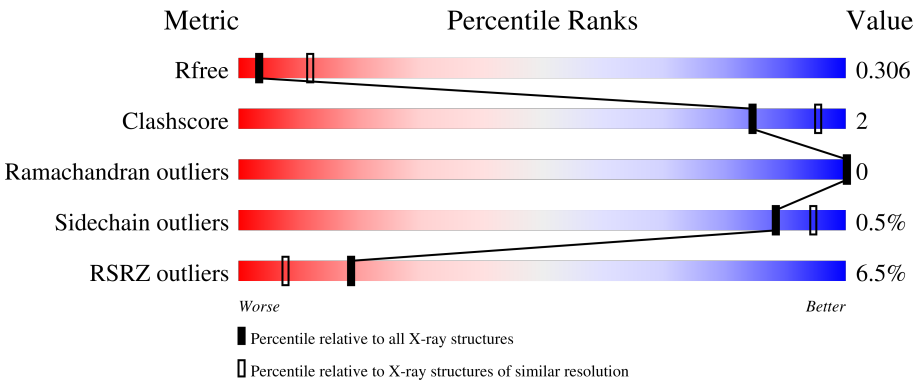
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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	325	3% 90% 6% •
1	D	325	2% 91% 6% •
1	G	325	5% 90% 6% •
2	B	395	10% 87% 6% 7%
2	E	395	3% 86% 8% 7%

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Mol	Chain	Length	Quality of chain
2	H	395	8% 85% 7% 7%
3	C	247	2% 85% 6% 8%
3	F	247	% 87% 8%
3	I	247	23% 89% 8%

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	CRO	C	66	X	-	-	-
3	CRO	F	66	X	-	-	-
3	CRO	I	66	X	-	-	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 41668 atoms, of which 20622 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 DD_Off7_10_3G124.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	313	4696	1486	2332	418	456	4	0	0	0
1	D	313	4696	1486	2332	418	456	4	0	0	0
1	G	311	4675	1480	2322	416	453	4	0	0	0

- Molecule 2 is a protein called Maltose-binding periplasmic protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	B	368	5635	1825	2797	462	545	6	0	0	0
2	E	369	5642	1827	2800	463	546	6	0	0	0
2	H	366	5602	1815	2780	459	542	6	0	0	0

