



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 01:36 pm BST

PDB ID : 2BJE
Title : Acylphosphatase from *Sulfolobus solfataricus*. Monclinic P21 space group
Authors : Rosano, C.; Zuccotti, S.
Deposited on : 2005-02-02
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

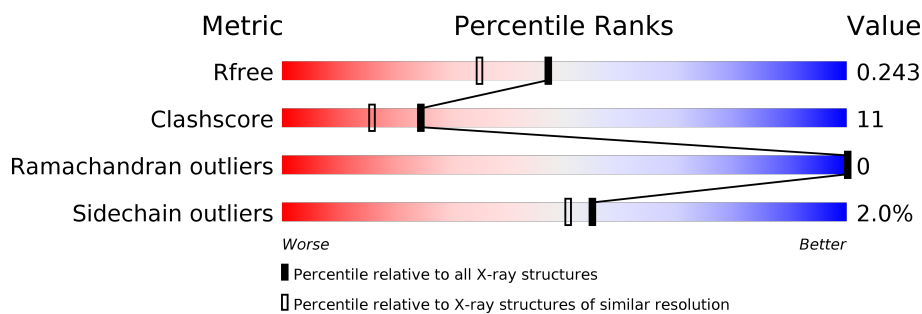
1 Overall quality at a glance

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)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	101	
1	C	101	
1	E	101	
1	G	101	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	G	1095	-	-	X	-

2 Entry composition [i](#)

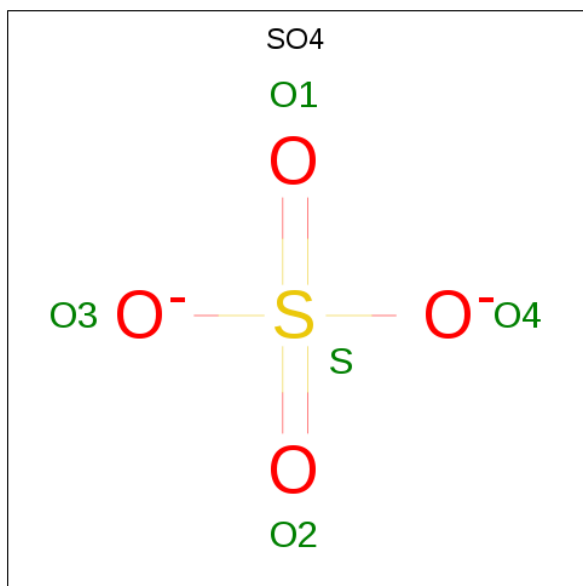
There are 4 unique types of molecules in this entry. The entry contains 3127 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ACYLPHOSPHATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	90	Total	C	N	O	S	0	0	0
			725	469	119	135	2			
1	C	90	Total	C	N	O	S	0	1	0
			737	478	120	137	2			
1	E	90	Total	C	N	O	S	0	0	0
			725	469	119	135	2			
1	G	90	Total	C	N	O	S	0	0	0
			725	469	119	135	2			

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



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

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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	42	Total	O	0	0
			42	42		
4	C	53	Total	O	0	0
			53	53		
4	E	44	Total	O	0	0
			44	44		
4	G	45	Total	O	0	0
			45	45		

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. 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. 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: ACYLPHOSPHATASE

Chain A: 



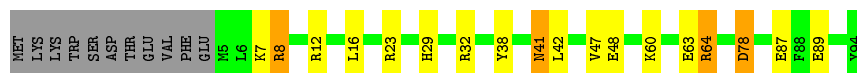
• Molecule 1: ACYLPHOSPHATASE

Chain C: 



• Molecule 1: ACYLPHOSPHATASE

Chain E: 



• Molecule 1: ACYLPHOSPHATASE

Chain G: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.98Å 56.53Å 60.80Å 90.00° 103.69° 90.00°	Depositor
Resolution (Å)	8.00 – 1.90 7.99 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (8.00-1.90) 98.8 (7.99-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.162 , 0.215 0.168 , 0.243	Depositor DCC
R_{free} test set	1266 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	28.2	Xtriage
Anisotropy	0.275	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3127	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.66% 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: SO4, CL

