wwPDB X-ray Structure Validation Summary Report (i)

Sep 16, 2023 – 03:33 PM EDT

PDB ID	:	4P05
Title	:	Bacterial arylsulfate sulfotransferase (ASST) H436N mutant with 4-nitrophenyl sulfate (PNS) in the active site
Authors	:	Malojcic, G.; Owen, R.L.; Glockshuber, R.
Deposited on	:	2014-02-20
Resolution	:	2.05 Å(reported)

The following versions of software and data (see references (i)) 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	:	2.35.1
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)	:	2.35.1

1   Overall quality at a glance ⓘ

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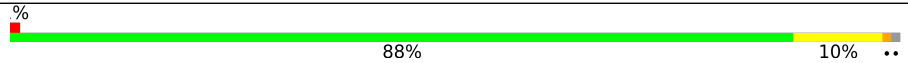*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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.
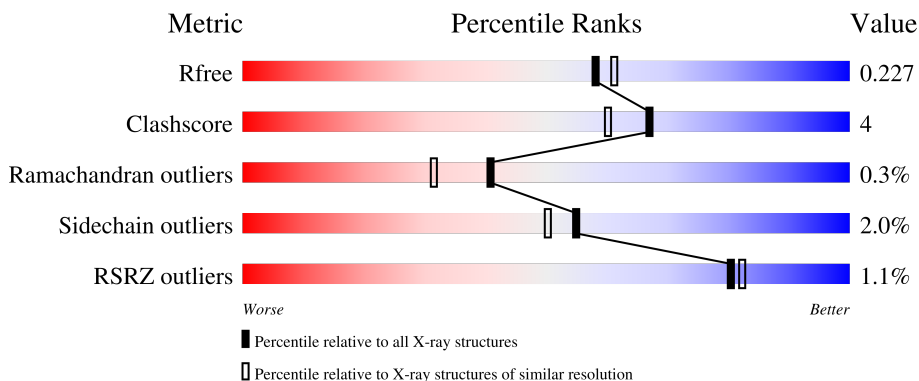
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 of 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
1	A	571	
1	B	571	

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 9573 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 Arylsulfate sulfotransferase AssT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	564	Total	C	N	O	S	11	2	0
			4463	2833	768	852	10			
1	B	564	Total	C	N	O	S	11	2	0
			4463	2833	768	852	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	436	ASN	HIS	engineered mutation	UNP E2QE64
B	436	ASN	HIS	engineered mutation	UNP E2QE64

- Molecule 2 is 4-nitrophenyl sulfate (three-letter code: 4NS) (formula: $C_6H_5NO_6S$).

4NS
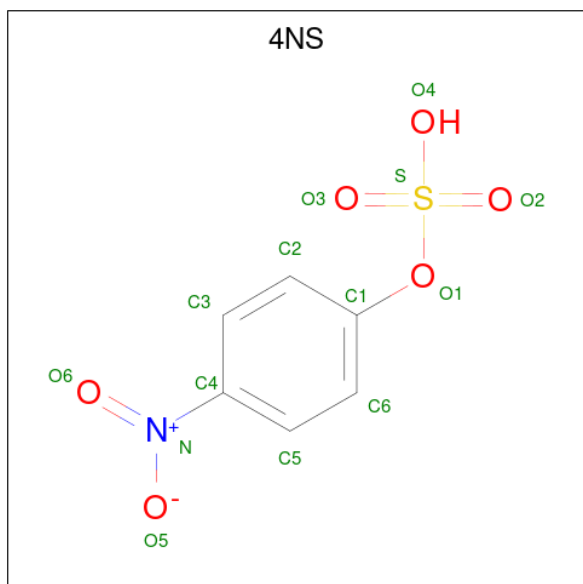
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			14	6	1	6	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			14	6	1	6	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	309	Total	O	0	0
			309	309		
4	B	295	Total	O	0	0
			295	295		

