



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:28 am GMT

PDB ID : 1E61
Title : OXIDIZED DMSO REDUCTASE EXPOSED TO HEPES - STRUCTURE II BUFFER
Authors : Bailey, S.; Bennett, B.; Adams, B.; Smith, A.T.; Bray, R.C.
Deposited on : 2000-08-06
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

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

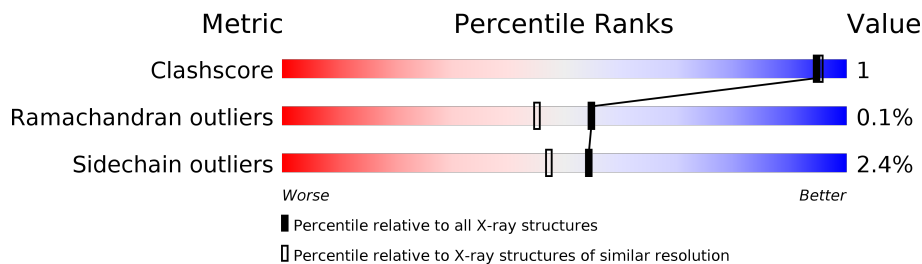
1 Overall quality at a glance

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))
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (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. 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	823	
1	C	823	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12739 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.

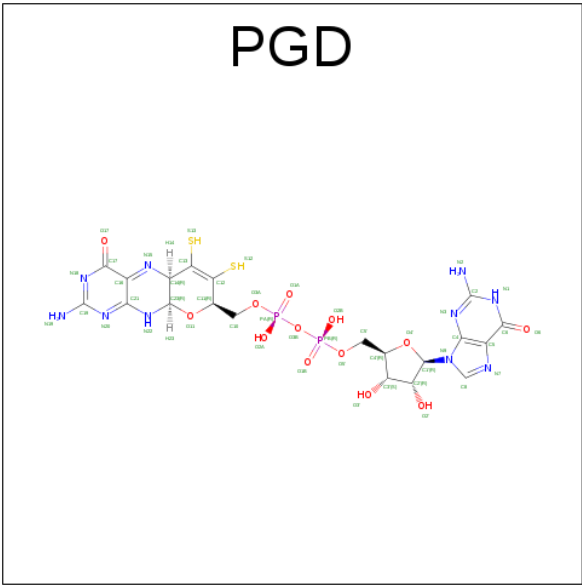
- Molecule 1 is a protein called DMSO REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	766	Total	C	N	O	S	0	0	0
			5880	3737	995	1121	27			
1	C	767	Total	C	N	O	S	0	0	0
			5888	3743	996	1122	27			

There are 24 discrepancies between the modelled and reference sequences:

