



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:51 PM GMT

PDB ID : 4GC7
Title : Crystal structure of Dpo4 in complex with S-MC-dADP opposite dT
Authors : Eoff, R.L.; Ketkar, A.; Banerjee, S.; Zafar, M.K.
Deposited on : 2012-07-29
Resolution : 2.89 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
<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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

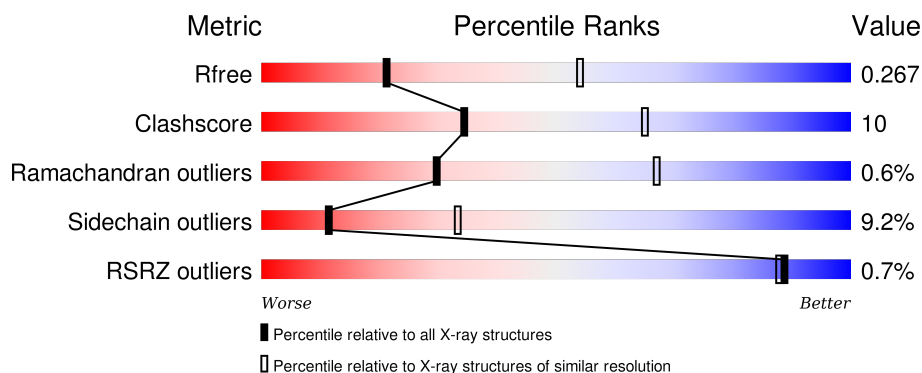
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.89 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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	359	<div> <div></div> <div>72% 20% • 5%</div> </div>
1	B	359	<div> <div></div> <div>66% 26% • 5%</div> </div>
2	C	14	<div> <div>29% 29% 36% 7%</div> </div>
2	E	14	<div> <div>29% 64% 7%</div> </div>
3	D	18	<div> <div>44% 28% 11% 17%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	18	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: green (33%), yellow (39%), orange (17%), and grey (11%).

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6775 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 DNA polymerase IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2743	1760	472	504	7			
1	B	341	Total	C	N	O	S	0	0	0
			2743	1760	472	504	7			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	HIS	-	EXPRESSION TAG	UNP Q97W02
A	-5	HIS	-	EXPRESSION TAG	UNP Q97W02
A	-4	HIS	-	EXPRESSION TAG	UNP Q97W02
A	-3	HIS	-	EXPRESSION TAG	UNP Q97W02
A	-2	HIS	-	EXPRESSION TAG	UNP Q97W02
A	-1	HIS	-	EXPRESSION TAG	UNP Q97W02
A	0	HIS	-	EXPRESSION TAG	UNP Q97W02
B	-6	HIS	-	EXPRESSION TAG	UNP Q97W02
B	-5	HIS	-	EXPRESSION TAG	UNP Q97W02
B	-4	HIS	-	EXPRESSION TAG	UNP Q97W02
B	-3	HIS	-	EXPRESSION TAG	UNP Q97W02
B	-2	HIS	-	EXPRESSION TAG	UNP Q97W02
B	-1	HIS	-	EXPRESSION TAG	UNP Q97W02
B	0	HIS	-	EXPRESSION TAG	UNP Q97W02

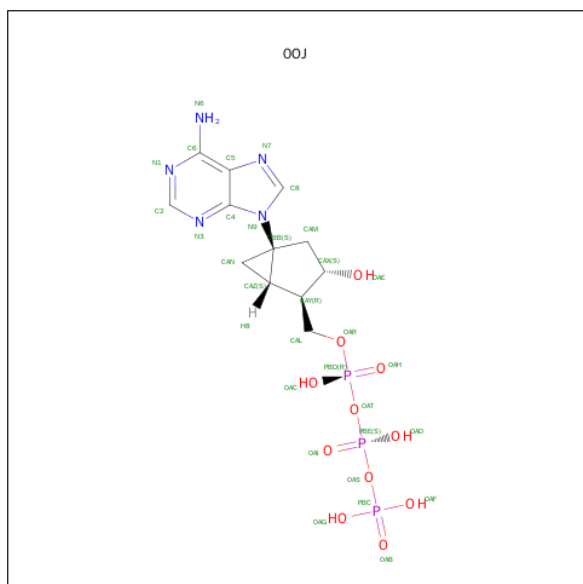
- Molecule 2 is a DNA chain called DNA (5'-D(*G*GP*GP*GP*GP*AP*AP*GP*GP*AP*TP*TP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	13	Total	C	N	O	P	1	0	0
			270	128	55	75	12			
2	E	13	Total	C	N	O	P	2	0	0
			270	128	55	75	12			