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Arylsulfate sulfotransferase AssT
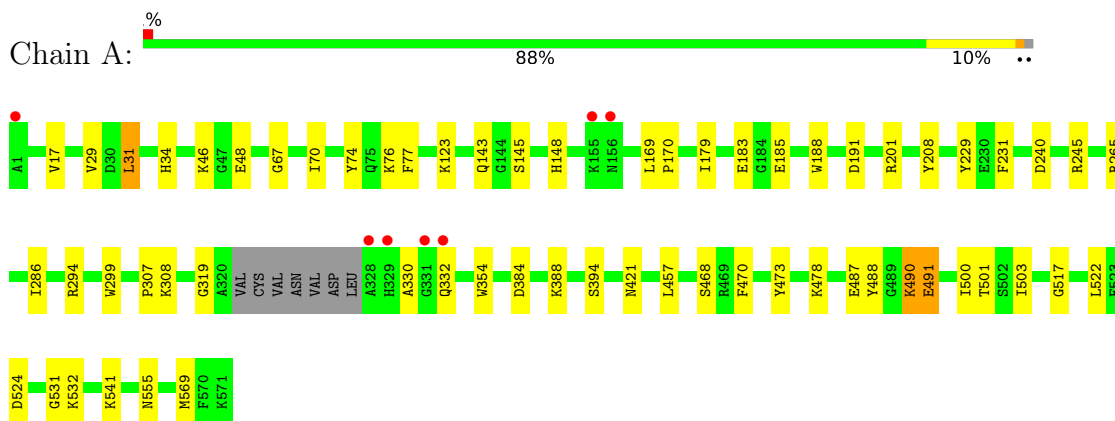
• Molecule 1: Arylsulfate sulfotransferase AssT
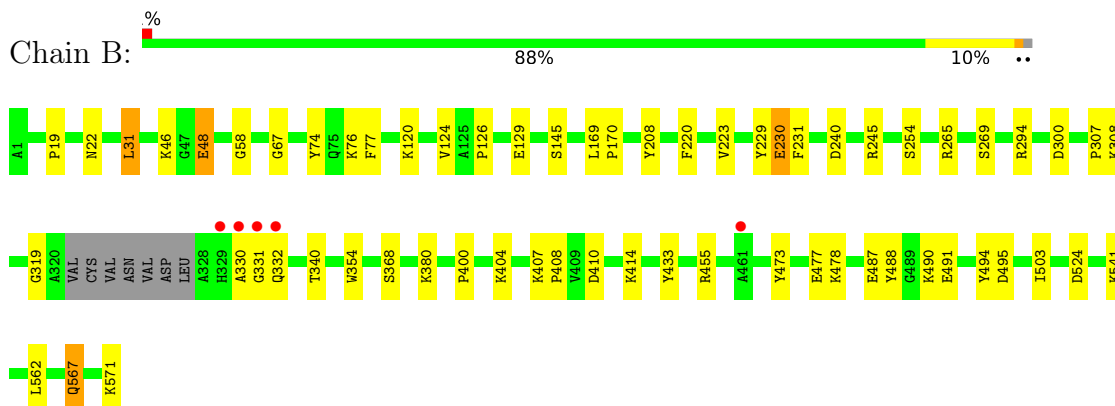
4   Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, α, β, γ	181.02Å 181.02Å 99.42Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.95 – 2.05 50.90 – 2.05	Depositor EDS
% Data completeness (in resolution range)	89.7 (50.95-2.05) 89.7 (50.90-2.05)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	0.90 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.7.0029, PHENIX	Depositor
R, R_{free}	0.188 , 0.225 0.193 , 0.227	Depositor DCC
R_{free} test set	5807 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	30.2	Xtriage
Anisotropy	0.787	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 34.4	EDS
L-test for twinning[2]	$< |L| > = 0.44, < L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.089 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	9573	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical 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.

5   Model quality ⓘ

5.1   Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 4NS, 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	1.23	19/4578 (0.4%)	0.96	5/6208 (0.1%)
1	B	1.18	21/4578 (0.5%)	0.94	3/6208 (0.0%)
All	All	1.21	40/9156 (0.4%)	0.95	8/12416 (0.1%)

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	473	TYR	CE1-CZ	-15.04	1.19	1.38
1	B	74	TYR	CE1-CZ	-12.38	1.22	1.38
1	A	74	TYR	CE1-CZ	-12.09	1.22	1.38
1	A	473	TYR	CG-CD2	-10.86	1.25	1.39
1	B	473	TYR	CG-CD1	-10.18	1.25	1.39

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	245	ARG	NE-CZ-NH1	8.30	124.45	120.30
1	A	245	ARG	NE-CZ-NH1	7.45	124.02	120.30
1	A	201	ARG	NE-CZ-NH2	-7.19	116.71	120.30
1	A	294	ARG	NE-CZ-NH1	-6.10	117.25	120.30
1	B	294	ARG	NE-CZ-NH1	-5.97	117.31	120.30

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	4463	0	4348	37	0
1	B	4463	0	4348	32	0
2	A	14	0	5	0	0
2	B	14	0	5	0	0
3	A	5	0	0	0	0
3	B	10	0	0	0	0
4	A	309	0	0	15	0
4	B	295	0	0	9	1
All	All	9573	0	8706	69	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 4.