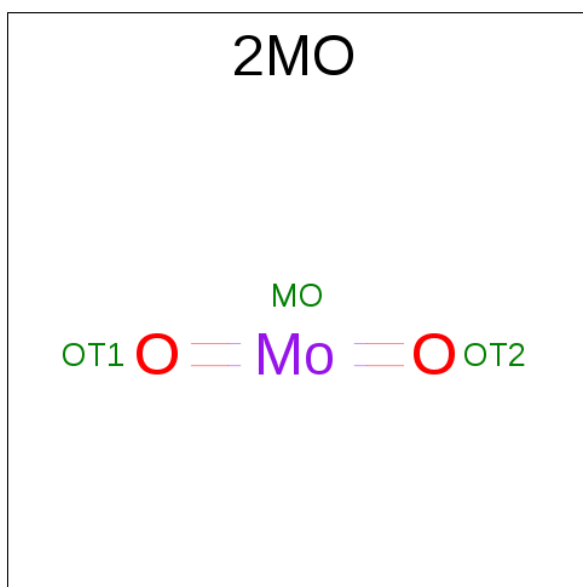
Chain	Residue	Modelled	Actual	Comment	Reference
A	39	SER	THR	SEQUENCED FROM MAP	UNP Q52675
A	43	ALA	GLU	SEQUENCED FROM MAP	UNP Q52675
A	107	GLU	GLN	SEQUENCED FROM MAP	UNP Q52675
A	234	GLU	ASP	SEQUENCED FROM MAP	UNP Q52675
A	236	ILE	VAL	SEQUENCED FROM MAP	UNP Q52675
A	280	ASP	MET	SEQUENCED FROM MAP	UNP Q52675
A	294	GLU	SER	SEQUENCED FROM MAP	UNP Q52675
A	295	GLY	ASP	SEQUENCED FROM MAP	UNP Q52675
A	312	GLU	ILE	SEQUENCED FROM MAP	UNP Q52675
A	374	ALA	SER	SEQUENCED FROM MAP	UNP Q52675
A	456	VAL	ILE	SEQUENCED FROM MAP	UNP Q52675
A	526	ALA	LYS	SEQUENCED FROM MAP	UNP Q52675
C	39	SER	THR	SEQUENCED FROM MAP	UNP Q52675
C	43	ALA	GLU	SEQUENCED FROM MAP	UNP Q52675
C	107	GLU	GLN	SEQUENCED FROM MAP	UNP Q52675
C	234	GLU	ASP	SEQUENCED FROM MAP	UNP Q52675
C	236	ILE	VAL	SEQUENCED FROM MAP	UNP Q52675
C	280	ASP	MET	SEQUENCED FROM MAP	UNP Q52675
C	294	GLU	SER	SEQUENCED FROM MAP	UNP Q52675
C	295	GLY	ASP	SEQUENCED FROM MAP	UNP Q52675
C	312	GLU	ILE	SEQUENCED FROM MAP	UNP Q52675
C	374	ALA	SER	SEQUENCED FROM MAP	UNP Q52675
C	456	VAL	ILE	SEQUENCED FROM MAP	UNP Q52675
C	526	ALA	LYS	SEQUENCED FROM MAP	UNP Q52675

- 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: C₂₀H₂₄N₁₀O₁₃P₂S₂).



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

- Molecule 3 is MOLYBDENUM (IV)OXIDE (three-letter code: 2MO) (formula: MoO₂).



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

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 5 is water.

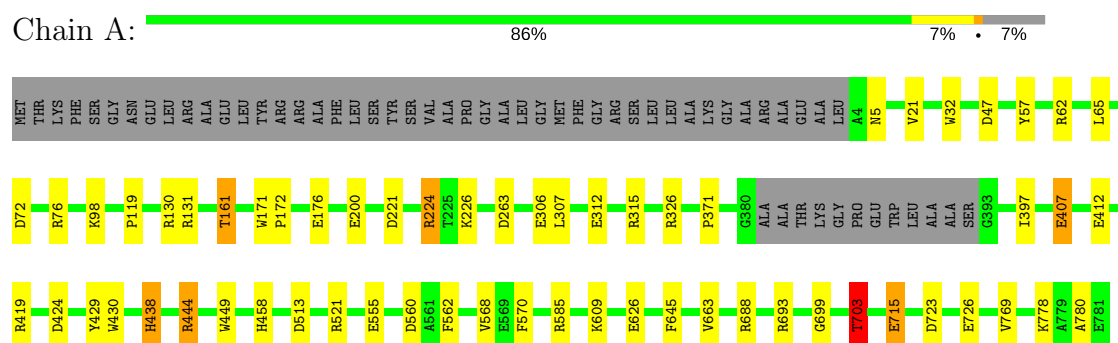
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	428	Total 428	O 428	0	0
5	C	339	Total 339	O 339	0	0

