



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 25, 2017 – 05:50 AM EDT

PDB ID : 5LE7
Title : Crystal structure of DARPin-DARPin rigid fusion, variant DD_D12_13_D12
Authors : Batyuk, A.; Wu, Y.; Mittl, P.R.; Plueckthun, A.
Deposited on : unknown
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

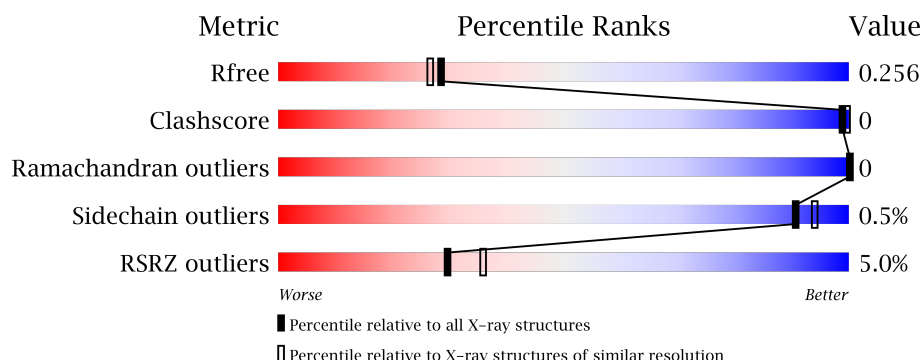
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	328	<div> <div>8%</div> <div>95%</div> <div>..</div> </div>
1	B	328	<div> <div>4%</div> <div>95%</div> <div>..</div> </div>
1	C	328	<div> <div>5%</div> <div>96%</div> <div>..</div> </div>
1	D	328	<div> <div>3%</div> <div>95%</div> <div>..</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 19107 atoms, of which 9385 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_D12_13_D12.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	316	Total	C	H	N	O	S	0	1	0
			4731	1495	2345	420	469	2			
1	B	317	Total	C	H	N	O	S	0	0	0
			4735	1495	2348	421	469	2			
1	C	318	Total	C	H	N	O	S	0	0	0
			4741	1497	2350	422	470	2			
1	D	316	Total	C	H	N	O	S	0	0	0
			4723	1492	2342	420	467	2			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	26	Total	O	0	0
			26	26		
3	B	42	Total	O	0	0
			42	42		
3	C	40	Total	O	0	0
			40	40		
3	D	44	Total	O	0	0
			44	44		

- Molecule 1: DD D12 13 D12



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	147.94Å 75.25Å 131.83Å 90.00° 96.94° 90.00°	Depositor
Resolution (Å)	46.16 – 2.10 46.16 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.2 (46.16-2.10) 99.3 (46.16-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 2.10Å)	Xtriage
Refinement program	PHENIX (dev_2386)	Depositor
R, R_{free}	0.225 , 0.258 0.224 , 0.256	Depositor DCC
R_{free} test set	4148 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	56.7	Xtriage
Anisotropy	0.119	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	19107	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: SO4

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	0.25	0/2429	0.41	0/3304
1	B	0.26	0/2427	0.42	0/3301
1	C	0.25	0/2431	0.41	0/3306
1	D	0.26	0/2421	0.42	0/3293
All	All	0.25	0/9708	0.42	0/13204

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	2386	2345	2346	4	0
1	B	2387	2348	2347	2	0
1	C	2391	2350	2350	2	0
1	D	2381	2342	2342	1	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	10	0	0	0	0
3	A	26	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	42	0	0	0	1
3	C	40	0	0	0	1
3	D	44	0	0	0	0
All	All	9722	9385	9385	9	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 0.

All (9) 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:B:319:ASP:OD1	1:B:320:ILE:N	2.31	0.62
1:B:271:ILE:HG22	1:B:271:ILE:O	2.13	0.49
1:A:110:ASP:OD1	1:A:114:THR:N	2.38	0.48
1:A:187:ASP:N	1:A:187:ASP:OD1	2.45	0.48
1:A:271:ILE:HG22	1:A:271:ILE:O	2.14	0.47
1:D:112:ILE:HG22	1:D:112:ILE:O	2.15	0.47
1:A:269:ASP:OD1	1:A:271:ILE:N	2.48	0.46
1:C:205:THR:HG1	1:C:207:PHE:HD2	1.65	0.45
1:C:271:ILE:HG22	1:C:271:ILE:O	2.17	0.44

All (1) 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)
3:B:535:HOH:O	3:C:537:HOH:O[3_545]	2.07	0.13

