



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 03:54 PM GMT

PDB ID : 4DSA
Title : Crystal Structure of DPP-IV with Compound C1
Authors : Xiong, B.; Zhu, L.R.; Chen, D.Q.; Zhao, Y.L.; Jiang, F.; Shen, J.K.
Deposited on : 2012-02-18
Resolution : 3.25 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

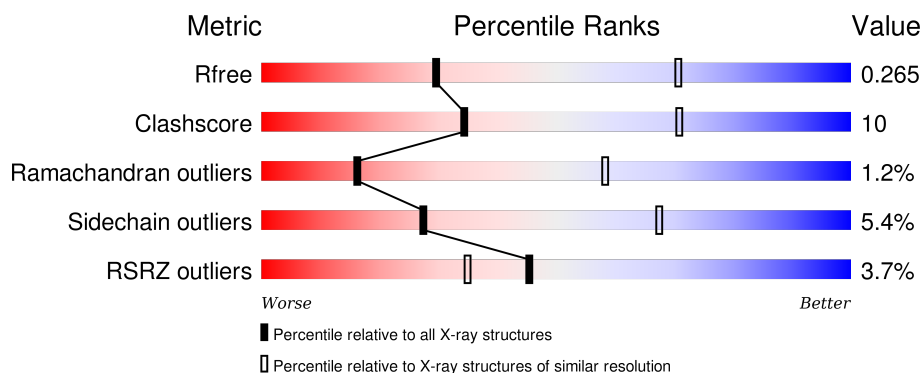
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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	1624 (3.32-3.20)
Clashscore	102246	1806 (3.32-3.20)
Ramachandran outliers	100387	1773 (3.32-3.20)
Sidechain outliers	100360	1771 (3.32-3.20)
RSRZ outliers	91569	1632 (3.32-3.20)

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.

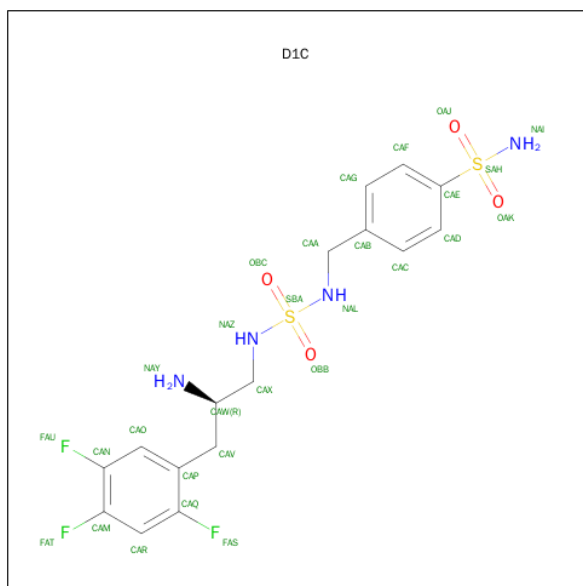
Mol	Chain	Length	Quality of chain
1	A	728	<div> <div>3%</div> <div>73%</div> <div>23%</div> <div>..</div> </div>
1	B	728	<div> <div>4%</div> <div>72%</div> <div>25%</div> <div>..</div> </div>

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 Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	724	Total 5931	C 3807	N 975	O 1123	S 26	0	0	0
1	B	724	Total 5931	C 3807	N 975	O 1123	S 26	0	0	0

- Molecule 2 is 4-[(2R)-2-AMINO-3-(2,4,5-TRIFLUOROPHENYL)PROPYL]SULFAMOYL)AMINO)METHYL]BENZENESULFONAMIDE (three-letter code: D1C) (formula: $C_{16}H_{19}F_3N_4O_4S_2$).