3 Residue-property plots

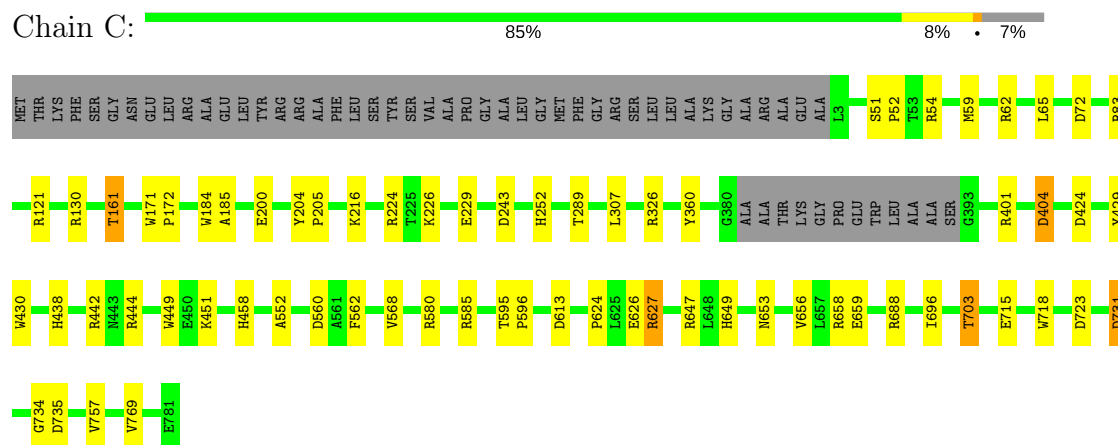
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

• Molecule 1: DMSO REDUCTASE



• Molecule 1: DMSO REDUCTASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.19Å 118.14Å 235.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90	Depositor
% Data completeness (in resolution range)	78.2 (20.00-1.90)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.178 , 0.216	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12739	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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: PGD, SO4, 2MO

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	0.54	1/6037 (0.0%)	1.21	41/8215 (0.5%)
1	C	0.54	0/6045	1.21	38/8226 (0.5%)
All	All	0.54	1/12082 (0.0%)	1.21	79/16441 (0.5%)

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	312	GLU	CD-OE1	-5.14	1.20	1.25

