



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 05:40 am BST

PDB ID : 5O1S
Title : Dimethyl fumarate is an allosteric covalent inhibitor of the p90 ribosomal S6 kinases
Authors : Andersen, J.L.; Nissen, P.
Deposited on : 2017-05-19
Resolution : 1.90 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

<https://www.wwpdb.org/validation/2017/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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

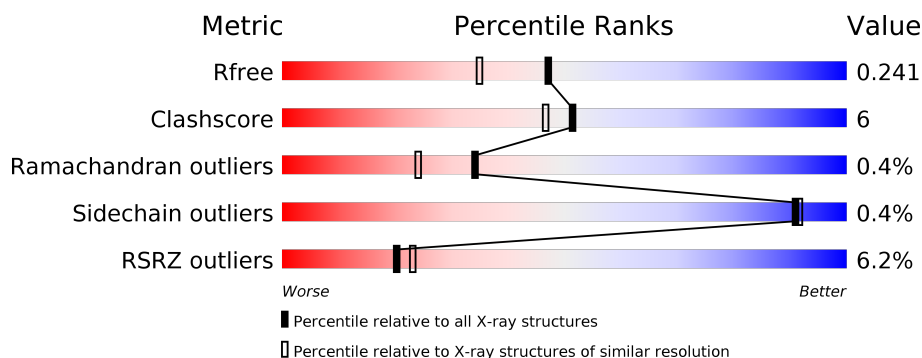
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 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 $\leq 5\%$. 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	364	<div> <div>5%</div> <div> <div></div> <div>70%</div> <div>10%</div> <div>20%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2431 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 Ribosomal protein S6 kinase alpha-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	290	Total	C	N	O	S	2	0	0
			2309	1473	393	432	11			

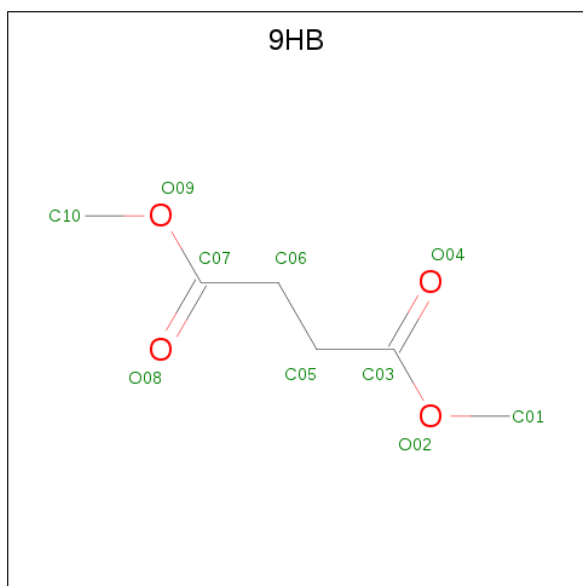
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	377	MET	-	initiating methionine	UNP P18654
A	378	HIS	-	expression tag	UNP P18654
A	379	HIS	-	expression tag	UNP P18654
A	380	HIS	-	expression tag	UNP P18654
A	381	HIS	-	expression tag	UNP P18654
A	382	HIS	-	expression tag	UNP P18654
A	383	HIS	-	expression tag	UNP P18654
A	384	HIS	-	expression tag	UNP P18654
A	385	HIS	-	expression tag	UNP P18654
A	386	ASP	-	expression tag	UNP P18654
A	387	TYR	-	expression tag	UNP P18654
A	388	ASP	-	expression tag	UNP P18654
A	389	ILE	-	expression tag	UNP P18654
A	390	PRO	-	expression tag	UNP P18654
A	391	THR	-	expression tag	UNP P18654
A	392	THR	-	expression tag	UNP P18654
A	393	GLU	-	expression tag	UNP P18654
A	394	ASN	-	expression tag	UNP P18654
A	395	LEU	-	expression tag	UNP P18654
A	396	TYR	-	expression tag	UNP P18654
A	397	PHE	-	expression tag	UNP P18654
A	398	GLN	-	expression tag	UNP P18654
A	399	GLY	-	expression tag	UNP P18654
A	591	GLU	LYS	conflict	UNP P18654

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0

- Molecule 3 is Dimethyl fumarate (three-letter code: 9HB) (formula: $C_6H_{10}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 10 6 4	0	0
3	A	1	Total C O 10 6 4	0	0

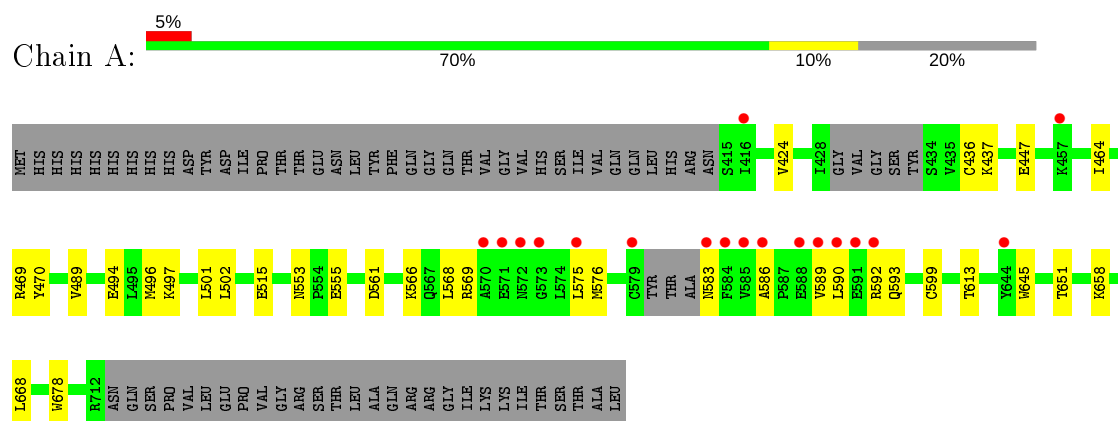
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	101	Total O 101 101	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Ribosomal protein S6 kinase alpha-3



