



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:01 PM GMT

PDB ID : 1DMS
Title : STRUCTURE OF DMSO REDUCTASE
Authors : Schneider, F.; Loewe, J.; Huber, R.; Schindelin, H.; Kisker, C.; Knaeblein, J.
Deposited on : 1996-09-03
Resolution : 1.88 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

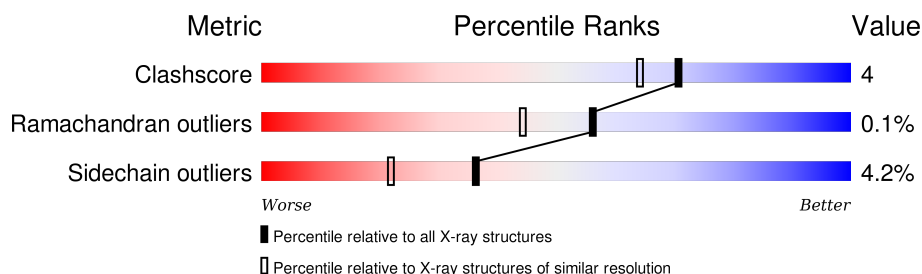
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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	102246	7778 (1.90-1.86)
Ramachandran outliers	100387	7691 (1.90-1.86)
Sidechain outliers	100360	7692 (1.90-1.86)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	781	

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
3	MM4	A	784	-	-	X	-

2 Entry composition [i](#)

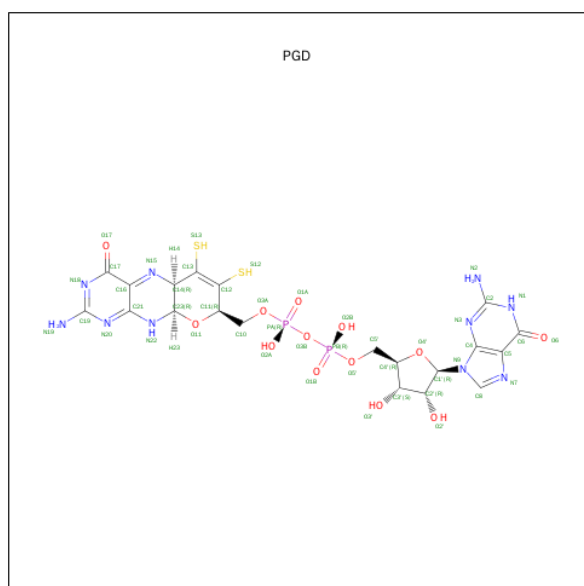
There are 4 unique types of molecules in this entry. The entry contains 6342 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DMSO REDUCTASE.

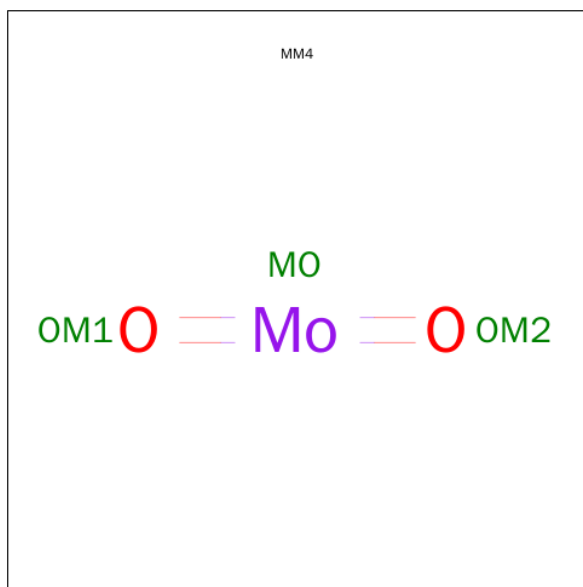
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	766	5890	3744	998	1120	28	0	0	0

- Molecule 2 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (three-letter code: PGD) (formula: $C_{20}H_{24}N_{10}O_{13}P_2S_2$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
2	A	1	47	20	10	13	2	2	0	0
2	A	1	47	20	10	13	2	2	0	0

- Molecule 3 is MOLYBDENUM (IV) OXIDE (three-letter code: MM4) (formula: MoO_2).



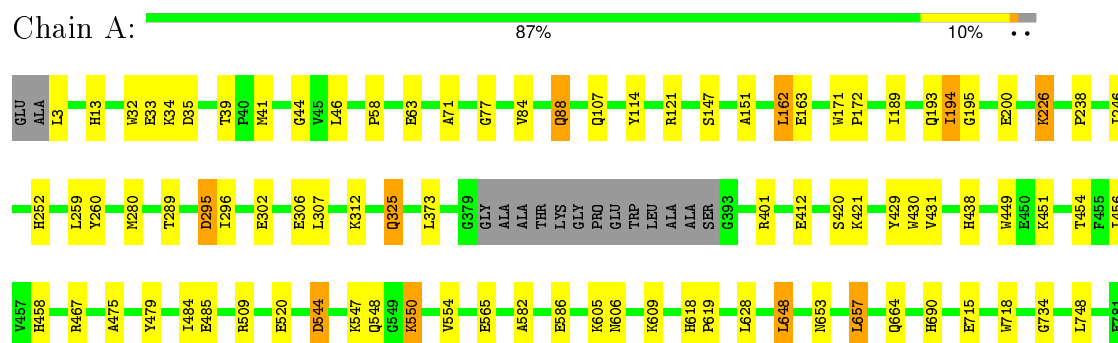
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 3	Mo 1	O 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	355	Total 355	O 355	0	0

Note EDS was not executed.