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	MET	-	initiating methionine	UNP P0AEY0
B	-13	ARG	-	expression tag	UNP P0AEY0
B	-12	GLY	-	expression tag	UNP P0AEY0
B	-11	SER	-	expression tag	UNP P0AEY0
B	-10	HIS	-	expression tag	UNP P0AEY0
B	-9	HIS	-	expression tag	UNP P0AEY0
B	-8	HIS	-	expression tag	UNP P0AEY0
B	-7	HIS	-	expression tag	UNP P0AEY0
B	-6	HIS	-	expression tag	UNP P0AEY0
B	-5	HIS	-	expression tag	UNP P0AEY0
B	-4	GLY	-	expression tag	UNP P0AEY0
B	-3	SER	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	expression tag	UNP P0AEY0
B	-1	SER	-	expression tag	UNP P0AEY0
B	0	MET	-	expression tag	UNP P0AEY0
B	1	LYS	-	expression tag	UNP P0AEY0
B	2	THR	-	expression tag	UNP P0AEY0
B	6	ASN	LYS	conflict	UNP P0AEY0
B	367	GLY	-	expression tag	UNP P0AEY0
B	368	SER	-	expression tag	UNP P0AEY0
B	369	GLY	-	expression tag	UNP P0AEY0
B	370	GLY	-	expression tag	UNP P0AEY0
B	371	THR	-	expression tag	UNP P0AEY0
B	372	PRO	-	expression tag	UNP P0AEY0
B	373	GLY	-	expression tag	UNP P0AEY0
B	374	ARG	-	expression tag	UNP P0AEY0
B	375	PRO	-	expression tag	UNP P0AEY0
B	376	ALA	-	expression tag	UNP P0AEY0
B	377	ALA	-	expression tag	UNP P0AEY0
B	378	LYS	-	expression tag	UNP P0AEY0
B	379	LEU	-	expression tag	UNP P0AEY0
B	380	ASN	-	expression tag	UNP P0AEY0
E	-14	MET	-	initiating methionine	UNP P0AEY0
E	-13	ARG	-	expression tag	UNP P0AEY0
E	-12	GLY	-	expression tag	UNP P0AEY0
E	-11	SER	-	expression tag	UNP P0AEY0
E	-10	HIS	-	expression tag	UNP P0AEY0
E	-9	HIS	-	expression tag	UNP P0AEY0
E	-8	HIS	-	expression tag	UNP P0AEY0
E	-7	HIS	-	expression tag	UNP P0AEY0
E	-6	HIS	-	expression tag	UNP P0AEY0
E	-5	HIS	-	expression tag	UNP P0AEY0
E	-4	GLY	-	expression tag	UNP P0AEY0
E	-3	SER	-	expression tag	UNP P0AEY0
E	-2	GLY	-	expression tag	UNP P0AEY0
E	-1	SER	-	expression tag	UNP P0AEY0
E	0	MET	-	expression tag	UNP P0AEY0
E	1	LYS	-	expression tag	UNP P0AEY0
E	2	THR	-	expression tag	UNP P0AEY0
E	6	ASN	LYS	conflict	UNP P0AEY0
E	367	GLY	-	expression tag	UNP P0AEY0
E	368	SER	-	expression tag	UNP P0AEY0
E	369	GLY	-	expression tag	UNP P0AEY0
E	370	GLY	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	371	THR	-	expression tag	UNP P0AEY0
E	372	PRO	-	expression tag	UNP P0AEY0
E	373	GLY	-	expression tag	UNP P0AEY0
E	374	ARG	-	expression tag	UNP P0AEY0
E	375	PRO	-	expression tag	UNP P0AEY0
E	376	ALA	-	expression tag	UNP P0AEY0
E	377	ALA	-	expression tag	UNP P0AEY0
E	378	LYS	-	expression tag	UNP P0AEY0
E	379	LEU	-	expression tag	UNP P0AEY0
E	380	ASN	-	expression tag	UNP P0AEY0
H	-14	MET	-	initiating methionine	UNP P0AEY0
H	-13	ARG	-	expression tag	UNP P0AEY0
H	-12	GLY	-	expression tag	UNP P0AEY0
H	-11	SER	-	expression tag	UNP P0AEY0
H	-10	HIS	-	expression tag	UNP P0AEY0
H	-9	HIS	-	expression tag	UNP P0AEY0
H	-8	HIS	-	expression tag	UNP P0AEY0
H	-7	HIS	-	expression tag	UNP P0AEY0
H	-6	HIS	-	expression tag	UNP P0AEY0
H	-5	HIS	-	expression tag	UNP P0AEY0
H	-4	GLY	-	expression tag	UNP P0AEY0
H	-3	SER	-	expression tag	UNP P0AEY0
H	-2	GLY	-	expression tag	UNP P0AEY0
H	-1	SER	-	expression tag	UNP P0AEY0
H	0	MET	-	expression tag	UNP P0AEY0
H	1	LYS	-	expression tag	UNP P0AEY0
H	2	THR	-	expression tag	UNP P0AEY0
H	6	ASN	LYS	conflict	UNP P0AEY0
H	367	GLY	-	expression tag	UNP P0AEY0
H	368	SER	-	expression tag	UNP P0AEY0
H	369	GLY	-	expression tag	UNP P0AEY0
H	370	GLY	-	expression tag	UNP P0AEY0
H	371	THR	-	expression tag	UNP P0AEY0
H	372	PRO	-	expression tag	UNP P0AEY0
H	373	GLY	-	expression tag	UNP P0AEY0
H	374	ARG	-	expression tag	UNP P0AEY0
H	375	PRO	-	expression tag	UNP P0AEY0
H	376	ALA	-	expression tag	UNP P0AEY0
H	377	ALA	-	expression tag	UNP P0AEY0
H	378	LYS	-	expression tag	UNP P0AEY0
H	379	LEU	-	expression tag	UNP P0AEY0
H	380	ASN	-	expression tag	UNP P0AEY0