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	62	ARG	NE-CZ-NH2	-18.03	111.28	120.30
1	C	62	ARG	NE-CZ-NH1	16.18	128.39	120.30
1	A	326	ARG	NE-CZ-NH1	13.24	126.92	120.30
1	A	62	ARG	NE-CZ-NH1	12.38	126.49	120.30
1	A	62	ARG	NE-CZ-NH2	-9.14	115.73	120.30
1	C	72	ASP	CB-CG-OD1	8.66	126.10	118.30
1	C	326	ARG	NE-CZ-NH1	8.25	124.42	120.30
1	A	585	ARG	NE-CZ-NH1	8.13	124.37	120.30
1	C	83	ARG	CD-NE-CZ	8.04	134.86	123.60
1	A	693	ARG	NE-CZ-NH2	-7.92	116.34	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	442	ARG	NE-CZ-NH2	-7.86	116.37	120.30
1	A	130	ARG	NE-CZ-NH2	-7.83	116.39	120.30
1	A	224	ARG	NE-CZ-NH1	7.80	124.20	120.30
1	A	130	ARG	NE-CZ-NH1	7.65	124.12	120.30
1	A	521	ARG	NE-CZ-NH1	7.57	124.09	120.30
1	A	131	ARG	NE-CZ-NH1	7.56	124.08	120.30
1	C	54	ARG	NE-CZ-NH1	7.51	124.06	120.30
1	A	312	GLU	OE1-CD-OE2	-7.30	114.54	123.30
1	C	83	ARG	NE-CZ-NH1	7.28	123.94	120.30
1	A	263	ASP	CB-CG-OD1	7.26	124.84	118.30
1	A	715	GLU	OE1-CD-OE2	-7.23	114.62	123.30
1	C	703	THR	CB-CA-C	-7.21	92.15	111.60
1	A	585	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	C	121	ARG	NE-CZ-NH1	7.04	123.82	120.30
1	C	688	ARG	NE-CZ-NH1	6.99	123.80	120.30
1	C	161	THR	N-CA-CB	6.94	123.48	110.30
1	A	703	THR	CB-CA-C	-6.75	93.38	111.60
1	C	580	ARG	NE-CZ-NH1	6.72	123.66	120.30
1	C	224	ARG	NE-CZ-NH1	6.47	123.53	120.30
1	C	585	ARG	NE-CZ-NH1	6.37	123.48	120.30
1	A	32	TRP	CA-CB-CG	6.34	125.74	113.70
1	C	59	MET	CA-CB-CG	6.33	124.05	113.30
1	C	438	HIS	CA-CB-CG	6.28	124.28	113.60
1	A	693	ARG	NE-CZ-NH1	6.23	123.42	120.30
1	A	513	ASP	CB-CG-OD1	6.22	123.90	118.30
1	A	444	ARG	NE-CZ-NH2	6.20	123.40	120.30
1	C	647	ARG	NE-CZ-NH1	-6.17	117.21	120.30
1	C	627	ARG	NE-CZ-NH2	-6.08	117.26	120.30
1	A	72	ASP	CB-CG-OD1	6.08	123.77	118.30
1	A	47	ASP	CB-CG-OD2	6.04	123.74	118.30
1	A	438	HIS	CA-CB-CG	6.03	123.86	113.60
1	C	458	HIS	N-CA-CB	5.99	121.38	110.60
1	A	723	ASP	CB-CG-OD1	5.96	123.66	118.30
1	C	658	ARG	NE-CZ-NH1	5.89	123.25	120.30
1	C	560	ASP	CB-CG-OD2	5.88	123.59	118.30
1	A	693	ARG	CD-NE-CZ	5.80	131.72	123.60
1	A	312	GLU	CG-CD-OE2	5.77	129.84	118.30
1	A	626	GLU	OE1-CD-OE2	-5.74	116.41	123.30
1	A	76	ARG	NE-CZ-NH2	5.71	123.16	120.30
1	A	688	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	C	360	TYR	CB-CG-CD2	5.69	124.41	121.00
1	A	57	TYR	CB-CA-C	-5.67	99.06	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	444	ARG	NE-CZ-NH2	-5.65	117.47	120.30
1	C	442	ARG	NE-CZ-NH1	5.61	123.10	120.30
1	A	723	ASP	CB-CG-OD2	-5.58	113.28	118.30
1	C	626	GLU	OE1-CD-OE2	-5.55	116.64	123.30
1	C	731	ASP	CB-CG-OD1	5.54	123.28	118.30
1	A	57	TYR	CB-CG-CD1	-5.53	117.68	121.00
1	A	315	ARG	NE-CZ-NH2	-5.49	117.55	120.30
1	C	735	ASP	CB-CG-OD1	5.47	123.23	118.30
1	A	161	THR	N-CA-CB	5.46	120.68	110.30
1	C	360	TYR	CB-CG-CD1	-5.36	117.78	121.00
1	C	458	HIS	CA-CB-CG	5.35	122.70	113.60
1	A	424	ASP	CB-CG-OD1	5.31	123.08	118.30
1	A	221	ASP	CB-CG-OD1	5.31	123.08	118.30
1	A	326	ARG	NH1-CZ-NH2	-5.23	113.65	119.40
1	C	243	ASP	CB-CG-OD1	5.21	122.99	118.30
1	A	407	GLU	OE1-CD-OE2	-5.20	117.06	123.30
1	C	656	VAL	CB-CA-C	-5.19	101.54	111.40
1	A	263	ASP	CB-CG-OD2	-5.18	113.64	118.30
1	C	757	VAL	CA-CB-CG2	5.16	118.63	110.90
1	C	161	THR	CB-CA-C	-5.15	97.69	111.60
1	A	560	ASP	CB-CG-OD1	5.14	122.92	118.30
1	C	613	ASP	CB-CG-OD1	5.13	122.91	118.30
1	C	404	ASP	CB-CG-OD1	5.10	122.89	118.30
1	C	130	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	C	723	ASP	CB-CG-OD1	5.08	122.87	118.30
1	A	726	GLU	OE1-CD-OE2	-5.05	117.23	123.30
1	A	458	HIS	CA-CB-CG	5.00	122.11	113.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	703	THR	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	5880	0	5680	15	0
1	C	5888	0	5691	17	0
2	A	94	0	41	0	0
2	C	94	0	41	2	0
3	A	3	0	0	0	0
3	C	3	0	0	0	0
4	A	5	0	0	0	0
4	C	5	0	0	0	0
5	A	428	0	0	4	0
5	C	339	0	0	2	0
All	All	12739	0	11453	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 1.