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	315/328 (96%)	307 (98%)	8 (2%)	0	100	100
1	B	315/328 (96%)	309 (98%)	6 (2%)	0	100	100
1	C	316/328 (96%)	310 (98%)	6 (2%)	0	100	100
1	D	314/328 (96%)	314 (100%)	0	0	100	100
All	All	1260/1312 (96%)	1240 (98%)	20 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	242/251 (96%)	240 (99%)	2 (1%)	85	89
1	B	242/251 (96%)	241 (100%)	1 (0%)	93	95
1	C	242/251 (96%)	242 (100%)	0	100	100
1	D	241/251 (96%)	239 (99%)	2 (1%)	85	89
All	All	967/1004 (96%)	962 (100%)	5 (0%)	91	94

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	187	ASP
1	A	248	TYR
1	B	123	TRP
1	D	248	TYR
1	D	282	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	218	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

5 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	$\# Z > 2$
2	SO4	A	401	-	4,4,4	0.17	0	6,6,6	0.07	0
2	SO4	B	401	-	4,4,4	0.20	0	6,6,6	0.07	0
2	SO4	C	401	-	4,4,4	0.20	0	6,6,6	0.11	0
2	SO4	D	401	-	4,4,4	0.17	0	6,6,6	0.08	0
2	SO4	D	402	-	4,4,4	0.17	0	6,6,6	0.10	0

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
2	SO4	A	401	-	-	0/0/0/0	0/0/0/0
2	SO4	B	401	-	-	0/0/0/0	0/0/0/0
2	SO4	C	401	-	-	0/0/0/0	0/0/0/0
2	SO4	D	401	-	-	0/0/0/0	0/0/0/0
2	SO4	D	402	-	-	0/0/0/0	0/0/0/0

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.

No monomer is involved in short contacts.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	316/328 (96%)	0.85	25 (7%) 13 17	43, 74, 99, 119	0
1	B	317/328 (96%)	0.76	13 (4%) 38 45	42, 61, 83, 106	0
1	C	318/328 (96%)	0.80	15 (4%) 32 38	45, 67, 97, 117	0
1	D	316/328 (96%)	0.73	10 (3%) 48 55	39, 64, 87, 114	0
All	All	1267/1312 (96%)	0.79	63 (4%) 30 36	39, 66, 95, 119	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	271	ILE	4.6
1	A	160	TRP	4.6
1	C	304	PHE	4.2
1	A	65	VAL	4.0
1	D	160	TRP	3.9
1	A	95	ILE	3.5
1	A	48	PHE	3.4
1	C	193	ILE	3.3
1	D	204	GLU	3.0
1	A	67	LEU	3.0
1	C	238	ARG	2.9
1	C	13	ASP	2.9
1	B	112	ILE	2.8
1	B	207	PHE	2.8
1	A	93	LEU	2.8
1	D	111	VAL	2.8
1	A	146	GLY	2.8
1	C	179	GLU	2.7
1	A	161	ILE	2.7
1	B	16	LYS	2.7
1	B	238	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	280	ALA	2.6
1	B	48	PHE	2.6
1	A	204	GLU	2.6
1	D	78	GLU	2.6
1	A	63	VAL	2.6
1	A	60	LEU	2.6
1	A	119	LEU	2.5
1	C	16	LYS	2.5
1	D	32	ILE	2.5
1	A	76	ASN	2.5
1	C	234	ALA	2.5
1	D	51	LEU	2.4
1	C	303	LYS	2.4
1	C	48	PHE	2.4
1	A	98	VAL	2.4
1	D	159	GLN	2.4
1	A	100	LEU	2.4
1	D	60	LEU	2.4
1	A	319	ASP	2.4
1	D	98	VAL	2.4
1	A	173	LEU	2.3
1	B	139	VAL	2.3
1	A	51	LEU	2.3
1	B	271	ILE	2.3
1	D	207	PHE	2.3
1	A	20	GLU	2.3
1	C	280	ALA	2.3
1	A	138	ASP	2.2
1	B	178	LEU	2.2
1	A	62	ILE	2.2
1	B	187	ASP	2.2
1	A	78	GLU	2.2
1	C	320	ILE	2.1
1	A	66	LEU	2.1
1	C	282	TRP	2.1
1	C	183	ALA	2.1
1	B	170	LYS	2.1
1	A	99	LEU	2.1
1	A	285	LEU	2.1
1	B	318	GLU	2.0
1	B	191	ASP	2.0
1	C	325	GLN	2.0

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	SO4	B	401	5/5	0.88	0.17	-0.01	84,85,86,88	0
2	SO4	C	401	5/5	0.83	0.16	-0.17	78,80,85,87	0
2	SO4	A	401	5/5	0.96	0.14	-1.28	93,93,95,95	0
2	SO4	D	402	5/5	0.92	0.11	-2.05	79,80,84,85	0
2	SO4	D	401	5/5	0.93	0.10	-2.45	87,88,89,91	0

6.5 Other polymers [i](#)

There are no such residues in this entry.