- Molecule 3 is a DNA chain called DNA (5'-D(*TP*CP*AP*TP*GP*GP*AP*AP*TP*CP*CP*TP*TP*CP*CP*CP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	15	Total	C	N	O	P	0	0	0
			301	144	51	91	15			
3	F	16	Total	C	N	O	P	0	0	0
			320	153	54	97	16			

- Molecule 4 is SOUTH-METHANOCARBA-2'-DEOXYADENOSINE TRIPHOSPHATE (three-letter code: 0OJ) (formula: C₁₂H₁₈N₅O₁₁P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			27	12	5	8	2		
4	B	1	Total	C	N	O	P	0	0
			27	12	5	8	2		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	4	Total	Ca	0	0
			4	4		
5	A	5	Total	Ca	0	0
			5	5		

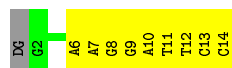
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	17	Total 17	O 17	0	0
6	B	21	Total 21	O 21	0	0
6	C	8	Total 8	O 8	0	0
6	D	6	Total 6	O 6	0	0
6	E	8	Total 8	O 8	0	0
6	F	5	Total 5	O 5	0	0

- Molecule 1: DNA polymerase IV

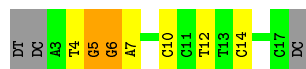


Chain E:  29% 64% 7%




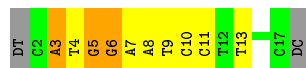
- Molecule 3: DNA (5'-D(*TP*CP*AP*TP*GP*GP*AP*AP*TP*CP*CP*TP*TP*CP*CP*CP*CP*C)-3')

Chain D:  44% 28% 11% 17%



- Molecule 3: DNA (5'-D(*TP*CP*AP*TP*GP*GP*AP*AP*TP*CP*CP*TP*TP*CP*CP*CP*CP*C)-3')

Chain F:  33% 39% 17% 11%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	52.72Å 101.08Å 99.99Å 90.00° 92.59° 90.00°	Depositor
Resolution (Å)	47.48 – 2.89 47.48 – 2.89	Depositor EDS
% Data completeness (in resolution range)	90.1 (47.48-2.89) 89.9 (47.48-2.89)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.206 , 0.265 0.204 , 0.267	Depositor DCC
R_{free} test set	1984 reflections (10.27%)	DCC
Wilson B-factor (Å ²)	61.0	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.2	EDS
Estimated twinning fraction	0.026 for -h,-l,-k 0.015 for -h,l,k 0.058 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 22641 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6775	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.48	0/2782	0.60	0/3736
1	B	0.48	0/2782	0.62	1/3736 (0.0%)
2	C	0.97	0/304	2.02	12/469 (2.6%)
2	E	0.97	1/304 (0.3%)	1.83	9/469 (1.9%)
3	D	0.90	0/335	1.89	9/513 (1.8%)
3	F	1.05	0/356	2.12	19/545 (3.5%)
All	All	0.61	1/6863 (0.0%)	1.06	50/9468 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	11	DT	N1-C2	5.25	1.42	1.38

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	C	13	DC	O4'-C4'-C3'	-11.99	98.81	106.00
3	D	5	DG	O4'-C4'-C3'	-10.94	99.44	106.00
2	E	11	DT	N3-C2-O2	-10.31	116.11	122.30
3	F	5	DG	C2-N3-C4	-9.75	107.02	111.90
2	C	11	DT	N3-C2-O2	-8.93	116.94	122.30

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	2743	0	2889	47	0
1	B	2743	0	2889	53	0
2	C	270	0	147	10	0
2	E	270	0	147	4	0
3	D	301	0	170	5	0
3	F	320	0	181	8	0
4	A	27	0	15	5	0
4	B	27	0	16	5	0
5	A	5	0	0	0	0
5	B	4	0	0	1	0
6	A	17	0	0	8	0
6	B	21	0	0	8	0
6	C	8	0	0	3	0
6	D	6	0	0	0	0
6	E	8	0	0	0	0
6	F	5	0	0	2	0
All	All	6775	0	6454	126	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 10.