- Molecule 1: DMSO REDUCTASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	80.70 Å 80.70 Å 229.20 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 1.88	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-1.88)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.169 , 0.203	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6342	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MM4, PGD

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	0.49	0/6046	0.71	1/8223 (0.0%)

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	648	LEU	N-CA-C	-5.83	95.26	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	114	TYR	Sidechain
1	A	479	TYR	Sidechain

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	5890	0	5705	50	1
2	A	94	0	42	1	0
3	A	3	0	0	2	0
4	A	355	0	0	3	1
All	All	6342	0	5747	52	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.

All (52) 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:39:THR:HG23	1:A:193:GLN:HE21	1.21	1.01
1:A:189:ILE:HG21	1:A:226:LYS:HG2	1.40	1.00
1:A:39:THR:HG23	1:A:193:GLN:NE2	1.84	0.93
1:A:39:THR:HG22	1:A:41:MET:H	1.43	0.82
1:A:582:ALA:O	1:A:586:GLU:HG2	1.87	0.73
1:A:151:ALA:H	1:A:325:GLN:HE21	1.42	0.66
1:A:189:ILE:CG2	1:A:226:LYS:HG2	2.24	0.63
3:A:784:MM4:OM1	3:A:784:MM4:MO	1.69	0.63
3:A:784:MM4:MO	3:A:784:MM4:OM2	1.71	0.62
1:A:44:GLY:HA3	1:A:657:LEU:HD22	1.85	0.59
1:A:33:GLU:HG3	4:A:828:HOH:O	2.03	0.58
1:A:84:VAL:HB	1:A:88:GLN:HG3	1.86	0.57
1:A:295:ASP:OD1	1:A:296:ILE:HG13	2.05	0.56
1:A:618:HIS:HD2	1:A:619:PRO:O	1.89	0.56
1:A:605:LYS:HA	1:A:605:LYS:HE2	1.87	0.56
1:A:194:ILE:HG12	1:A:648:LEU:HD13	1.91	0.53
1:A:121:ARG:HD3	1:A:485:GLU:OE1	2.09	0.53
1:A:451:LYS:HD2	1:A:451:LYS:N	2.24	0.53
1:A:690:HIS:HD2	4:A:936:HOH:O	1.90	0.53
1:A:147:SER:OG	2:A:783:PGD:S12	2.67	0.53
1:A:238:PRO:HB3	1:A:246:ILE:HD11	1.90	0.52
1:A:226:LYS:HG3	1:A:226:LYS:O	2.09	0.51
1:A:456:ILE:N	1:A:456:ILE:HD12	2.26	0.50
1:A:565:GLU:HB2	4:A:1115:HOH:O	2.11	0.50
1:A:454:THR:HG22	1:A:456:ILE:HD11	1.94	0.50
1:A:547:LYS:O	1:A:550:LYS:HD3	2.12	0.49
1:A:653:ASN:ND2	1:A:718:TRP:H	2.10	0.48
1:A:544:ASP:O	1:A:548:GLN:HG2	2.14	0.47
1:A:162:LEU:HD12	1:A:163:GLU:N	2.28	0.47
1:A:151:ALA:H	1:A:325:GLN:NE2	2.12	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:GLY:HA2	1:A:467:ARG:O	2.15	0.46
1:A:171:TRP:N	1:A:172:PRO:HD2	2.31	0.46
1:A:606:ASN:HA	1:A:609:LYS:HE3	1.96	0.46
1:A:412:GLU:HA	1:A:420:SER:O	2.15	0.46
1:A:431:VAL:HG12	1:A:458:HIS:HB2	1.98	0.46
1:A:302:GLU:O	1:A:306:GLU:HG3	2.17	0.45
1:A:63:GLU:HG3	1:A:71:ALA:HB1	1.98	0.45
1:A:226:LYS:HB2	1:A:226:LYS:HZ2	1.82	0.45
1:A:121:ARG:HG2	1:A:484:ILE:O	2.17	0.44
1:A:412:GLU:HG2	1:A:421:LYS:HG2	1.99	0.44
1:A:454:THR:HG22	1:A:456:ILE:CD1	2.48	0.44
1:A:32:TRP:CE2	1:A:34:LYS:HB2	2.52	0.43
1:A:58:PRO:HG2	1:A:84:VAL:O	2.18	0.42
1:A:606:ASN:HD22	1:A:609:LYS:HE3	1.84	0.42
1:A:13:HIS:HD2	1:A:195:GLY:O	2.03	0.42
1:A:312:LYS:HA	1:A:312:LYS:HD2	1.86	0.41
1:A:259:LEU:O	1:A:312:LYS:HE3	2.19	0.41
1:A:605:LYS:HB3	1:A:605:LYS:NZ	2.36	0.41
1:A:252:HIS:CE1	1:A:289:THR:HG22	2.55	0.41
1:A:260:TYR:HA	1:A:312:LYS:HE3	2.03	0.41
1:A:475:ALA:HA	1:A:509:ARG:O	2.21	0.41
1:A:401:ARG:NE	1:A:401:ARG:HA	2.35	0.41