- Molecule 3 is a protein called Green fluorescent protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
3	C	227	3574	1159	1753	308	348	6	0	0	0
3	F	227	3574	1159	1753	308	348	6	0	0	0
3	I	227	3574	1159	1753	308	348	6	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-10	MET	-	initiating methionine	UNP P42212
C	-9	ARG	-	expression tag	UNP P42212
C	-8	GLY	-	expression tag	UNP P42212
C	-7	SER	-	expression tag	UNP P42212
C	-6	HIS	-	expression tag	UNP P42212
C	-5	HIS	-	expression tag	UNP P42212
C	-4	HIS	-	expression tag	UNP P42212
C	-3	HIS	-	expression tag	UNP P42212
C	-2	HIS	-	expression tag	UNP P42212
C	-1	HIS	-	expression tag	UNP P42212
C	0	GLY	-	expression tag	UNP P42212
C	1	SER	-	expression tag	UNP P42212
C	?	CRO	SER	chromophore	UNP P42212
C	?	CRO	TYR	chromophore	UNP P42212
C	66	CRO	GLY	chromophore	UNP P42212
C	80	ARG	GLN	engineered mutation	UNP P42212
F	-10	MET	-	initiating methionine	UNP P42212
F	-9	ARG	-	expression tag	UNP P42212
F	-8	GLY	-	expression tag	UNP P42212
F	-7	SER	-	expression tag	UNP P42212
F	-6	HIS	-	expression tag	UNP P42212
F	-5	HIS	-	expression tag	UNP P42212
F	-4	HIS	-	expression tag	UNP P42212
F	-3	HIS	-	expression tag	UNP P42212
F	-2	HIS	-	expression tag	UNP P42212
F	-1	HIS	-	expression tag	UNP P42212
F	0	GLY	-	expression tag	UNP P42212
F	1	SER	-	expression tag	UNP P42212
F	?	CRO	SER	chromophore	UNP P42212
F	?	CRO	TYR	chromophore	UNP P42212
F	66	CRO	GLY	chromophore	UNP P42212
F	80	ARG	GLN	engineered mutation	UNP P42212

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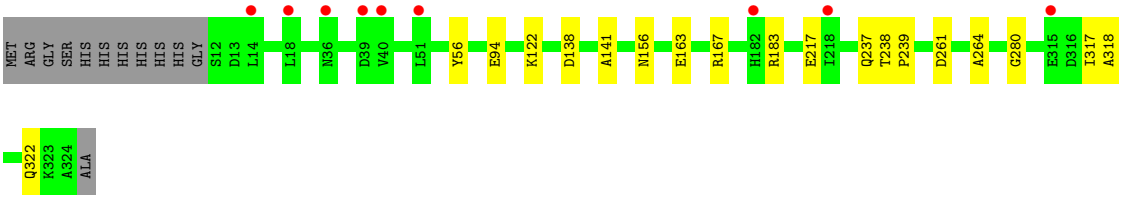
Chain	Residue	Modelled	Actual	Comment	Reference
I	-10	MET	-	initiating methionine	UNP P42212
I	-9	ARG	-	expression tag	UNP P42212
I	-8	GLY	-	expression tag	UNP P42212
I	-7	SER	-	expression tag	UNP P42212
I	-6	HIS	-	expression tag	UNP P42212
I	-5	HIS	-	expression tag	UNP P42212
I	-4	HIS	-	expression tag	UNP P42212
I	-3	HIS	-	expression tag	UNP P42212
I	-2	HIS	-	expression tag	UNP P42212
I	-1	HIS	-	expression tag	UNP P42212
I	0	GLY	-	expression tag	UNP P42212
I	1	SER	-	expression tag	UNP P42212
I	?	CRO	SER	chromophore	UNP P42212
I	?	CRO	TYR	chromophore	UNP P42212
I	66	CRO	GLY	chromophore	UNP P42212
I	80	ARG	GLN	engineered mutation	UNP P42212

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.

