



wwPDB X-ray Structure Validation Summary Report ⓘ

May 19, 2020 – 10:41 AM EDT

PDB ID : 6T58
Title : Structure determination of the transactivation domain of p53 in complex with S100A4 using annexin A2 as a crystallization chaperone
Authors : Ecsedi, P.; Gogl, G.; Nyitray, L.
Deposited on : 2019-10-15
Resolution : 3.10 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 : 2.10.1
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
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) : 2.10.1

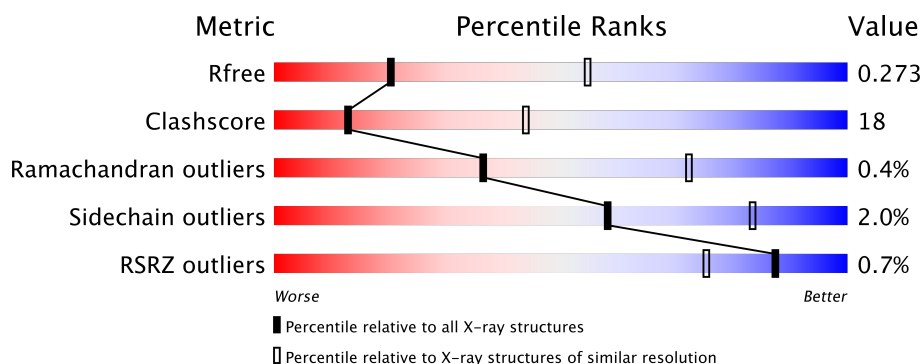
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	111664	1115 (3.12-3.08)
Clashscore	122126	1042 (3.10-3.10)
Ramachandran outliers	120053	1010 (3.10-3.10)
Sidechain outliers	120020	1010 (3.10-3.10)
RSRZ outliers	108989	1089 (3.12-3.08)

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	553	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 62%, green 32%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 62% 32% • 5% </div> </div>
1	B	553	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 39%, green 17%, grey 44%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 39% 17% 44% </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6605 atoms, of which 8 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 Cellular tumor antigen p53,Protein S100-A4,Protein S100-A4,Annexin A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	524	Total	C	N	O	S	6	1	0
			4093	2574	673	817	29			
1	B	311	Total	C	N	O	S	0	0	0
			2464	1542	422	489	11			

There are 36 discrepancies between the modelled and reference sequences:

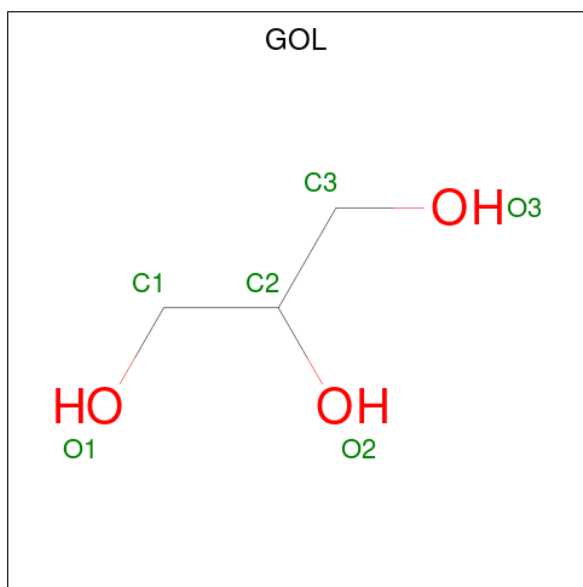
Chain	Residue	Modelled	Actual	Comment	Reference
A	13	GLY	-	expression tag	UNP P04637
A	14	SER	-	expression tag	UNP P04637
A	15	HIS	-	expression tag	UNP P04637
A	16	MET	-	expression tag	UNP P04637
A	57	GLY	-	linker	UNP P04637
A	58	GLY	-	linker	UNP P04637
A	59	SER	-	linker	UNP P04637
A	60	GLY	-	linker	UNP P04637
A	61	HIS	-	linker	UNP P04637
A	155	SER	-	linker	UNP P26447
A	156	ALA	-	linker	UNP P26447
A	157	GLY	-	linker	UNP P26447
A	158	SER	-	linker	UNP P26447
A	159	ALA	-	linker	UNP P26447
A	160	GLY	-	linker	UNP P26447
A	253	THR	-	linker	UNP P26447
A	254	SER	-	linker	UNP P26447
A	292	GLU	ALA	engineered mutation	UNP P07355
B	13	GLY	-	expression tag	UNP P04637
B	14	SER	-	expression tag	UNP P04637
B	15	HIS	-	expression tag	UNP P04637
B	16	MET	-	expression tag	UNP P04637
B	57	GLY	-	linker	UNP P04637
B	58	GLY	-	linker	UNP P04637

