



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 04:43 pm BST

PDB ID : 1DD1
Title : CRYSTAL STRUCTURE ANALYSIS OF THE SMAD4 ACTIVE FRAGMENT
Authors : Qin, B.Y.; Lam, S.W.; Lin, K.
Deposited on : 1999-11-05
Resolution : 2.62 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 ⓘ 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

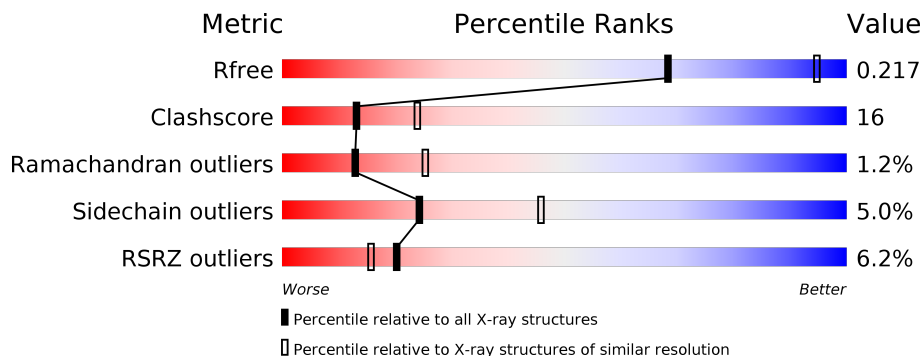
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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	268	<p>4% 63% 17% • 18%</p>
1	B	268	<p>6% 66% 24% • 7%</p>
1	C	268	<p>6% 63% 25% • 10%</p>

2 Entry composition [i](#)

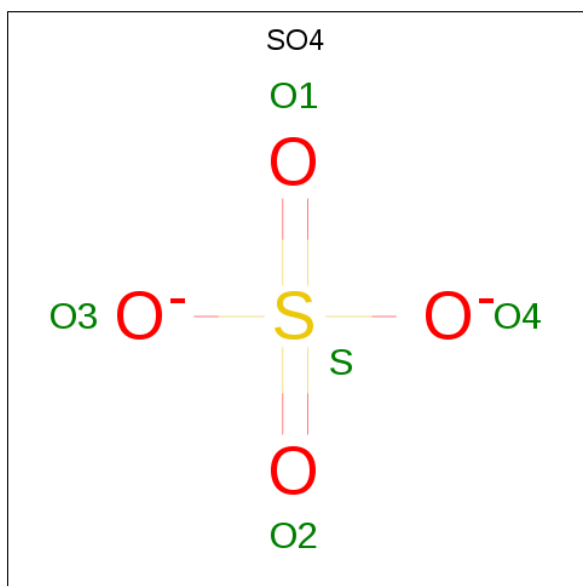
There are 3 unique types of molecules in this entry. The entry contains 5889 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 SMAD4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	221	Total 1738	C 1099	N 315	O 311	S 13	0	0	0
1	B	249	Total 1938	C 1224	N 347	O 354	S 13	0	1	0
1	C	241	Total 1866	C 1176	N 337	O 340	S 13	0	0	0

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



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

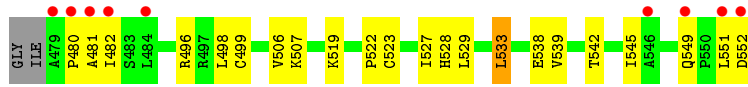
Continued on next page...

Continued from previous page...

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	106	Total	O	0	0
			106	106		
3	B	111	Total	O	0	0
			111	111		
3	C	85	Total	O	0	0
			85	85		



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	142.43Å 142.43Å 195.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.62 70.14 – 2.62	Depositor EDS
% Data completeness (in resolution range)	92.9 (100.00-2.62) 92.9 (70.14-2.62)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.62Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.218 , 0.175 0.173 , 0.217	Depositor DCC
R_{free} test set	1468 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	37.0	Xtrriage
Anisotropy	0.076	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 71.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.010 for $-1/2^*h+1/2^*k-1/2^*l, 1/2^*h-1/2^*k-1/2^*l, -h-k$ 0.018 for $-1/2^*h-1/2^*k+1/2^*l, -1/2^*h-1/2^*k-1/2^*l, h-k$	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5889	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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	0.36	0/1786	0.61	0/2427
1	B	0.41	0/1990	0.69	2/2708 (0.1%)
1	C	0.37	0/1915	0.61	0/2603
All	All	0.38	0/5691	0.64	2/7738 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	286	GLY	N-CA-C	7.39	131.58	113.10
1	B	467	GLY	N-CA-C	5.11	125.86	113.10

