



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 08:30 am GMT

PDB ID : 1VLB
Title : STRUCTURE REFINEMENT OF THE ALDEHYDE OXIDOREDUCTASE
FROM DESULFOVIBRIO GIGAS AT 1.28 Å
Authors : Rebelo, J.M.; Dias, J.M.; Huber, R.; Moura, J.J.G.; Romao, M.J.
Deposited on : 2004-07-20
Resolution : 1.28 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

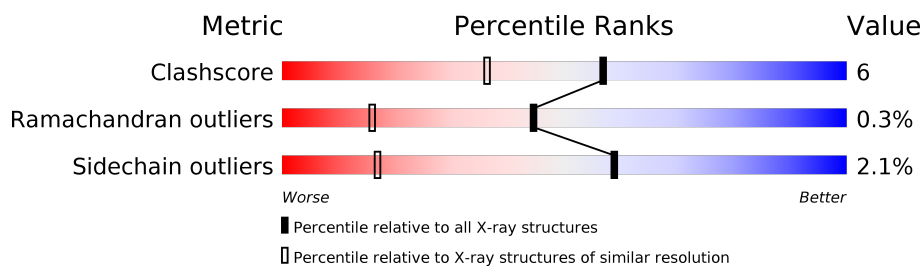
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.28 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	1447 (1.30-1.26)
Ramachandran outliers	110173	1392 (1.30-1.26)
Sidechain outliers	110143	1391 (1.30-1.26)

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	907	

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
6	IPA	A	915	-	X	-	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8192 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 ALDEHYDE OXIDOREDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	907	Total	C	N	O	S	12	17	0
			6885	4357	1172	1310	46			

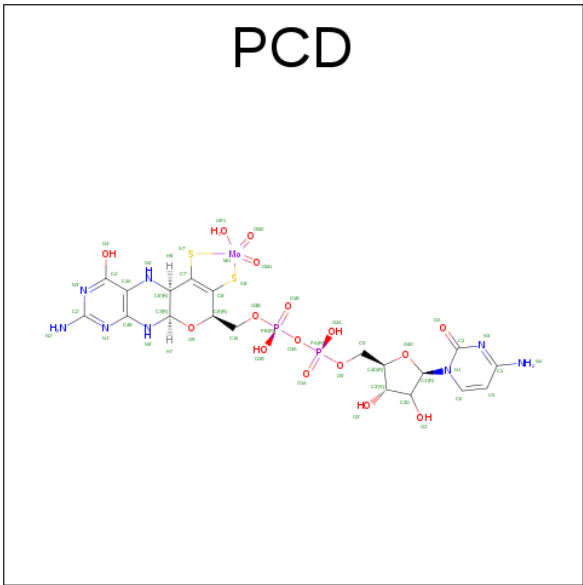
- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

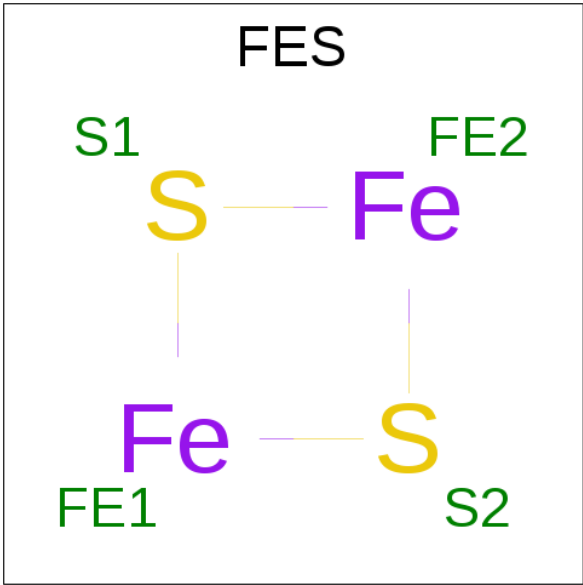
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		