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	59	SER	-	linker	UNP P04637
B	60	GLY	-	linker	UNP P04637
B	61	HIS	-	linker	UNP P04637
B	155	SER	-	linker	UNP P26447
B	156	ALA	-	linker	UNP P26447
B	157	GLY	-	linker	UNP P26447
B	158	SER	-	linker	UNP P26447
B	159	ALA	-	linker	UNP P26447
B	160	GLY	-	linker	UNP P26447
B	253	THR	-	linker	UNP P26447
B	254	SER	-	linker	UNP P26447
B	292	GLU	ALA	engineered mutation	UNP P07355

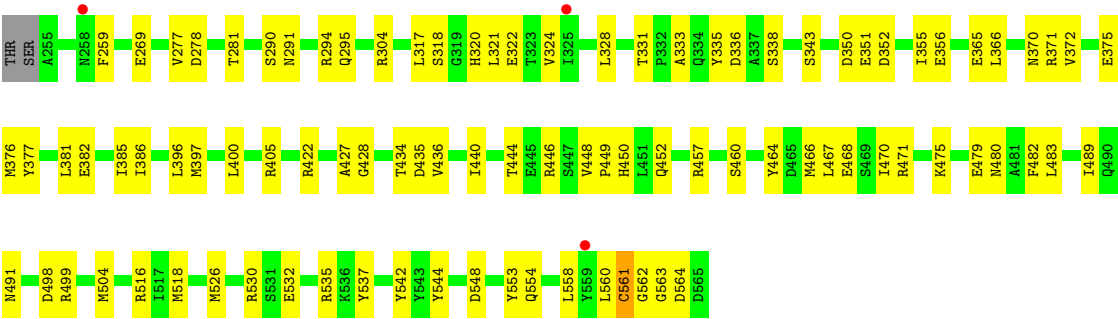
- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O		0	0
			6	3	3			
2	A	1	Total	C	O		0	0
			6	3	3			
2	B	1	Total	C	O		0	0
			6	3	3			
2	B	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	6	Total 6	Ca 6	0	0
3	A	10	Total 10	Ca 10	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.96Å 62.77Å 106.02Å 90.00° 90.26° 90.00°	Depositor
Resolution (Å)	47.98 – 3.10 47.98 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.98-3.10) 88.9 (47.98-3.10)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.230 , 0.272 0.231 , 0.273	Depositor DCC
R_{free} test set	1992 reflections (8.57%)	wwPDB-VP
Wilson B-factor (Å ²)	53.6	Xtriage
Anisotropy	0.740	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6605	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% 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: GOL, CA

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	0.30	0/4159	0.48	0/5607
1	B	0.28	0/2496	0.44	0/3361
All	All	0.29	0/6655	0.47	0/8968

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	4093	0	3902	161	0
1	B	2464	0	2425	70	0
2	A	12	0	16	2	0
2	B	12	8	16	3	0
3	A	10	0	0	0	0
3	B	6	0	0	0	0
All	All	6597	8	6359	229	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 18.