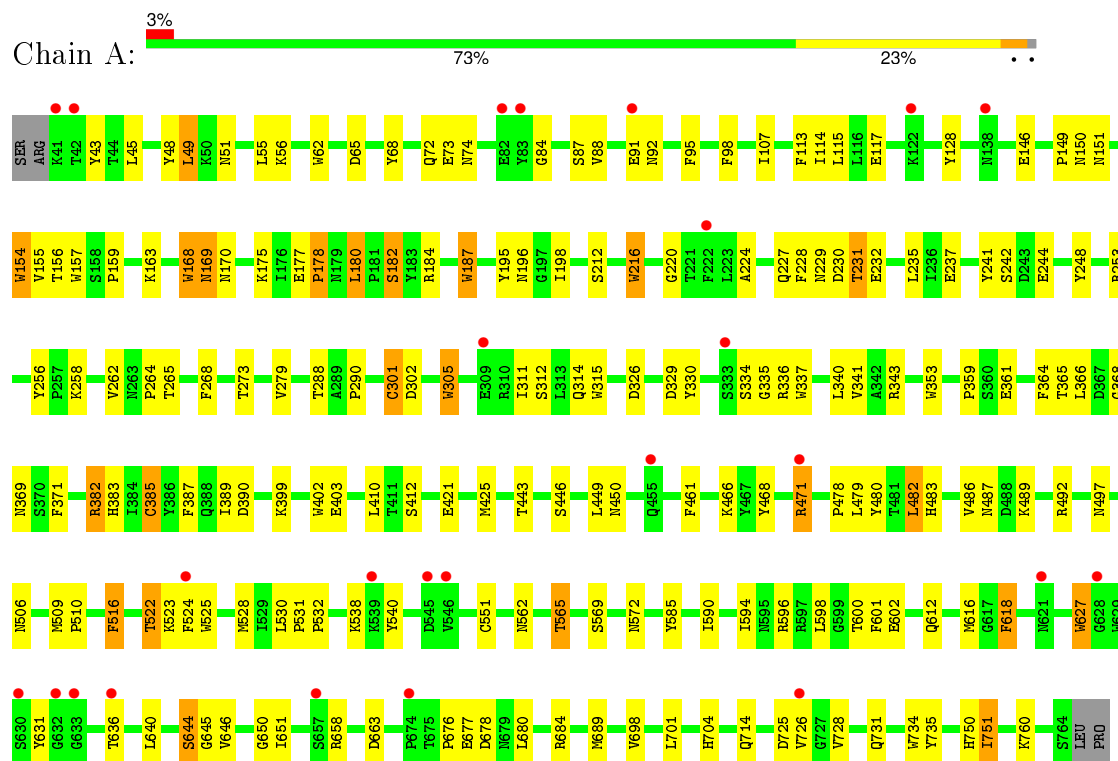


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			29	16	3	4	4	2		

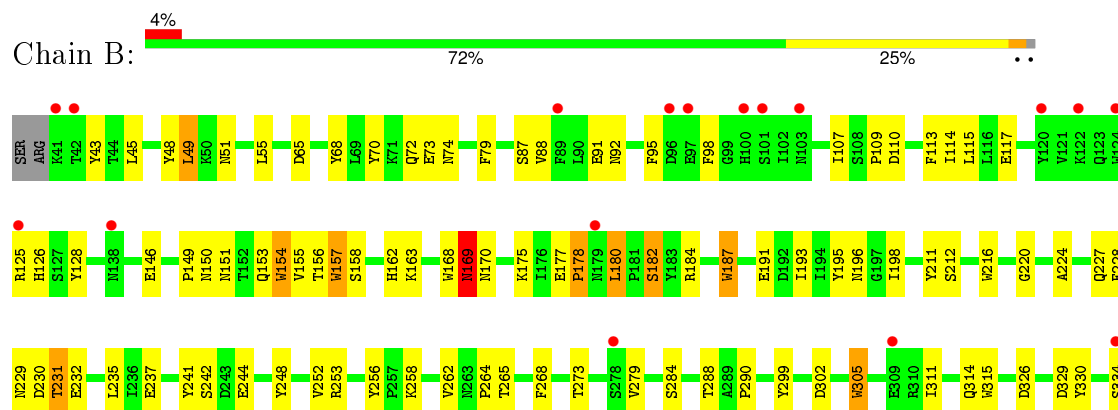
3 Residue-property plots

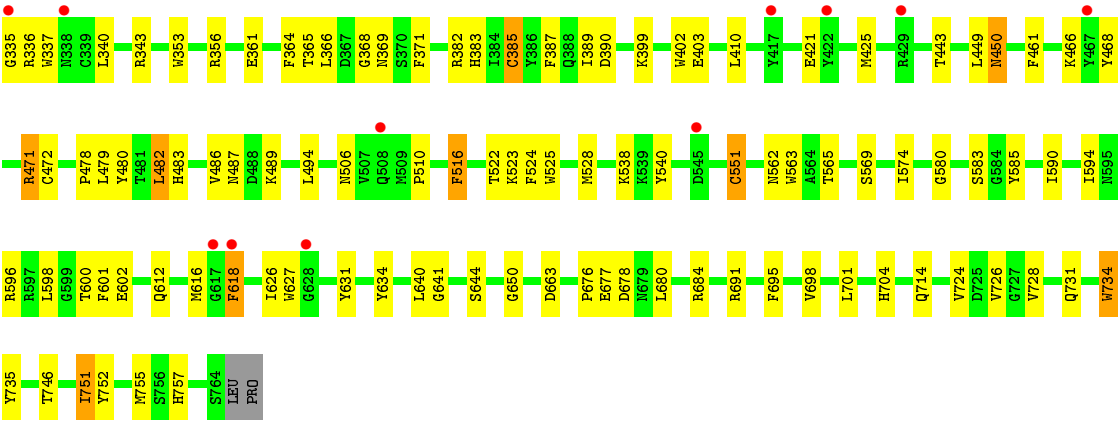
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Dipeptidyl peptidase 4