- Molecule 4 is (MOLYBDOPTERIN-CYTOSINE DINUCLEOTIDE-S,S)-DIOXO-AQUA-MOLYBDENUM(V) (three-letter code: PCD) (formula: C₁₉H₂₆MoN₈O₁₆P₂S₂).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
4	A	1	Total	C	Mo	N	O	P	S	0	0
			48	19	1	8	16	2	2		

- Molecule 5 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



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

- Molecule 6 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C₃H₈O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	3	1		
6	A	1	Total	C	O	0	0
			4	3	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1238	Total	O	0	0
			1238	1238		

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: ALDEHYDE OXIDOREDUCTASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	141.78Å 141.78Å 160.87Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.40 – 1.28	Depositor
% Data completeness (in resolution range)	(Not available) (24.40-1.28)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	0.04	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.145 , 0.193	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8192	wwPDB-VP
Average B, all atoms (Å ²)	25.0	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: MG, IPA, FES, PCD, 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	0.64	0/7104	1.23	41/9650 (0.4%)

There are no bond length outliers.

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	82	PRO	C-N-CA	-10.26	96.04	121.70
1	A	442	ARG	NE-CZ-NH2	-10.12	115.24	120.30
1	A	127	ARG	NE-CZ-NH2	9.22	124.91	120.30
1	A	857	ARG	NE-CZ-NH2	-9.17	115.71	120.30
1	A	82	PRO	O-C-N	-8.71	108.76	122.70
1	A	182	ARG	NE-CZ-NH1	-8.68	115.96	120.30
1	A	134	ARG	NE-CZ-NH2	-8.30	116.15	120.30
1	A	563	ARG	NE-CZ-NH1	8.21	124.40	120.30
1	A	205	ALA	C-N-CA	-7.38	106.81	122.30
1	A	447	ARG	NE-CZ-NH1	-7.15	116.72	120.30
1	A	568	TYR	CB-CG-CD1	7.08	125.25	121.00
1	A	563	ARG	NE-CZ-NH2	-6.84	116.88	120.30
1	A	532	PHE	CB-CG-CD1	6.69	125.48	120.80
1	A	510	TYR	CG-CD1-CE1	-6.55	116.06	121.30
1	A	123	ARG	NE-CZ-NH2	-6.52	117.04	120.30
1	A	572	ASP	CB-CG-OD1	-6.51	112.44	118.30
1	A	332	TYR	CB-CG-CD1	-6.48	117.11	121.00
1	A	164	ASP	CB-CG-OD2	-6.39	112.55	118.30
1	A	332	TYR	CB-CG-CD2	6.21	124.72	121.00
1	A	838	PHE	CB-CG-CD1	-6.20	116.46	120.80
1	A	447	ARG	NE-CZ-NH2	6.17	123.39	120.30
1	A	205	ALA	O-C-N	-6.11	112.82	123.20
1	A	28	ARG	NE-CZ-NH2	-5.94	117.33	120.30
1	A	528	TRP	CA-CB-CG	5.92	124.96	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	ASP	CB-CG-OD2	5.89	123.60	118.30
1	A	138	ARG	NE-CZ-NH2	5.69	123.15	120.30
1	A	510	TYR	CD1-CE1-CZ	5.65	124.89	119.80
1	A	450	TYR	CA-CB-CG	-5.64	102.68	113.40
1	A	771	PHE	CB-CG-CD2	-5.60	116.88	120.80
1	A	442	ARG	NH1-CZ-NH2	5.52	125.47	119.40
1	A	653	HIS	CA-CB-CG	5.41	122.79	113.60
1	A	310	TYR	CB-CG-CD2	-5.38	117.77	121.00
1	A	905	LEU	CA-CB-CG	5.35	127.61	115.30
1	A	748	SER	C-N-CA	-5.26	111.25	122.30
1	A	564	TYR	CG-CD1-CE1	5.10	125.38	121.30
1	A	709	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	A	44[A]	GLN	CB-CA-C	-5.09	100.21	110.40
1	A	44[B]	GLN	CB-CA-C	-5.09	100.21	110.40
1	A	474	ASP	CB-CG-OD1	5.09	122.88	118.30
1	A	182	ARG	NE-CZ-NH2	5.07	122.83	120.30
1	A	164	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	6885	0	6797	76	0
2	A	3	0	0	1	0
3	A	2	0	0	0	0
4	A	48	0	21	2	0
5	A	8	0	0	0	0
6	A	8	0	14	2	0
7	A	1238	0	0	31	0
All	All	8192	0	6832	78	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 6.