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	46.95Å 46.95Å 291.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.35 – 1.90 46.36 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.3 (46.35-1.90) 99.3 (46.36-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 1.90Å)	Xtriage
Refinement program	PHENIX (1.10 _2152: ???)	Depositor
R, R_{free}	0.207 , 0.241 0.207 , 0.241	Depositor DCC
R_{free} test set	1349 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2431	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.58% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 9HB, NA

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	0.63	0/2359	0.74	0/3196

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

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	2309	0	2291	26	0
2	A	1	0	0	0	0
3	A	20	0	0	6	0
4	A	101	0	0	1	0
All	All	2431	0	2291	26	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 6.

All (26) 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:436:CYS:SG	3:A:803:9HB:C06	2.10	1.40
1:A:599:CYS:SG	3:A:802:9HB:C05	2.10	1.38
1:A:436:CYS:HG	3:A:803:9HB:C06	1.84	0.87
1:A:599:CYS:SG	3:A:802:9HB:C03	2.66	0.83
1:A:568:LEU:HD13	1:A:593:GLN:HG3	1.64	0.77
1:A:651:THR:HG22	1:A:678:TRP:HB2	1.67	0.75
1:A:436:CYS:SG	3:A:803:9HB:C07	2.78	0.71
1:A:515:GLU:OE1	4:A:901:HOH:O	2.09	0.70
1:A:566:LYS:HE2	1:A:592:ARG:HH22	1.62	0.65
1:A:569:ARG:HG2	1:A:575:LEU:HD23	1.81	0.62
1:A:447:GLU:OE2	1:A:497:LYS:HE2	2.05	0.57
1:A:469:ARG:HD3	1:A:470:TYR:CZ	2.39	0.57
1:A:494:GLU:HG3	1:A:496:MET:CE	2.34	0.57
1:A:464:ILE:HD11	1:A:489:VAL:HG11	1.87	0.56
1:A:494:GLU:HG3	1:A:496:MET:HE1	1.91	0.52
1:A:599:CYS:SG	3:A:802:9HB:C06	2.94	0.52
1:A:658:LYS:HB3	1:A:668:LEU:HG	1.92	0.52
1:A:576:MET:HE3	1:A:583:ASN:HB2	1.95	0.49
1:A:613:THR:HG21	1:A:645:TRP:CE2	2.50	0.47
1:A:553:ASN:HB3	1:A:555:GLU:OE1	2.20	0.42
1:A:424:VAL:HG13	1:A:437:LYS:HD3	2.01	0.41
1:A:590:LEU:HA	1:A:590:LEU:HD23	1.85	0.41
1:A:586:ALA:HB3	1:A:589:VAL:HG23	2.02	0.40
1:A:575:LEU:HA	1:A:575:LEU:HD23	1.90	0.40
1:A:502:LEU:HA	1:A:502:LEU:HD12	1.87	0.40
1:A:424:VAL:CG1	1:A:437:LYS:HD3	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	284/364 (78%)	277 (98%)	6 (2%)	1 (0%)	34	24

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	561	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	252/317 (80%)	251 (100%)	1 (0%)	91	91

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	501	LEU

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

Mol	Chain	Res	Type
1	A	583	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](#)

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

Of 3 ligands modelled in this entry, 1 is 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	$\# Z > 2$
3	9HB	A	802	-	9,9,9	1.48	2 (22%)	10,10,10	1.43	2 (20%)
3	9HB	A	803	-	9,9,9	1.60	2 (22%)	10,10,10	1.55	3 (30%)

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	9HB	A	802	-	-	0/9/9/9	-
3	9HB	A	803	-	-	1/9/9/9	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	802	9HB	O02-C01	-2.99	1.38	1.45
3	A	803	9HB	O02-C01	-2.90	1.38	1.45
3	A	803	9HB	O09-C10	-2.88	1.38	1.45
3	A	802	9HB	O09-C10	-2.25	1.40	1.45

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	802	9HB	O09-C07-C06	2.66	122.75	112.23
3	A	803	9HB	O09-C07-C06	2.17	120.83	112.23
3	A	803	9HB	C06-C05-C03	2.06	119.42	113.43
3	A	803	9HB	C01-O02-C03	2.02	122.76	116.11
3	A	802	9HB	C01-O02-C03	2.01	122.73	116.11

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	803	9HB	C05-C06-C07-O08

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	9HB	3	0
3	A	803	9HB	3	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 ⓘ

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	290/364 (79%)	0.39	18 (6%) 20 23	35, 55, 88, 114	1 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	584	PHE	6.9
1	A	585	VAL	6.0
1	A	416	ILE	4.3
1	A	579	CYS	4.1
1	A	572	ASN	4.0
1	A	570	ALA	3.8
1	A	573	GLY	3.6
1	A	590	LEU	3.5
1	A	588	GLU	3.4
1	A	589	VAL	3.4
1	A	591	GLU	3.0
1	A	586	ALA	2.7
1	A	457	LYS	2.7
1	A	575	LEU	2.6
1	A	583	ASN	2.5
1	A	571	GLU	2.3
1	A	592	ARG	2.1
1	A	644	TYR	2.0

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

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. 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	9HB	A	803	10/10	0.76	0.20	84,93,96,97	0
3	9HB	A	802	10/10	0.95	0.18	51,58,68,72	0
2	NA	A	801	1/1	0.97	0.05	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.