All (33) 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:226:LYS:HG2	5:A:2137:HOH:O	1.89	0.71
1:A:226:LYS:HD2	1:A:645:PHE:CZ	2.37	0.58
1:A:562:PHE:HD1	1:A:568:VAL:HG23	1.71	0.55
1:C:552:ALA:HB2	5:C:2214:HOH:O	2.07	0.54
1:A:555:GLU:HG3	1:A:555:GLU:O	2.07	0.53
1:C:562:PHE:CD1	1:C:568:VAL:HG23	2.46	0.51
1:C:696:ILE:HG22	1:C:731:ASP:HB3	1.92	0.50
1:A:5:ASN:HA	1:A:21:VAL:O	2.13	0.49
1:A:306:GLU:HG2	5:A:2185:HOH:O	2.11	0.49
1:C:595:THR:HB	1:C:596:PRO:HD2	1.96	0.47
1:C:252:HIS:CE1	1:C:289:THR:HG22	2.50	0.47
1:C:624:PRO:HG2	1:C:627:ARG:HB3	1.96	0.47
1:A:412:GLU:OE1	1:A:419:ARG:NH1	2.45	0.46
1:C:424:ASP:OD1	1:C:451:LYS:NZ	2.41	0.46
1:A:780:ALA:HB1	5:A:2027:HOH:O	2.16	0.46
1:C:184:TRP:O	1:C:185:ALA:HB3	2.15	0.46
1:C:401:ARG:NE	1:C:404:ASP:OD2	2.35	0.45
1:C:595:THR:HB	1:C:596:PRO:CD	2.47	0.45
1:A:407:GLU:OE1	1:A:444:ARG:NH2	2.35	0.45
1:C:171:TRP:HB2	1:C:172:PRO:HD3	2.00	0.44
1:C:226:LYS:HD3	5:C:2102:HOH:O	2.16	0.44
1:A:224:ARG:HD2	5:A:2140:HOH:O	2.18	0.44
1:A:371:PRO:HD2	1:A:570:PHE:CZ	2.52	0.44
1:C:562:PHE:HD1	1:C:568:VAL:HG23	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:ILE:HG13	1:A:397:ILE:O	2.18	0.43
1:A:562:PHE:CD1	1:A:568:VAL:HG23	2.52	0.43
1:C:653:ASN:ND2	1:C:718:TRP:H	2.17	0.42
1:C:204:TYR:HB2	1:C:205:PRO:HD3	2.01	0.42
1:C:51:SER:HB2	1:C:52:PRO:CD	2.51	0.41
1:A:663:VAL:HB	1:A:699:GLY:HA3	2.03	0.40
1:A:171:TRP:N	1:A:172:PRO:HD2	2.37	0.40
1:C:649:HIS:CG	2:C:801:PGD:H102	2.57	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	762/823 (93%)	740 (97%)	22 (3%)	0	100	100
1	C	763/823 (93%)	742 (97%)	20 (3%)	1 (0%)	55	45
All	All	1525/1646 (93%)	1482 (97%)	42 (3%)	1 (0%)	55	45

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	734	GLY

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	609/648 (94%)	593 (97%)	16 (3%)	51	43
1	C	610/648 (94%)	597 (98%)	13 (2%)	59	53
All	All	1219/1296 (94%)	1190 (98%)	29 (2%)	54	47

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	LEU
1	A	98	LYS
1	A	119	PRO
1	A	161	THR
1	A	176	GLU
1	A	200	GLU
1	A	307	LEU
1	A	429	TYR
1	A	430	TRP
1	A	438	HIS
1	A	449	TRP
1	A	609	LYS
1	A	703	THR
1	A	715	GLU
1	A	769	VAL
1	A	778	LYS
1	C	65	LEU
1	C	161	THR
1	C	200	GLU
1	C	216	LYS
1	C	229	GLU
1	C	307	LEU
1	C	429	TYR
1	C	430	TRP
1	C	449	TRP
1	C	659	GLU
1	C	703	THR
1	C	715	GLU
1	C	769	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	241	GLN

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Mol	Chain	Res	Type
1	A	606	ASN
1	A	653	ASN
1	C	241	GLN
1	C	606	ASN
1	C	653	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 ⓘ