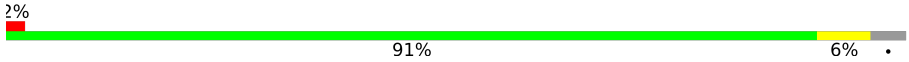
• Molecule 1: DD_Off7_10_3G124

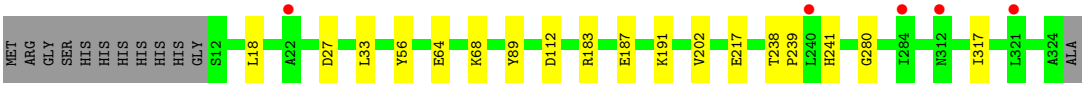
Chain A:



• Molecule 1: DD_Off7_10_3G124

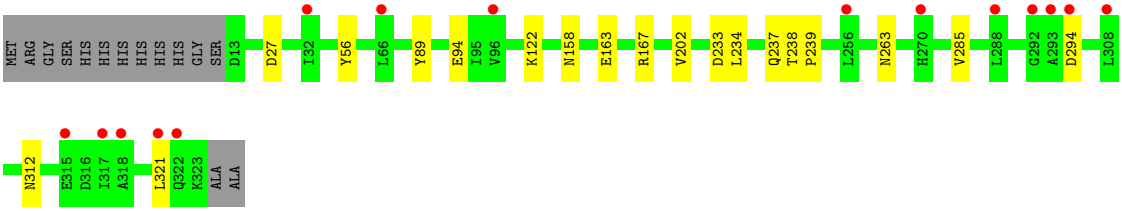
Chain D:





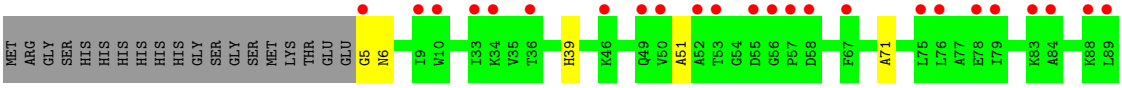
• Molecule 1: DD_Off7_10_3G124

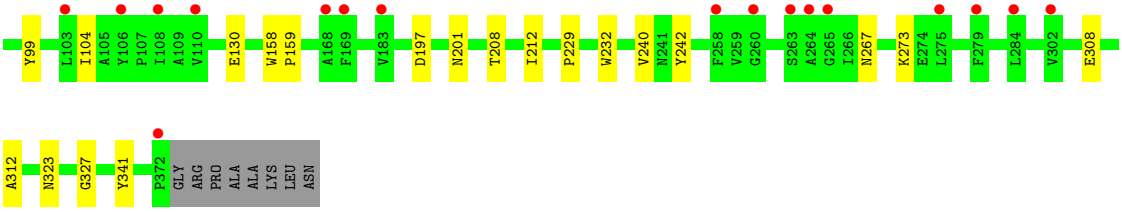
Chain G:



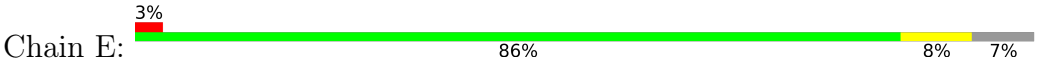
• Molecule 2: Maltose-binding periplasmic protein

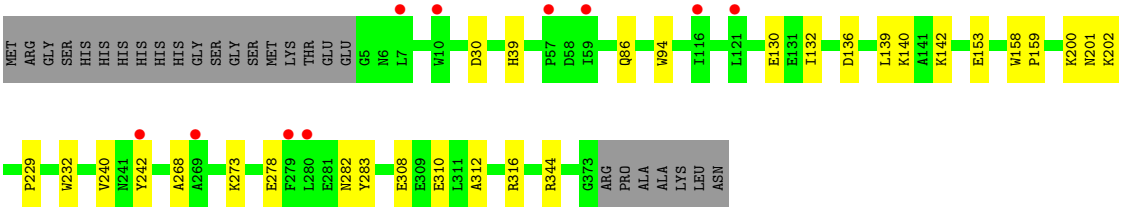
Chain B:



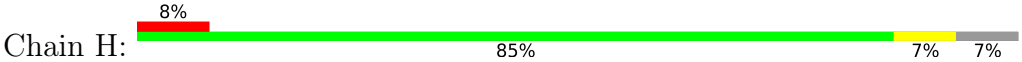


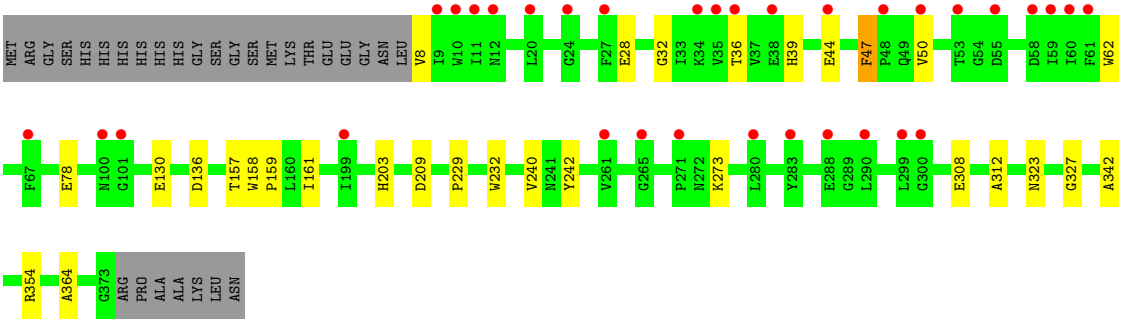
• Molecule 2: Maltose-binding periplasmic protein



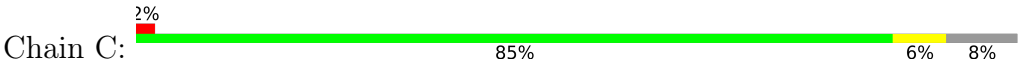


• Molecule 2: Maltose-binding periplasmic protein

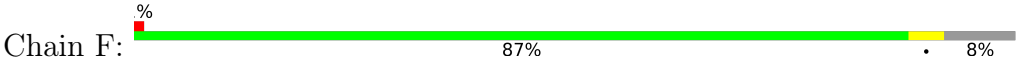


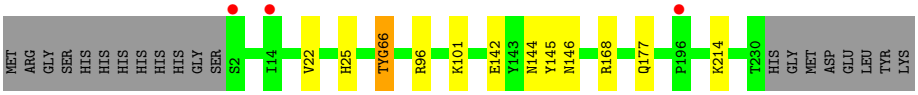


• Molecule 3: Green fluorescent protein



• Molecule 3: Green fluorescent protein

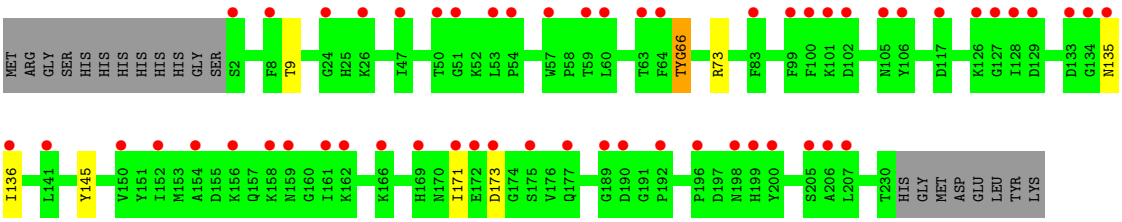




• Molecule 3: Green fluorescent protein

Chain I:

23%
89%
8%


MET ARG GLY SER HIS HIS HIS HIS HIS HIS GLY SER S2 F8 T9 G24 H25 K26 I47 T50 G51 K52 L53 P54 W57 P58 T59 L60 T63 F64 TYG66 R73 F83 F99 F100 K101 D102 N105 Y106 D117 K126 G127 I128 D129 D133 G134 N135
I136 L141 Y145 V150 Y151 I152 M153 A154 D155 K156 Q157 K158 N159 G160 I161 K162 K166 H169 N170 I171 E172 D173 G174 S175 V176 Q177 G189 D190 G191 P192 P196 D197 N198 H199 Y200 S205 A206 L207 T230 HIS GLY MET ASP GLU LEU TYR LYS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	235.00Å 103.14Å 156.84Å 90.00° 131.35° 90.00°	Depositor
Resolution (Å)	46.63 – 3.10 47.17 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.63-3.10) 99.7 (47.17-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.32 (at 3.12Å)	Xtriage
Refinement program	PHENIX (DEV_2429)	Depositor
R, R_{free}	0.258 , 0.306 0.259 , 0.306	Depositor DCC
R_{free} test set	2558 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	85.2	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 33.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	0.020 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	41668	wwPDB-VP
Average B, all atoms (Å^2)	118.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% of the height of the origin peak. No significant pseudotranslation is detected.*

[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)

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

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	0.24	0/2406	0.39	0/3275
1	D	0.24	0/2406	0.39	0/3275
1	G	0.24	0/2395	0.39	0/3260
2	B	0.25	0/2908	0.41	0/3951
2	E	0.25	0/2912	0.40	0/3956
2	H	0.25	0/2892	0.41	0/3929
3	C	0.25	0/1840	0.46	0/2485
3	F	0.25	0/1840	0.45	0/2485
3	I	0.25	0/1840	0.46	0/2485
All	All	0.25	0/21439	0.41	0/29101

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
3	C	1	0
3	F	1	0
3	I	1	0
All	All	3	0

There are no bond length outliers.

There are no bond angle outliers.

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	C	66	CRO	CB1
3	F	66	CRO	CB1
3	I	66	CRO	CB1

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	2364	2332	2332	10	0
1	D	2364	2332	2332	11	0
1	G	2353	2322	2322	10	0
2	B	2838	2797	2797	15	0
2	E	2842	2800	2800	18	0
2	H	2822	2780	2780	17	0
3	C	1821	1753	1765	9	0
3	F	1821	1753	1765	6	0
3	I	1821	1753	1765	6	0
All	All	21046	20622	20658	95	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 2.

The worst 5 of 95 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:122:LYS:O	1:A:156:ASN:ND2	2.16	0.79
2:B:39:HIS:O	2:B:39:HIS:ND1	2.22	0.73
2:E:30:ASP:OD1	2:E:283:TYR:OH	2.06	0.72
3:F:101:LYS:O	3:F:177:GLN:NE2	2.23	0.70
2:B:267:ASN:O	2:B:273:LYS:NZ	2.24	0.70

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	311/325 (96%)	300 (96%)	11 (4%)	0	100	100
1	D	311/325 (96%)	298 (96%)	13 (4%)	0	100	100
1	G	309/325 (95%)	297 (96%)	12 (4%)	0	100	100
2	B	366/395 (93%)	359 (98%)	7 (2%)	0	100	100
2	E	367/395 (93%)	360 (98%)	7 (2%)	0	100	100
2	H	364/395 (92%)	354 (97%)	10 (3%)	0	100	100
3	C	222/247 (90%)	217 (98%)	5 (2%)	0	100	100
3	F	222/247 (90%)	217 (98%)	5 (2%)	0	100	100
3	I	222/247 (90%)	216 (97%)	6 (3%)	0	100	100
All	All	2694/2901 (93%)	2618 (97%)	76 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	239/248 (96%)	238 (100%)	1 (0%)	91	96
1	D	239/248 (96%)	238 (100%)	1 (0%)	91	96
1	G	238/248 (96%)	235 (99%)	3 (1%)	69	87
2	B	292/313 (93%)	292 (100%)	0	100	100
2	E	292/313 (93%)	292 (100%)	0	100	100
2	H	290/313 (93%)	289 (100%)	1 (0%)	92	96
3	C	198/215 (92%)	196 (99%)	2 (1%)	76	90
3	F	198/215 (92%)	197 (100%)	1 (0%)	88	94
3	I	198/215 (92%)	197 (100%)	1 (0%)	88	94
All	All	2184/2328 (94%)	2174 (100%)	10 (0%)	88	94