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	1.02	0/740	1.03	1/991 (0.1%)
1	C	0.98	0/753	0.99	1/1009 (0.1%)
1	E	1.07	0/740	1.09	2/991 (0.2%)
1	G	0.94	1/740 (0.1%)	1.05	1/991 (0.1%)
All	All	1.00	1/2973 (0.0%)	1.04	5/3982 (0.1%)

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	1
1	E	0	3
1	G	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	84	TYR	CE1-CZ	-5.31	1.31	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	8	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	C	12	ARG	NE-CZ-NH1	-5.93	117.34	120.30
1	E	78	ASP	CB-CG-OD2	5.47	123.23	118.30
1	G	32	ARG	NE-CZ-NH2	-5.39	117.61	120.30
1	A	62	LEU	CB-CG-CD2	-5.10	102.33	111.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	47	VAL	Mainchain
1	E	23	ARG	Sidechain
1	E	38	TYR	Sidechain
1	E	41	ASN	Mainchain
1	G	73	GLU	Mainchain

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	725	0	721	9	0
1	C	737	0	729	17	0
1	E	725	0	721	13	0
1	G	725	0	721	24	0
2	A	15	0	0	1	0
2	C	5	0	0	0	0
2	E	5	0	0	0	0
2	G	5	0	0	5	0
3	A	1	0	0	0	0
4	A	42	0	0	4	0
4	C	53	0	0	7	0
4	E	44	0	0	5	1
4	G	45	0	0	7	1
All	All	3127	0	2892	61	1

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 11.

All (61) 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:82:SER:HB2	4:A:2032:HOH:O	1.57	1.03
1:C:10[B]:TYR:HE1	1:C:82:SER:HG	1.02	0.98
1:G:24:LYS:HG2	4:G:2004:HOH:O	1.70	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:89:GLU:CG	4:E:2038:HOH:O	2.20	0.88
1:G:24:LYS:HD3	4:G:2004:HOH:O	1.74	0.86
1:G:24:LYS:HG3	2:G:1095:SO4:O2	1.80	0.82
1:G:24:LYS:CD	4:G:2004:HOH:O	2.34	0.74
1:G:24:LYS:CG	4:G:2004:HOH:O	2.33	0.73
1:E:89:GLU:HG3	4:E:2038:HOH:O	1.85	0.72
1:C:28:ILE:HG13	4:C:2009:HOH:O	1.90	0.71
1:G:24:LYS:HE2	2:G:1095:SO4:O4	1.92	0.70
2:A:1098:SO4:O2	4:A:2041:HOH:O	2.10	0.69
1:G:24:LYS:CE	2:G:1095:SO4:O4	2.42	0.67
1:E:8:ARG:HH22	1:E:87:GLU:CD	1.97	0.67
1:A:66:LYS:HE2	4:A:2042:HOH:O	1.95	0.65
1:G:62:LEU:HD21	1:G:79:TYR:CZ	2.32	0.65
1:C:10[A]:TYR:CE2	4:C:2045:HOH:O	2.49	0.64
1:C:94:TYR:OXT	4:C:2052:HOH:O	2.15	0.63
1:G:24:LYS:HE3	2:G:1095:SO4:S	2.43	0.58
1:C:7:LYS:NZ	1:C:55:GLU:OE2	2.35	0.57
1:C:10[A]:TYR:CD2	4:C:2045:HOH:O	2.60	0.55
1:E:89:GLU:HG2	4:E:2038:HOH:O	1.97	0.55
1:G:24:LYS:NZ	4:G:2009:HOH:O	2.38	0.54
1:G:62:LEU:O	1:G:66:LYS:HG3	2.07	0.54
1:C:7:LYS:HD2	1:C:55:GLU:HG3	1.89	0.54
1:E:78:ASP:OD2	4:E:2034:HOH:O	2.18	0.54
1:C:40:LYS:HD2	4:C:2020:HOH:O	2.08	0.54
1:C:92:GLU:HA	1:C:92:GLU:OE1	2.07	0.54
1:C:69:PRO:HD2	1:C:72:ALA:CB	2.37	0.53
1:E:29:HIS:CE1	1:E:32:ARG:HH21	2.27	0.52
1:E:16:LEU:HD11	1:G:31:ILE:HG22	1.93	0.51
1:A:28:ILE:CD1	1:C:20:VAL:HA	2.41	0.51
1:C:27:GLN:O	1:C:31:ILE:HG13	2.10	0.51
1:G:24:LYS:HE3	2:G:1095:SO4:O4	2.10	0.50
1:E:60:LYS:HE2	1:E:64:ARG:NH1	2.26	0.49
1:C:69:PRO:HD2	1:C:72:ALA:HB3	1.94	0.49
1:G:37:GLY:HA2	1:G:88:PHE:CG	2.48	0.48
1:G:37:GLY:O	1:G:91:PHE:HA	2.14	0.48
1:G:24:LYS:CE	4:G:2008:HOH:O	2.63	0.47
1:G:10:TYR:HE1	1:G:82:SER:HG	1.63	0.46
1:G:65:ILE:HG21	1:G:65:ILE:HD13	1.76	0.46
1:C:10[A]:TYR:CE1	1:C:48:GLU:HG3	2.51	0.45
1:C:10[A]:TYR:HE2	4:C:2045:HOH:O	1.90	0.45
1:A:8:ARG:HD3	1:A:10:TYR:CZ	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:ARG:HH11	1:A:67:GLN:HE22	1.66	0.44
1:A:69:PRO:HD2	1:A:72:ALA:HB3	1.99	0.44
1:C:92:GLU:HG2	4:C:2018:HOH:O	2.17	0.43
1:E:41:ASN:HD22	1:E:47:VAL:HG22	1.83	0.43
1:A:66:LYS:CE	4:A:2042:HOH:O	2.63	0.42
1:E:16:LEU:HD11	1:G:31:ILE:CG2	2.49	0.42
1:G:35:ILE:CG2	1:G:51:ALA:HB1	2.49	0.42
1:G:62:LEU:HD21	1:G:79:TYR:CE1	2.54	0.42
1:G:84:TYR:CZ	1:G:86:GLY:HA2	2.55	0.41
1:E:12:ARG:NE	1:E:42:LEU:HD12	2.35	0.41
1:E:64:ARG:NH2	4:E:2026:HOH:O	2.27	0.41
1:G:56:GLU:O	1:G:60:LYS:HG3	2.20	0.41
1:A:33:LEU:HA	1:A:33:LEU:HD23	1.82	0.41
1:C:10[A]:TYR:CD2	1:C:10[A]:TYR:C	2.93	0.41
1:A:73:GLU:O	1:A:73:GLU:HG3	2.21	0.41
1:E:64:ARG:HG2	1:E:64:ARG:HH11	1.85	0.41
1:G:24:LYS:HD3	4:G:2008:HOH:O	2.19	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:2019:HOH:O	4:G:2027:HOH:O[2_645]	2.17	0.03

