



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:08 AM UTC

PDB ID : 1NQK / pdb_00001nqk
Title : Structural Genomics, Crystal structure of Alkanesulfonate monooxygenase
Authors : Zhang, R.; Skarina, T.; Savchenko, A.; Edwards, A.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2003-01-21
Resolution : 2.20 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

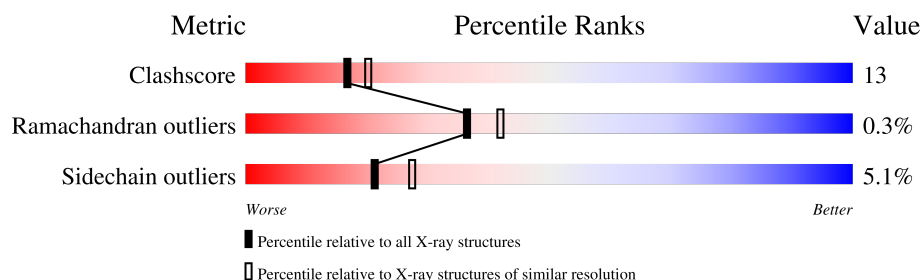
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	381	 64% 24% •• 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2816 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 Alkanesulfonate monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	S	0	0	0
			2672	1702	470	496	4			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	144	Total	O	0	0
			144	144		

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	84.25Å 84.25Å 234.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.13 – 2.20	Depositor
% Data completeness (in resolution range)	84.2 (42.13-2.20)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.201 , 0.266	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2816	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0.47	0/2736	0.96	13/3727 (0.3%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	283	ASN	N-CA-C	-6.94	104.07	112.54
1	A	309	GLY	CA-C-N	6.19	125.41	118.97
1	A	309	GLY	C-N-CA	6.19	125.41	118.97
1	A	149	ASP	N-CA-C	-6.06	98.64	108.52
1	A	338	ALA	N-CA-C	-5.90	104.93	111.36
1	A	21	GLU	N-CA-C	-5.83	105.93	113.16
1	A	79	ARG	CA-C-N	5.76	127.04	119.84
1	A	79	ARG	C-N-CA	5.76	127.04	119.84
1	A	148	VAL	N-CA-C	5.73	116.13	108.11
1	A	147	THR	N-CA-C	-5.69	100.01	109.46
1	A	56	GLU	N-CA-C	-5.52	102.30	110.48
1	A	229	HIS	N-CA-C	-5.17	102.10	110.32
1	A	334	HIS	N-CA-C	5.06	118.71	112.54

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	2672	0	2634	68	0
2	A	144	0	0	3	0
All	All	2816	0	2634	68	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 13.