• Molecule 1: Dipeptidyl peptidase 4





4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	78.68Å 78.68Å 289.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.37 – 3.25 29.37 – 3.25	Depositor EDS
% Data completeness (in resolution range)	97.2 (29.37-3.25) 97.3 (29.37-3.25)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 3.24Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.198 , 0.266 0.193 , 0.265	Depositor DCC
R_{free} test set	1596 reflections (5.47%)	DCC
Wilson B-factor (Å ²)	122.7	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 93.5	EDS
Estimated twinning fraction	0.000 for -h,-k,l 0.056 for h,-h-k,-l 0.024 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 30700 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11891	wwPDB-VP
Average B, all atoms (Å ²)	144.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: D1C

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	0.61	13/6102 (0.2%)	0.67	0/8299
1	B	0.62	10/6102 (0.2%)	0.67	0/8299
All	All	0.61	23/12204 (0.2%)	0.67	0/16598

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	337	TRP	CD2-CE2	6.13	1.48	1.41
1	A	157	TRP	CD2-CE2	5.96	1.48	1.41
1	B	337	TRP	CD2-CE2	5.92	1.48	1.41
1	B	563	TRP	CD2-CE2	5.69	1.48	1.41
1	A	187	TRP	CD2-CE2	5.65	1.48	1.41

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	5931	0	5649	118	0
1	B	5931	0	5649	121	0
2	A	29	0	19	0	0
All	All	11891	0	11317	231	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 231 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:175:LYS:HG3	1:A:182:SER:HB3	1.52	0.90
1:B:175:LYS:HG3	1:B:182:SER:HB3	1.56	0.86
1:B:383:HIS:HD2	1:B:399:LYS:HA	1.41	0.85
1:A:383:HIS:HD2	1:A:399:LYS:HA	1.41	0.84
1:A:383:HIS:CD2	1:A:399:LYS:HA	2.15	0.81

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	722/728 (99%)	643 (89%)	69 (10%)	10 (1%)	14	54
1	B	722/728 (99%)	640 (89%)	75 (10%)	7 (1%)	19	62
All	All	1444/1456 (99%)	1283 (89%)	144 (10%)	17 (1%)	16	58

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	PRO
1	A	644	SER
1	A	645	GLY
1	B	169	ASN
1	B	178	PRO

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	649/653 (99%)	615 (95%)	34 (5%)	29	68
1	B	649/653 (99%)	613 (94%)	36 (6%)	27	67
All	All	1298/1306 (99%)	1228 (95%)	70 (5%)	27	67

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	627	TRP
1	B	180	LEU
1	B	516	PHE
1	A	704	HIS
1	B	51	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	748	HIS
1	B	247	GLN
1	B	66	HIS
1	A	247	GLN
1	B	138	ASN

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	D1C	A	800	-	30,30,30	6.13	11 (36%)	36,44,44	2.44	9 (25%)

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	D1C	A	800	-	-	0/21/22/22	0/2/2/2

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	800	D1C	SBA-NAZ	-21.19	1.40	1.61
2	A	800	D1C	CAV-CAP	-9.83	1.37	1.51
2	A	800	D1C	CAE-SAH	-4.62	1.70	1.77
2	A	800	D1C	CAA-CAB	-4.41	1.41	1.51
2	A	800	D1C	FAU-CAN	-2.90	1.28	1.35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	800	D1C	OBC-SBA-OB	-7.99	107.01	120.04
2	A	800	D1C	OAJ-SAH-OAK	-5.48	111.09	118.80
2	A	800	D1C	CAR-CAQ-CAP	-3.65	119.48	124.13
2	A	800	D1C	CAW-CAX-NAZ	-2.79	104.47	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	800	D1C	OBC-SBA-NAL	2.19	111.27	106.83

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 [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	724/728 (99%)	0.07	25 (3%)	48 38	87, 141, 186, 246	0
1	B	724/728 (99%)	0.09	28 (3%)	43 33	86, 144, 192, 229	0
All	All	1448/1456 (99%)	0.08	53 (3%)	45 35	86, 143, 189, 246	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	524	PHE	5.7
1	A	82	GLU	5.0
1	B	309	GLU	4.8
1	A	83	TYR	4.8
1	A	455	GLN	3.8

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	D1C	A	800	29/29	0.90	0.27	-0.15	98,148,204,207	0

6.5 Other polymers ⓘ

There are no such residues in this entry.