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	1738	0	1689	50	0
1	B	1938	0	1880	77	0
1	C	1866	0	1814	56	0
2	A	10	0	0	0	0
2	B	15	0	0	0	0
2	C	20	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	106	0	0	9	0
3	B	111	0	0	7	0
3	C	85	0	0	9	0
All	All	5889	0	5383	179	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 16.

The worst 5 of 179 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:287:HIS:HA	1:B:420:ARG:NH2	1.70	1.07
1:B:287:HIS:HA	1:B:420:ARG:HH21	1.14	1.05
1:B:465:VAL:C	1:B:467:GLY:H	1.55	1.00
1:C:417:GLU:HB2	3:C:640:HOH:O	1.61	1.00
1:A:287:HIS:HA	1:A:420:ARG:HH21	1.26	0.97

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	215/268 (80%)	206 (96%)	8 (4%)	1 (0%)	29 50
1	B	244/268 (91%)	223 (91%)	15 (6%)	6 (2%)	5 9
1	C	235/268 (88%)	222 (94%)	12 (5%)	1 (0%)	34 55
All	All	694/804 (86%)	651 (94%)	35 (5%)	8 (1%)	13 25

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	286	GLY
1	B	466	ALA
1	B	546	ALA
1	B	357	SER
1	A	331	MET

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	185/217 (85%)	176 (95%)	9 (5%)	25	46
1	B	204/217 (94%)	193 (95%)	11 (5%)	22	42
1	C	196/217 (90%)	187 (95%)	9 (5%)	27	50
All	All	585/651 (90%)	556 (95%)	29 (5%)	24	46

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	440	LEU
1	B	482	ILE
1	C	527	ILE
1	B	449	GLN
1	B	490	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	405	HIS
1	B	446	GLN
1	C	446	GLN
1	B	427	HIS
1	A	388	GLN

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 [i](#)

9 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	C	555	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	B	553	-	4,4,4	0.27	0	6,6,6	0.07	0
2	SO4	C	556	-	4,4,4	0.25	0	6,6,6	0.12	0
2	SO4	B	555	-	4,4,4	0.31	0	6,6,6	0.15	0
2	SO4	C	553	-	4,4,4	0.19	0	6,6,6	0.10	0
2	SO4	A	553	-	4,4,4	0.30	0	6,6,6	0.08	0
2	SO4	C	554	-	4,4,4	0.26	0	6,6,6	0.06	0
2	SO4	A	554	-	4,4,4	0.27	0	6,6,6	0.11	0
2	SO4	B	554	-	4,4,4	0.18	0	6,6,6	0.22	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 [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	221/268 (82%)	0.01	12 (5%) 25 20	20, 37, 90, 115	1 (0%)
1	B	249/268 (92%)	0.07	16 (6%) 19 15	17, 40, 105, 133	1 (0%)
1	C	241/268 (89%)	-0.01	16 (6%) 18 14	19, 38, 93, 128	1 (0%)
All	All	711/804 (88%)	0.02	44 (6%) 20 16	17, 38, 98, 133	3 (0%)

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	487	ALA	8.1
1	A	488	ALA	5.9
1	B	285	ASN	5.7
1	B	469	ILE	5.2
1	B	307	GLU	4.8

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. 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(\AA^2)	Q<0.9
2	SO4	B	555	5/5	0.77	0.24	104,104,105,106	5
2	SO4	C	556	5/5	0.86	0.23	100,100,100,101	5
2	SO4	B	553	5/5	0.89	0.27	114,114,115,115	0
2	SO4	A	554	5/5	0.92	0.26	93,95,95,95	0
2	SO4	C	555	5/5	0.94	0.41	98,98,99,99	5
2	SO4	C	554	5/5	0.96	0.17	92,92,93,94	5
2	SO4	A	553	5/5	0.96	0.20	96,96,97,97	0
2	SO4	B	554	5/5	0.98	0.13	65,68,72,72	0
2	SO4	C	553	5/5	0.99	0.15	38,39,44,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.