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	88/101 (87%)	87 (99%)	1 (1%)	0	100	100
1	C	89/101 (88%)	87 (98%)	2 (2%)	0	100	100
1	E	88/101 (87%)	88 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	88/101 (87%)	87 (99%)	1 (1%)	0	100	100
All	All	353/404 (87%)	349 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	74/85 (87%)	73 (99%)	1 (1%)	67	65
1	C	75/85 (88%)	75 (100%)	0	100	100
1	E	74/85 (87%)	70 (95%)	4 (5%)	22	13
1	G	74/85 (87%)	73 (99%)	1 (1%)	67	65
All	All	297/340 (87%)	291 (98%)	6 (2%)	55	51

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	GLU
1	E	7	LYS
1	E	48	GLU
1	E	63	GLU
1	E	64	ARG
1	G	28	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	41	ASN
1	A	67	GLN
1	C	18	GLN
1	C	41	ASN

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Mol	Chain	Res	Type
1	E	18	GLN
1	E	29	HIS
1	E	41	ASN
1	G	18	GLN
1	G	41	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	SO4	A	1097	-	4,4,4	0.13	0	6,6,6	0.15	0
2	SO4	A	1098	-	4,4,4	0.35	0	6,6,6	0.47	0
2	SO4	E	1095	-	4,4,4	0.49	0	6,6,6	1.00	0
2	SO4	C	1095	-	4,4,4	0.24	0	6,6,6	1.11	1 (16%)
2	SO4	G	1095	-	4,4,4	0.15	0	6,6,6	0.44	0
2	SO4	A	1095	-	4,4,4	0.29	0	6,6,6	0.54	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	C	1095	SO4	O4-S-O3	2.29	118.82	109.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1098	SO4	1	0
2	G	1095	SO4	5	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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.