10 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	801	3	39,52,52	2.39	14 (35%)	35,81,81	1.96	10 (28%)
2	PGD	A	802	3	39,52,52	2.45	14 (35%)	35,81,81	2.09	7 (20%)
3	2MO	A	803[A]	1,3,2	0,1,2	0.00	-	0,0,1	0.00	-
3	2MO	A	803[B]	1,3,2	0,1,2	0.00	-	0,0,1	0.00	-
4	SO4	A	901	-	4,4,4	0.56	0	6,6,6	0.32	0
2	PGD	C	801	3	39,52,52	2.28	13 (33%)	35,81,81	1.92	9 (25%)
2	PGD	C	802	3	39,52,52	2.41	13 (33%)	35,81,81	2.34	9 (25%)
3	2MO	C	803[A]	1,3,2	0,1,2	0.00	-	0,0,1	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	2MO	C	803[B]	1,3,2	0,1,2	0.00	-	0,0,1	0.00	-
4	SO4	C	901	-	4,4,4	0.59	0	6,6,6	0.43	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	PGD	A	801	3	-	0/18/82/82	0/6/6/6
2	PGD	A	802	3	-	0/18/82/82	0/6/6/6
3	2MO	A	803[A]	1,3,2	-	0/0/0/0	0/0/0/0
3	2MO	A	803[B]	1,3,2	-	0/0/0/0	0/0/0/0
4	SO4	A	901	-	-	0/0/0/0	0/0/0/0
2	PGD	C	801	3	-	0/18/82/82	0/6/6/6
2	PGD	C	802	3	-	0/18/82/82	0/6/6/6
3	2MO	C	803[A]	1,3,2	-	0/0/0/0	0/0/0/0
3	2MO	C	803[B]	1,3,2	-	0/0/0/0	0/0/0/0
4	SO4	C	901	-	-	0/0/0/0	0/0/0/0

All (54) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	802	PGD	C5-C4	-2.45	1.35	1.40
2	C	802	PGD	C5-C4	-2.24	1.35	1.40
2	A	801	PGD	C5-C4	-2.09	1.35	1.40
2	C	801	PGD	C5-C4	-2.04	1.35	1.40
2	A	801	PGD	O4'-C1'	2.04	1.44	1.41
2	A	802	PGD	C8-N7	2.15	1.38	1.34
2	A	801	PGD	C21-N20	2.23	1.37	1.32
2	C	801	PGD	C6-N1	2.26	1.37	1.33
2	A	802	PGD	C21-N20	2.38	1.38	1.32
2	C	801	PGD	O4'-C1'	2.47	1.44	1.41
2	A	802	PGD	C6-N1	2.50	1.37	1.33
2	C	801	PGD	PA-O2A	2.60	1.68	1.55
2	A	801	PGD	PA-O2A	2.64	1.68	1.55
2	C	802	PGD	PA-O2A	2.74	1.69	1.55
2	C	802	PGD	C19-N19	2.83	1.41	1.34
2	A	801	PGD	C14-N15	2.85	1.49	1.46
2	A	801	PGD	C6-N1	2.89	1.38	1.33
2	C	801	PGD	PB-O2B	2.95	1.70	1.55
2	A	802	PGD	PB-O2B	3.01	1.70	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	802	PGD	C6-N1	3.01	1.38	1.33
2	A	801	PGD	PB-O2B	3.12	1.70	1.55
2	C	801	PGD	C2-N2	3.20	1.40	1.34
2	C	802	PGD	O4'-C1'	3.24	1.45	1.41
2	C	801	PGD	C19-N19	3.28	1.42	1.34
2	A	802	PGD	PA-O2A	3.29	1.71	1.55
2	A	801	PGD	PA-O3A	3.35	1.73	1.59
2	C	801	PGD	PB-O5'	3.35	1.73	1.59
2	C	801	PGD	C10-C11	3.38	1.56	1.52
2	A	802	PGD	PA-O3A	3.39	1.73	1.59
2	A	802	PGD	C2-N2	3.40	1.41	1.34
2	A	802	PGD	PB-O5'	3.44	1.73	1.59
2	A	802	PGD	O4'-C1'	3.49	1.46	1.41
2	C	802	PGD	PB-O2B	3.57	1.73	1.55
2	A	801	PGD	PB-O5'	3.58	1.74	1.59
2	A	801	PGD	C10-C11	3.59	1.57	1.52
2	C	802	PGD	C14-N15	3.62	1.49	1.46
2	A	802	PGD	C19-N19	3.71	1.43	1.34
2	C	801	PGD	PA-O3A	3.93	1.75	1.59
2	C	802	PGD	PB-O5'	3.97	1.76	1.59
2	A	801	PGD	PB-O1B	4.01	1.65	1.50
2	C	802	PGD	PA-O3A	4.26	1.77	1.59
2	C	802	PGD	PB-O1B	4.30	1.67	1.50
2	A	801	PGD	C2-N2	4.43	1.43	1.34
2	C	802	PGD	C2-N2	4.49	1.43	1.34
2	A	802	PGD	PB-O1B	4.71	1.68	1.50
2	A	802	PGD	PA-O1A	4.98	1.69	1.50
2	C	801	PGD	PB-O1B	5.02	1.69	1.50
2	C	802	PGD	PA-O1A	5.11	1.70	1.50
2	C	801	PGD	PA-O1A	5.18	1.70	1.50
2	A	801	PGD	PA-O1A	5.65	1.72	1.50
2	C	802	PGD	C16-N15	5.93	1.43	1.28
2	C	801	PGD	C16-N15	6.33	1.44	1.28
2	A	801	PGD	C16-N15	6.79	1.45	1.28
2	A	802	PGD	C16-N15	7.04	1.46	1.28

