

Full wwPDB X-ray Structure Validation Report (i)

May 24, 2020 – 09:15 pm BST

PDB ID : 1GV9

Title : p58/ERGIC-53

Authors: Velloso, L.M.; Svensson, K.; Schneider, G.; Pettersson, R.F.; Lindqvist, Y.

Deposited on : 2002-02-07

Resolution : 1.46 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

 $\begin{array}{ccc} \text{Xtriage (Phenix)} & : & 1.13 \\ \text{EDS} & : & 2.11 \end{array}$

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)

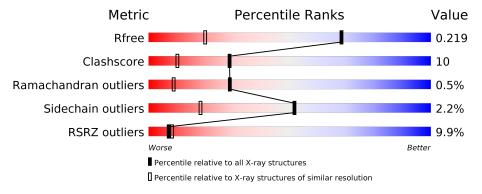
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 1.46 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
R_{free}	130704	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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 <=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				
			8%				
1	Α	260	75%	9%		14%	



2 Entry composition (i)

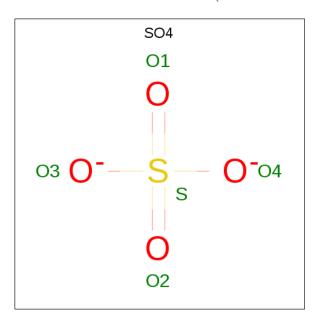
There are 3 unique types of molecules in this entry. The entry contains 1941 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 P58/ERGIC-53.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	223	Total	С	N	О	S	0	0	0
1	A	223	1740	1108	299	328	5	0	U	

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



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

• Molecule 3 is water.

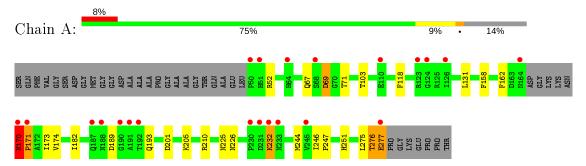
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	191	Total O 191 191	0	0



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: P58/ERGIC-53





4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants	49.04Å 85.41Å 127.67Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.64 - 1.46	Depositor
resolution (A)	23.18 - 1.46	EDS
% Data completeness	100.0 (23.64-1.46)	Depositor
(in resolution range)	94.9 (23.18-1.46)	EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	346.10 (at 1.46Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
P. P.	0.191 , 0.212	Depositor
R, R_{free}	0.200 , 0.219	DCC
R_{free} test set	2195 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	12.3	Xtriage
Anisotropy	0.594	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.45, 50.7	EDS
L-test for twinning ²	$ < L >=0.58, < L^2>=0.47$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	1941	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 60.68 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4680e-05.

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



¹Intensities estimated from amplitudes.

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	Boı	nd lengths	Bo	nd angles
WIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.61	$2/1788 \; (0.1\%)$	0.85	$4/2430 \ (0.2\%)$

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	${ m Observed}({ m \AA})$	$\operatorname{Ideal}(ext{\AA})$
1	A	276	THR	C-N	14.71	1.67	1.34
1	A	277	GLU	N-CA	5.19	1.56	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	A	276	THR	C-N-CA	8.28	142.40	121.70
1	A	277	GLU	N-CA-CB	6.41	122.13	110.60
1	A	189	ASP	CB-CG-OD2	5.56	123.31	118.30
1	A	69	ASP	CB-CG-OD2	5.50	123.25	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

\mathbf{Mol}	Chain	${f Res}$	Type	Group
1	A	170	ASN	Mainchain,Peptide



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	1740	0	1638	33	0
2	A	10	0	0	0	0
3	A	191	0	0	1	0
All	All	1941	0	1638	33	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.