All (78) 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)
6:A:915:IPA:C2	6:A:915:IPA:C1	1.76	1.62
1:A:807:GLN:HE22	4:A:921:PCD:H8'	1.08	1.01
1:A:169:MET:HE3	1:A:170:PRO:HD2	1.59	0.84
1:A:163:THR:HA	1:A:166:GLU:OE1	1.84	0.78
6:A:915:IPA:O2	6:A:915:IPA:C1	2.32	0.76
1:A:626:LEU:HD12	7:A:5144:HOH:O	1.88	0.74
1:A:716:LEU:O	1:A:720:GLU:HG3	1.94	0.68
1:A:396[B]:LEU:HD11	1:A:410[B]:LEU:HD13	1.75	0.67
1:A:604:GLN:HB3	7:A:5076:HOH:O	1.96	0.66
1:A:261:LYS:HD3	1:A:329:PRO:HG3	1.78	0.66
1:A:255:ILE:HD13	7:A:5145:HOH:O	1.99	0.62
1:A:261:LYS:HD3	1:A:329:PRO:CG	2.34	0.58
1:A:365:HIS:HE1	1:A:531:ALA:O	1.88	0.57
1:A:318:ALA:HB1	1:A:320:ASP:OD1	2.04	0.57
1:A:95:HIS:HE1	1:A:151:ASP:OD2	1.87	0.57
1:A:520:ARG:HD2	7:A:4723:HOH:O	2.04	0.56
1:A:396[B]:LEU:CD1	1:A:410[B]:LEU:HD13	2.35	0.56
1:A:95:HIS:HD2	7:A:4428:HOH:O	1.90	0.54
1:A:170:PRO:HB2	1:A:172:ASP:OD1	2.07	0.54
1:A:237:HIS:HD2	1:A:238:SER:OG	1.90	0.54
1:A:240[B]:ILE:HD13	1:A:436:ALA:HA	1.89	0.54
1:A:826:ASP:HB3	7:A:5011:HOH:O	2.08	0.54
1:A:246:LYS:HE3	7:A:4902:HOH:O	2.08	0.54
1:A:635:TRP:CD1	1:A:742[B]:THR:HG22	2.43	0.53
1:A:246:LYS:HD3	1:A:246:LYS:N	2.24	0.53
1:A:163:THR:HG23	7:A:4763:HOH:O	2.09	0.53
1:A:334:GLU:HG2	1:A:520:ARG:HG2	1.92	0.51
1:A:680:LYS:HD3	7:A:4859:HOH:O	2.09	0.51
1:A:319:GLU:HG2	7:A:5074:HOH:O	2.11	0.51
1:A:728:THR:OG1	1:A:731:GLU:HG3	2.10	0.51
1:A:205:ALA:HA	7:A:5137:HOH:O	2.11	0.51
1:A:112:LYS:HE3	7:A:4865:HOH:O	2.11	0.49
1:A:112:LYS:HE2	7:A:4648:HOH:O	2.13	0.49
1:A:174:ARG:NH1	1:A:176:TRP:HD1	2.11	0.48
1:A:352:VAL:HG21	1:A:555:LEU:CD2	2.43	0.48
1:A:609:ALA:N	7:A:4966:HOH:O	2.46	0.48
1:A:609:ALA:HB3	7:A:4966:HOH:O	2.12	0.48
1:A:393:HIS:HE1	7:A:4082:HOH:O	1.96	0.47
1:A:365:HIS:HD2	7:A:4199:HOH:O	1.96	0.47
1:A:407:PRO:HA	1:A:410[B]:LEU:CD1	2.45	0.47
1:A:393:HIS:HD2	7:A:4077:HOH:O	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:661[B]:CYS:SG	1:A:708:ILE:HD11	2.55	0.47
1:A:533:ARG:HD3	1:A:872[B]:LEU:HD12	1.97	0.47
1:A:129:TRP:O	1:A:133:HIS:HD2	1.98	0.47
1:A:229:GLU:OE1	1:A:299:LYS:HE3	2.14	0.47
1:A:170:PRO:HG3	7:A:5170:HOH:O	2.15	0.47