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	802	PGD	C4'-O4'-C1'	-6.35	103.01	109.77
2	A	802	PGD	N20-C19-N18	-5.78	117.56	126.41
2	C	802	PGD	N20-C19-N18	-5.29	118.29	126.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	802	PGD	C4'-O4'-C1'	-4.89	104.57	109.77
2	A	801	PGD	N3-C2-N1	-4.87	120.34	127.46
2	A	801	PGD	C4'-O4'-C1'	-4.66	104.81	109.77
2	C	802	PGD	N3-C2-N1	-4.63	120.69	127.46
2	A	802	PGD	C5-C6-N1	-4.26	117.42	123.48
2	C	801	PGD	N20-C19-N18	-3.95	120.36	126.41
2	C	801	PGD	C5-C6-N1	-3.79	118.08	123.48
2	C	802	PGD	C5-C6-N1	-3.73	118.17	123.48
2	A	802	PGD	N3-C2-N1	-3.63	122.15	127.46
2	C	801	PGD	N3-C2-N1	-3.61	122.18	127.46
2	A	801	PGD	C5-C6-N1	-2.63	119.74	123.48
2	A	801	PGD	N20-C19-N18	-2.51	122.56	126.41
2	C	801	PGD	C4'-O4'-C1'	-2.39	107.22	109.77
2	C	801	PGD	N19-C19-N18	2.02	119.82	117.09
2	A	801	PGD	N19-C19-N18	2.06	119.87	117.09
2	A	801	PGD	C16-C21-N22	2.26	122.46	116.53
2	A	802	PGD	O11-C23-C14	2.44	112.15	108.71
2	C	801	PGD	C1'-N9-C4	2.45	130.87	126.64
2	C	801	PGD	N19-C19-N20	2.46	119.80	116.54
2	A	801	PGD	C6-N1-C2	2.49	119.64	116.06
2	C	802	PGD	N19-C19-N20	2.66	120.08	116.54
2	A	801	PGD	N2-C2-N3	2.71	122.76	117.75
2	C	801	PGD	C6-N1-C2	2.75	120.01	116.06
2	C	802	PGD	C2-N3-C4	3.11	118.79	115.16
2	C	802	PGD	C6-N1-C2	3.20	120.66	116.06
2	A	802	PGD	C6-N1-C2	3.33	120.84	116.06
2	C	802	PGD	N19-C19-N18	3.36	121.63	117.09
2	A	801	PGD	C2-N3-C4	3.39	119.12	115.16
2	A	801	PGD	C17-C16-N15	4.45	122.95	118.06
2	A	802	PGD	N19-C19-N20	4.76	122.86	116.54
2	C	802	PGD	C17-C16-N15	4.95	123.50	118.06
2	C	801	PGD	C17-C16-N15	5.58	124.18	118.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	801	PGD	1	0
2	C	802	PGD	1	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 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.