All (33) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A 1 1	A 4 0	Interatomic	Clash
Atom-1	Atom-2	${f distance} \; ({f \AA})$	overlap (Å)
1:A:276:THR:C	1:A:277:GLU:N	1.67	1.45
1:A:170:ASN:ND2	1:A:170:ASN:O	1.65	1.26
1:A:162:PHE:HB2	1:A:171:PRO:CD	1.81	1.09
1:A:162:PHE:HB2	1:A:171:PRO:HD3	1.38	1.04
1:A:162:PHE:CB	1:A:171:PRO:HD3	2.01	0.89
1:A:162:PHE:CA	1:A:171:PRO:HD3	2.09	0.83
1:A:170:ASN:C	1:A:170:ASN:HD22	1.83	0.81
1:A:162:PHE:CB	1:A:171:PRO:CD	2.59	0.80
1:A:170:ASN:C	1:A:170:ASN:ND2	2.35	0.80
1:A:67:GLN:HB2	1:A:69:ASP:OD1	1.83	0.78
1:A:232:LYS:H	1:A:232:LYS:HD3	1.54	0.72
1:A:158:PHE:HB2	1:A:174:VAL:HG12	1.79	0.65
1:A:162:PHE:CD1	1:A:171:PRO:HD2	2.35	0.62
1:A:158:PHE:HB2	1:A:174:VAL:CG1	2.30	0.61
1:A:103:THR:O	1:A:251:HIS:HD2	1.84	0.60
1:A:162:PHE:HD1	1:A:171:PRO:HD2	1.64	0.60
1:A:67:GLN:CB	1:A:69:ASP:OD1	2.50	0.58
1:A:162:PHE:HB2	1:A:171:PRO:CG	2.34	0.56
1:A:251:HIS:HE1	3:A:2182:HOH:O	1.89	0.55
1:A:52:ARG:HG2	1:A:275:LEU:CD2	2.37	0.54
1:A:276:THR:CA	1:A:277:GLU:N	2.70	0.49
1:A:162:PHE:N	1:A:171:PRO:HD3	2.29	0.47
1:A:232:LYS:HD3	1:A:232:LYS:N	2.27	0.47
1:A:118:PHE:CD2	1:A:131:LEU:HD21	2.51	0.46

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Atom-1	Atom-2	Interatomic	Clash
		$\operatorname{distance}\left(ext{\AA} ight)$	overlap (Å)
1:A:210:ARG:HB2	1:A:225:ASN:HB3	1.99	0.45
1:A:162:PHE:HA	1:A:171:PRO:HD3	1.95	0.44
1:A:182:ILE:HG21	1:A:193:GLN:HE22	1.81	0.44
1:A:201:ASP:O	1:A:205:LYS:HE3	2.17	0.43
1:A:246:ILE:HB	1:A:247:PRO:HD2	2.00	0.43
1:A:69:ASP:OD2	1:A:71:THR:HG23	2.20	0.42
1:A:162:PHE:CA	1:A:171:PRO:CD	2.89	0.41
1:A:52:ARG:HG2	1:A:275:LEU:HD23	2.02	0.41
1:A:158:PHE:O	1:A:173:ILE:HA	2.21	0.41

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	219/260 (84%)	214 (98%)	4 (2%)	1 (0%)	29 9	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	171	PRO

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	180/206 (87%)	176 (98%)	4 (2%)	52 18	

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	170	ASN
1	A	226	ASN
1	A	232	LYS
1	A	244	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	ASN
1	A	181	GLN
1	A	193	GLN
1	A	251	HIS

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)

2 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	Туре	Chain	Res	Link	B	ond leng	${ m gths}$	В	ond ang	gles
	MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
	2	SO4	A	1278	-	4,4,4	0.13	0	6,6,6	0.37	0
ĺ	2	SO4	A	1279	_	4,4,4	0.14	0	6,6,6	0.31	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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

\mathbf{Model}	Chain	Residue-1	Atom-1	Residue-2	Atom-2	${f Distance} ({f A})$
1	A	276:THR	С	277:GLU	N	1.67



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, 95^{th} 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>	$\#\mathrm{RSRZ}{>}2$		$OWAB(A^2)$	Q < 0.9
1	A	223/260 (85%)	0.41	22 (9%)	7 8	6, 13, 28, 43	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res Type		RSRZ	
1	A	191	ALA	6.7	
1	A	192	THR	6.5	
1	A	170	ASN	5.2	
1	A	123	ARG	4.4	
1	A	230	PRO	3.9	
1	A	245	VAL	3.8	
1	A	164	ASN	3.4	
1	A	277	GLU	3.1	
1	A	68	SER	3.1	
1	A	171	PRO	3.1	
1	A	188	ASN	3.0	
1	A	190	GLY	2.9	
1	A	231	ASP	2.8	
1	A	64	HIS	2.7	
1	A	124	GLY	2.7	
1	A	51	HIS	2.6	
1	A	232	LYS	2.6	
1	A	187	GLN	2.5	
1	A	233	ASN	2.5	
1	A	110	GLU	2.3	
1	A	50	PRO	2.2	
1	A	126	ILE	2.0	

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, 95^{th} 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	${f B-factors}({f \AA}^2)$	Q<0.9
2	SO4	A	1279	5/5	0.90	0.15	19,21,22,23	5
2	SO4	A	1278	5/5	0.95	0.16	34,34,35,35	5

6.5 Other polymers (i)

There are no such residues in this entry.