All (68) 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:198:GLY:HA2	1:A:226:ILE:HD11	1.75	0.69
1:A:32:LEU:C	1:A:65:MET:HE1	2.19	0.68
1:A:18:LEU:HD12	1:A:247:ILE:HG22	1.76	0.68
1:A:206:GLU:O	1:A:210:GLN:HG3	1.93	0.67
1:A:53:ARG:HD2	1:A:115:GLU:HG3	1.77	0.65
1:A:211:VAL:CG1	1:A:222:ILE:HD11	2.29	0.63
1:A:53:ARG:CG	1:A:115:GLU:HG3	2.30	0.62
1:A:176:PHE:CB	1:A:191:VAL:HG11	2.31	0.60
1:A:223:ARG:HD2	1:A:325:ASP:OD2	2.01	0.60
1:A:262:PHE:HB2	1:A:283:ASN:HB3	1.84	0.60
1:A:176:PHE:HB3	1:A:191:VAL:HG11	1.84	0.59
1:A:75:LEU:HD11	1:A:106:ASN:HB2	1.85	0.57
1:A:100:ASN:ND2	1:A:357:PRO:HB2	2.20	0.57
1:A:290:LEU:HD22	1:A:303:THR:HB	1.86	0.57
1:A:18:LEU:HD12	1:A:247:ILE:CG2	2.36	0.56
1:A:53:ARG:CD	1:A:115:GLU:HG3	2.37	0.55
1:A:80:PRO:HG3	1:A:107:LEU:HD11	1.87	0.55
1:A:116:LEU:CD1	1:A:128:ARG:HD3	2.37	0.55
1:A:156:HIS:HB2	2:A:438:HOH:O	2.07	0.54
1:A:51:THR:HB	1:A:77:ALA:HB3	1.89	0.53
1:A:240:TRP:O	1:A:244:GLU:HG2	2.09	0.53
1:A:228:LEU:O	1:A:329:LEU:HA	2.09	0.53
1:A:179:SER:OG	1:A:197:TRP:CZ2	2.59	0.53
1:A:22:GLU:HG2	1:A:249:HIS:CD2	2.44	0.52
1:A:250:LEU:HB2	1:A:255:ILE:HD11	1.92	0.52
1:A:258:ALA:O	1:A:262:PHE:HD2	1.94	0.50
1:A:204:VAL:HG21	1:A:319:TYR:HE1	1.77	0.48
1:A:189:GLU:O	1:A:189:GLU:HG2	2.14	0.48
1:A:6:PHE:HB2	1:A:328:VAL:HA	1.95	0.47
1:A:2:SER:HB3	1:A:352:ALA:HB2	1.96	0.47
1:A:204:VAL:HG21	1:A:319:TYR:CE1	2.50	0.47
1:A:111:SER:O	1:A:113:PRO:HD3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:PRO:HD2	1:A:203:LEU:HD12	1.96	0.47
1:A:78:LEU:HD22	1:A:135:PHE:CE2	2.51	0.46
1:A:33:GLN:N	1:A:65:MET:HE1	2.31	0.46
1:A:48:LEU:HD12	1:A:49:ILE:N	2.30	0.46
1:A:20:THR:OG1	1:A:22:GLU:HB3	2.16	0.46
1:A:123:LEU:HB3	1:A:127:GLU:HB2	1.98	0.46
1:A:342:GLY:O	1:A:346:PHE:HB2	2.17	0.45
1:A:87:VAL:O	1:A:91:GLN:HG3	2.16	0.45
1:A:139:TRP:CZ2	1:A:143:LEU:HD11	2.51	0.45
1:A:176:PHE:HB2	1:A:191:VAL:HG11	1.99	0.45
1:A:316:ILE:HD12	1:A:345:LEU:HD21	1.99	0.44
1:A:211:VAL:HG12	1:A:222:ILE:HD11	2.00	0.44
1:A:211:VAL:HG11	1:A:222:ILE:HD11	1.98	0.44
1:A:53:ARG:HG3	1:A:115:GLU:HG3	1.98	0.44
1:A:175:TYR:N	1:A:175:TYR:CD1	2.85	0.43
1:A:223:ARG:NH1	1:A:325:ASP:OD1	2.51	0.43
1:A:262:PHE:CB	1:A:283:ASN:HB3	2.46	0.43
1:A:7:TRP:HB3	1:A:47:VAL:HG12	2.00	0.43
1:A:7:TRP:CG	1:A:8:PHE:H	2.37	0.43
1:A:153:LYS:HD3	2:A:481:HOH:O	2.18	0.43
1:A:207:LYS:HE3	1:A:207:LYS:HB2	1.88	0.43
1:A:289:ASN:HD22	1:A:315:ARG:HH21	1.66	0.42
1:A:78:LEU:HD22	1:A:135:PHE:HE2	1.85	0.42
1:A:79:ARG:HH11	1:A:79:ARG:HB3	1.84	0.42
1:A:290:LEU:HD23	1:A:290:LEU:HA	1.81	0.42
1:A:150:PHE:O	1:A:156:HIS:HA	2.18	0.42
1:A:229:HIS:HE1	2:A:402:HOH:O	2.02	0.42
1:A:175:TYR:N	1:A:175:TYR:HD1	2.18	0.42
1:A:140:ARG:O	1:A:144:GLN:HG3	2.20	0.41
1:A:31:TYR:CE2	1:A:35:ILE:HD11	2.56	0.41
1:A:289:ASN:HD22	1:A:315:ARG:NH2	2.17	0.41
1:A:80:PRO:CG	1:A:107:LEU:HD11	2.49	0.41
1:A:124:ASP:OD2	1:A:127:GLU:HG3	2.21	0.41
1:A:346:PHE:HB2	1:A:347:PRO:HD3	2.03	0.40
1:A:116:LEU:HB3	1:A:121:VAL:HB	2.03	0.40
1:A:149:ASP:OD1	1:A:159:GLY:N	2.53	0.40

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	341/381 (90%)	325 (95%)	15 (4%)	1 (0%)	36	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	80	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	274/303 (90%)	260 (95%)	14 (5%)	21	27

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	HIS
1	A	56	GLU
1	A	78	LEU
1	A	80	PRO
1	A	141	ARG
1	A	169	GLN
1	A	175	TYR
1	A	195	LEU
1	A	197	TRP
1	A	283	ASN

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Mol	Chain	Res	Type
1	A	290	LEU
1	A	316	ILE
1	A	353	ILE
1	A	355	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	HIS
1	A	91	GLN
1	A	137	GLN
1	A	210	GLN
1	A	283	ASN
1	A	289	ASN
1	A	317	ASN
1	A	358	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.