The worst 5 of 229 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:162:CYS:H	1:A:163:PRO:HD2	1.14	1.12
1:B:518:MET:CE	1:B:561:CYS:HB2	1.99	0.92
1:B:561:CYS:O	1:B:561:CYS:SG	2.27	0.92
1:A:36:PRO:HD3	1:A:247:GLU:HG3	1.54	0.88
1:B:518:MET:HE1	1:B:561:CYS:HB2	1.58	0.85

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	517/553 (94%)	474 (92%)	41 (8%)	2 (0%)	36	72
1	B	309/553 (56%)	295 (96%)	13 (4%)	1 (0%)	43	77
All	All	826/1106 (75%)	769 (93%)	54 (6%)	3 (0%)	36	72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	CYS
1	A	277	VAL
1	B	277	VAL

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	437/489 (89%)	428 (98%)	9 (2%)	56	82
1	B	263/489 (54%)	258 (98%)	5 (2%)	60	84
All	All	700/978 (72%)	686 (98%)	14 (2%)	58	83

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	352	ASP
1	A	548	ASP
1	B	548	ASP
1	A	249	PHE
1	B	464	TYR

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 20 ligands modelled in this entry, 16 are monoatomic - leaving 4 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
2	GOL	B	601	-	5,5,5	0.96	0	5,5,5	1.01	0
2	GOL	A	601	-	5,5,5	1.05	0	5,5,5	0.94	0
2	GOL	B	602	-	5,5,5	0.71	0	5,5,5	0.78	0
2	GOL	A	602	-	5,5,5	0.86	0	5,5,5	0.97	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	GOL	B	601	-	-	1/4/4/4	-
2	GOL	A	601	-	-	2/4/4/4	-
2	GOL	B	602	-	-	4/4/4/4	-
2	GOL	A	602	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	GOL	O1-C1-C2-C3
2	B	602	GOL	C1-C2-C3-O3
2	A	601	GOL	O1-C1-C2-O2
2	B	602	GOL	O2-C2-C3-O3
2	A	602	GOL	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	GOL	2	0
2	A	601	GOL	1	0
2	B	602	GOL	1	0
2	A	602	GOL	1	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	524/553 (94%)	-0.21	3 (0%) 89 78	30, 62, 132, 156	1 (0%)
1	B	311/553 (56%)	-0.12	3 (0%) 82 67	54, 74, 99, 127	0
All	All	835/1106 (75%)	-0.17	6 (0%) 87 75	30, 70, 126, 156	1 (0%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	258	ASN	5.0
1	A	52	GLN	3.3
1	B	325	ILE	2.7
1	A	47	PRO	2.7
1	A	48	ASP	2.4

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
3	CA	A	609	1/1	0.80	0.15	140,140,140,140	0
3	CA	A	605	1/1	0.83	0.23	57,57,57,57	0
3	CA	B	607	1/1	0.84	0.11	101,101,101,101	0
3	CA	B	606	1/1	0.89	0.10	80,80,80,80	0
3	CA	A	607	1/1	0.90	0.06	112,112,112,112	0
2	GOL	B	602	6/6	0.92	0.27	61,78,93,93	0
2	GOL	A	602	6/6	0.92	0.36	43,53,60,66	0
2	GOL	B	601	6/6	0.93	0.41	54,56,62,62	0
3	CA	A	611	1/1	0.94	0.12	48,48,48,48	0
3	CA	A	612	1/1	0.95	0.14	53,53,53,53	0
2	GOL	A	601	6/6	0.95	0.37	37,43,49,51	0
3	CA	B	605	1/1	0.95	0.07	71,71,71,71	0
3	CA	B	603	1/1	0.95	0.11	107,107,107,107	0
3	CA	B	608	1/1	0.95	0.10	98,98,98,98	0
3	CA	A	606	1/1	0.95	0.10	64,64,64,64	0
3	CA	A	610	1/1	0.96	0.12	45,45,45,45	0
3	CA	A	608	1/1	0.96	0.20	78,78,78,78	0
3	CA	B	604	1/1	0.97	0.07	62,62,62,62	0
3	CA	A	604	1/1	0.97	0.15	59,59,59,59	0
3	CA	A	603	1/1	0.98	0.18	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.