The worst 5 of 126 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)
4:B:401:OOJ:H16	6:B:516:HOH:O	1.50	1.10
2:C:10:DA:N3	6:C:104:HOH:O	1.96	0.98
2:E:13:DC:N3	3:F:6:DG:N2	2.11	0.98
3:F:6:DG:H8	6:F:104:HOH:O	1.47	0.97
2:C:13:DC:N3	3:D:6:DG:N2	2.13	0.96

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	339/359 (94%)	312 (92%)	25 (7%)	2 (1%)	30	67
1	B	339/359 (94%)	319 (94%)	18 (5%)	2 (1%)	30	67
All	All	678/718 (94%)	631 (93%)	43 (6%)	4 (1%)	30	67

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	161	ASN
1	B	161	ASN
1	A	49	GLU
1	B	111	ILE

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	300/316 (95%)	274 (91%)	26 (9%)	13	36
1	B	300/316 (95%)	271 (90%)	29 (10%)	10	30
All	All	600/632 (95%)	545 (91%)	55 (9%)	11	33

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	310	THR
1	B	99	ILE
1	B	307	SER
1	A	331	ARG
1	B	49	GLU

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

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 ⓘ

Of 11 ligands modelled in this entry, 9 are monoatomic - leaving 2 for Mogul analysis.

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$
4	0OJ	A	401	5	24,30,34	2.03	6 (25%)	23,49,56	3.09	7 (30%)
4	0OJ	B	401	5	24,30,34	1.77	6 (25%)	23,49,56	2.37	5 (21%)

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
4	0OJ	A	401	5	-	0/12/39/45	0/3/4/4
4	0OJ	B	401	5	-	0/12/39/45	0/3/4/4

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	401	0OJ	CAL-CAY	-5.99	1.44	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	401	0OJ	CBB-N9	-3.77	1.46	1.51
4	A	401	0OJ	OAE-CAX	-3.75	1.34	1.43
4	B	401	0OJ	C2-N1	-3.57	1.27	1.33
4	B	401	0OJ	CAL-CAY	-3.22	1.47	1.51

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	401	0OJ	N3-C2-N1	-10.38	120.95	128.89
4	B	401	0OJ	N3-C2-N1	-7.54	123.12	128.89
4	B	401	0OJ	PBD-OAT-PBE	-3.18	121.99	132.67
4	A	401	0OJ	PBD-OAT-PBE	-2.91	122.92	132.67
4	A	401	0OJ	C8-N9-CBB	-2.03	120.81	125.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	401	0OJ	5	0
4	B	401	0OJ	5	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, 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	341/359 (94%)	0.05	2 (0%) 90 89	43, 64, 85, 95	0
1	B	341/359 (94%)	0.05	3 (0%) 85 84	35, 61, 90, 108	0
2	C	13/14 (92%)	-0.59	0 100 100	55, 61, 79, 83	0
2	E	13/14 (92%)	-0.49	0 100 100	53, 59, 68, 71	1 (7%)
3	D	15/18 (83%)	-0.40	0 100 100	55, 63, 66, 92	0
3	F	16/18 (88%)	-0.41	0 100 100	47, 62, 70, 89	0
All	All	739/782 (94%)	0.01	5 (0%) 89 88	35, 63, 88, 108	1 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	213	LEU	4.0
1	A	210	PHE	2.6
1	A	213	LEU	2.5
1	B	214	LYS	2.4
1	B	156	ASP	2.2

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(Å ²)	Q<0.9
5	CA	A	403	1/1	0.83	0.26	1.81	70,70,70,70	0
4	0OJ	B	401	27/31	0.95	0.18	-0.13	53,63,76,79	2
4	0OJ	A	401	27/31	0.96	0.15	-0.84	55,67,82,87	1
5	CA	A	405	1/1	0.89	0.14	-0.84	80,80,80,80	0
5	CA	B	402	1/1	0.96	0.14	-1.51	64,64,64,64	0
5	CA	A	406	1/1	0.77	0.15	-1.60	75,75,75,75	0
5	CA	A	404	1/1	0.76	0.14	-1.81	83,83,83,83	0
5	CA	B	403	1/1	0.71	0.17	-	82,82,82,82	0
5	CA	B	405	1/1	0.71	0.14	-	88,88,88,88	0
5	CA	A	402	1/1	0.82	0.09	-	87,87,87,87	0
5	CA	B	404	1/1	0.86	0.12	-	85,85,85,85	0

6.5 Other polymers [i](#)

There are no such residues in this entry.