The worst 5 of 69 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:48:GLU:OE1	4:A:897:HOH:O	1.95	0.83
1:B:124:VAL:O	4:B:961:HOH:O	2.01	0.76
1:B:48:GLU:H	1:B:48:GLU:CD	1.90	0.74
1:A:569:MET:HG2	4:A:878:HOH:O	1.89	0.72
1:A:183:GLU:O	4:A:843:HOH:O	2.09	0.71

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:B:753:HOH:O	4:B:855:HOH:O[5_554]	2.06	0.14

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	562/571 (98%)	532 (95%)	29 (5%)	1 (0%)	47	39
1	B	562/571 (98%)	536 (95%)	24 (4%)	2 (0%)	34	24
All	All	1124/1142 (98%)	1068 (95%)	53 (5%)	3 (0%)	41	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	319	GLY
1	B	319	GLY
1	B	331	GLY

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	478/483 (99%)	469 (98%)	9 (2%)	57	53
1	B	478/483 (99%)	468 (98%)	10 (2%)	53	48
All	All	956/966 (99%)	937 (98%)	19 (2%)	55	50

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	491	GLU
1	B	562	LEU
1	B	567	GLN
1	B	524	ASP
1	A	524	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	GLN
1	B	567	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

5 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	$\#|Z| > 2$
3	SO4	B	603	-	4,4,4	0.57	0	6,6,6	0.83	0
2	4NS	B	601	-	13,14,14	1.96	3 (23%)	17,20,20	2.01	8 (47%)
3	SO4	B	602	-	4,4,4	0.22	0	6,6,6	1.08	0
2	4NS	A	601	-	13,14,14	1.88	3 (23%)	17,20,20	1.80	5 (29%)
3	SO4	A	602	-	4,4,4	0.52	0	6,6,6	0.72	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	4NS	A	601	-	-	0/7/9/9	0/1/1/1
2	4NS	B	601	-	-	0/7/9/9	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	4NS	O1-C1	-5.53	1.33	1.42
2	A	601	4NS	O1-C1	-4.56	1.35	1.42
2	A	601	4NS	C4-N	-3.02	1.37	1.45
2	A	601	4NS	O1-S	-2.73	1.54	1.58
2	B	601	4NS	O4-S	2.42	1.65	1.50

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	601	4NS	C2-C3-C4	-3.39	115.36	120.08
2	B	601	4NS	C5-C4-N	-3.24	116.93	119.38
2	A	601	4NS	C5-C4-N	-3.18	116.98	119.38
2	B	601	4NS	O4-S-O3	3.12	119.34	108.49
2	A	601	4NS	C3-C4-C5	2.91	124.67	119.86

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 ⓘ

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	564/571 (98%)	-0.51	7 (1%)	79	81	23, 37, 66, 131	0
1	B	564/571 (98%)	-0.47	5 (0%)	84	86	24, 36, 68, 139	0
All	All	1128/1142 (98%)	-0.49	12 (1%)	80	82	23, 37, 67, 139	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	331	GLY	9.4
1	B	330	ALA	7.5
1	A	1	ALA	3.8
1	A	328	ALA	3.4
1	A	329	HIS	3.4

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 ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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
2	4NS	A	601	14/14	0.98	0.11	34,42,58,59	0
2	4NS	B	601	14/14	0.98	0.11	37,44,69,69	0
3	SO4	B	602	5/5	0.98	0.06	64,64,72,76	0
3	SO4	A	602	5/5	0.99	0.06	48,51,60,60	0
3	SO4	B	603	5/5	0.99	0.07	43,46,52,54	0

6.5 Other polymers ⓘ

There are no such residues in this entry.