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

Mol	Chain	Res	Type
1	G	234	LEU
2	H	47	PHE
3	I	145	TYR
1	D	56	TYR
3	F	145	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	156	ASN
2	B	6	ASN
1	D	158	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)

3 non-standard protein/DNA/RNA residues 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	CRO	I	66	3	23,23,24	5.65	8 (34%)	30,32,34	3.52	19 (63%)
3	CRO	C	66	3	23,23,24	5.75	8 (34%)	30,32,34	3.51	18 (60%)
3	CRO	F	66	3	23,23,24	5.68	8 (34%)	30,32,34	3.43	17 (56%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CRO	I	66	3	1/1/6/8	6/12/31/32	0/2/2/2
3	CRO	C	66	3	1/1/6/8	6/12/31/32	0/2/2/2
3	CRO	F	66	3	1/1/6/8	7/12/31/32	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	66	CRO	CB2-CA2	22.93	1.54	1.35
3	I	66	CRO	CB2-CA2	22.33	1.53	1.35
3	F	66	CRO	CB2-CA2	22.18	1.53	1.35
3	F	66	CRO	OG1-CB1	-9.35	1.17	1.43
3	C	66	CRO	OG1-CB1	-9.33	1.17	1.43

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	F	66	CRO	CA2-C2-N3	11.22	108.68	103.37
3	C	66	CRO	CA2-C2-N3	10.99	108.57	103.37
3	I	66	CRO	CA2-C2-N3	10.08	108.14	103.37
3	I	66	CRO	CG2-CB2-CA2	-8.55	119.46	129.94
3	C	66	CRO	CG2-CB2-CA2	-7.37	120.91	129.94

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	C	66	CRO	CB1
3	F	66	CRO	CB1
3	I	66	CRO	CB1

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	66	CRO	C1-CA1-CB1-CG1
3	C	66	CRO	N2-C1-CA1-CB1
3	C	66	CRO	N3-C1-CA1-CB1
3	F	66	CRO	N1-CA1-CB1-OG1
3	F	66	CRO	C1-CA1-CB1-OG1

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	66	CRO	1	0
3	C	66	CRO	2	0
3	F	66	CRO	1	0

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	313/325 (96%)	0.13	9 (2%)	51	28	47, 85, 148, 224	0
1	D	313/325 (96%)	0.19	5 (1%)	72	51	47, 86, 140, 186	0
1	G	311/325 (95%)	0.26	15 (4%)	30	14	62, 108, 181, 295	0
2	B	368/395 (93%)	0.56	41 (11%)	5	2	61, 128, 187, 243	0
2	E	369/395 (93%)	0.19	10 (2%)	54	31	47, 95, 150, 225	0
2	H	366/395 (92%)	0.39	33 (9%)	9	3	58, 115, 215, 291	0
3	C	226/247 (91%)	0.04	4 (1%)	68	47	46, 76, 118, 176	0
3	F	226/247 (91%)	0.16	3 (1%)	77	59	49, 82, 129, 172	0
3	I	226/247 (91%)	1.16	56 (24%)	0	0	71, 151, 214, 276	0
All	All	2718/2901 (93%)	0.33	176 (6%)	18	8	46, 101, 186, 295	0

The worst 5 of 176 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	129	ASP	10.7
2	H	59	ILE	8.5
1	G	315	GLU	8.5
2	H	265	GLY	8.0
2	H	11	ILE	7.2

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95th 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^2)	Q<0.9
3	CRO	C	66	22/23	0.91	0.27	51,58,85,105	0
3	CRO	F	66	22/23	0.91	0.31	59,72,85,88	0
3	CRO	I	66	22/23	0.94	0.32	142,147,155,159	0

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.