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)
1:A:35:ASP:OD2	4:A:804:HOH:O[6_555]	1.87	0.33

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	762/781 (98%)	739 (97%)	22 (3%)	1 (0%)	56 44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	734	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	613/621 (99%)	587 (96%)	26 (4%)	36 22

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	46	LEU
1	A	88	GLN
1	A	107	GLN
1	A	162	LEU
1	A	194	ILE
1	A	200	GLU
1	A	226	LYS
1	A	280	MET
1	A	295	ASP
1	A	307	LEU
1	A	325	GLN
1	A	373	LEU
1	A	429	TYR
1	A	430	TRP
1	A	438	HIS
1	A	449	TRP
1	A	520	GLU
1	A	544	ASP
1	A	550	LYS

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Mol	Chain	Res	Type
1	A	554	VAL
1	A	628	LEU
1	A	657	LEU
1	A	664	GLN
1	A	715	GLU
1	A	748	LEU

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

Mol	Chain	Res	Type
1	A	13	HIS
1	A	193	GLN
1	A	241	GLN
1	A	325	GLN
1	A	606	ASN
1	A	618	HIS
1	A	653	ASN
1	A	690	HIS

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 ⓘ

3 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	$\# Z > 2$
2	PGD	A	782	3	34,52,52	2.68	8 (23%)	39,81,81	2.36	8 (20%)
2	PGD	A	783	-	34,52,52	2.48	7 (20%)	39,81,81	2.58	9 (23%)
3	MM4	A	784	1,2	0,2,2	0.00	-	0,1,1	0.00	-

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	PGD	A	782	3	-	0/18/82/82	0/6/6/6
2	PGD	A	783	-	-	0/18/82/82	0/6/6/6
3	MM4	A	784	1,2	-	0/0/0/0	0/0/0/0

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	783	PGD	C2-N1	2.03	1.39	1.35
2	A	782	PGD	C2-N1	2.39	1.39	1.35
2	A	782	PGD	C5-C4	2.79	1.46	1.40
2	A	783	PGD	C5-C4	2.92	1.47	1.40
2	A	782	PGD	C2-N2	3.59	1.41	1.34
2	A	782	PGD	O6-C6	4.19	1.34	1.24
2	A	783	PGD	O6-C6	4.30	1.35	1.24
2	A	783	PGD	C16-N15	4.76	1.41	1.28
2	A	782	PGD	C23-C14	5.01	1.57	1.52
2	A	783	PGD	C23-C14	5.17	1.57	1.52
2	A	782	PGD	C16-N15	5.46	1.43	1.28
2	A	783	PGD	O17-C17	6.72	1.35	1.24
2	A	783	PGD	C21-N20	7.47	1.37	1.28
2	A	782	PGD	O17-C17	7.49	1.36	1.24
2	A	782	PGD	C21-N20	7.77	1.38	1.28

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	782	PGD	C6-C5-C4	-6.35	113.31	120.90
2	A	782	PGD	O17-C17-N18	-6.13	112.44	120.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	783	PGD	O17-C17-N18	-6.08	112.49	120.41
2	A	783	PGD	C6-C5-C4	-5.50	114.32	120.90
2	A	783	PGD	C17-C16-C21	-4.31	112.84	117.63
2	A	783	PGD	C4'-O4'-C1'	-4.29	105.00	109.72
2	A	782	PGD	C17-C16-C21	-2.92	114.38	117.63
2	A	782	PGD	O2A-PA-O1A	2.02	123.49	112.53
2	A	782	PGD	PA-O3B-PB	2.10	138.62	132.73
2	A	782	PGD	O2'-C2'-C3'	2.31	119.35	111.83
2	A	783	PGD	O2A-PA-O1A	2.38	125.43	112.53
2	A	783	PGD	O2'-C2'-C3'	2.61	120.32	111.83
2	A	783	PGD	PA-O3B-PB	4.08	144.19	132.73
2	A	783	PGD	C17-C16-N15	5.97	123.57	117.87
2	A	782	PGD	C16-C17-N18	6.50	123.42	117.83
2	A	782	PGD	C17-C16-N15	7.20	124.74	117.87
2	A	783	PGD	C16-C17-N18	8.12	124.82	117.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	783	PGD	1	0
3	A	784	MM4	2	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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.