1:A:807:GLN:HE21	1:A:868:GLY:HA2	1.80	0.46
1:A:237:HIS:HE1	7:A:4899:HOH:O	1.98	0.45
1:A:744[A]:ASN:ND2	7:A:4535:HOH:O	2.49	0.45
1:A:171:ALA:O	1:A:172:ASP:HB3	2.17	0.45
1:A:319:GLU:N	1:A:319:GLU:OE1	2.50	0.45
1:A:649:ALA:O	7:A:5139:HOH:O	2.21	0.44
1:A:44[A]:GLN:NE2	7:A:4459:HOH:O	2.49	0.44
1:A:610:THR:N	7:A:4966:HOH:O	2.50	0.44
1:A:761:LYS:NZ	7:A:4996:HOH:O	2.49	0.44
1:A:535:TYR:HA	2:A:916:CL:CL	2.55	0.43
1:A:551:LEU:HD23	1:A:562:LEU:HD21	2.00	0.43
1:A:170:PRO:O	1:A:171:ALA:HB3	2.18	0.43
1:A:655:GLN:HG3	4:A:921:PCD:H5'2	2.00	0.43
1:A:169:MET:CE	1:A:170:PRO:HD2	2.39	0.42
1:A:175:ILE:HD13	1:A:676:PRO:HB3	2.00	0.42
1:A:867:VAL:HG22	1:A:867:VAL:O	2.19	0.42
1:A:365:HIS:H	1:A:365:HIS:CD2	2.37	0.42
1:A:815:GLY:HA3	1:A:875:PRO:HG2	2.01	0.42
1:A:881:ASN:ND2	1:A:890:ARG:HH22	2.18	0.42
1:A:610:THR:HG23	7:A:4966:HOH:O	2.20	0.42
1:A:752:HIS:HD2	7:A:4342:HOH:O	2.03	0.41
1:A:597:GLN:HE21	1:A:597:GLN:HB3	1.53	0.41
1:A:352:VAL:HG21	1:A:555:LEU:HD23	2.01	0.41
1:A:855:HIS:HD2	7:A:4385:HOH:O	2.02	0.41
1:A:174:ARG:NH2	7:A:5167:HOH:O	2.49	0.41
1:A:735:ALA:O	1:A:736[B]:ASP:HB3	2.21	0.41
1:A:701:GLN:O	1:A:705:GLY:HA3	2.21	0.40
1:A:828[B]:LYS:HD2	1:A:828[B]:LYS:HA	1.73	0.40
1:A:322[A]:ILE:HD12	7:A:4777:HOH:O	2.20	0.40
1:A:761:LYS:NZ	7:A:4766:HOH:O	2.49	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	922/907 (102%)	896 (97%)	23 (2%)	3 (0%)	44 16

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	ASP
1	A	533	ARG
1	A	874	SER

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	728/711 (102%)	711 (98%)	17 (2%)	56 14

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2[A]	ILE
1	A	2[B]	ILE
1	A	11	ILE
1	A	92	TRP
1	A	124	GLU
1	A	246	LYS
1	A	319	GLU
1	A	342	ASP

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Mol	Chain	Res	Type
1	A	355	GLU
1	A	420	THR
1	A	528	TRP
1	A	532	PHE
1	A	604	GLN
1	A	605	LYS
1	A	828[A]	LYS
1	A	828[B]	LYS
1	A	905	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	HIS
1	A	133	HIS
1	A	135	ASN
1	A	237	HIS
1	A	365	HIS
1	A	393	HIS
1	A	591	GLN
1	A	597	GLN
1	A	639	ASN
1	A	701	GLN
1	A	752	HIS
1	A	807	GLN
1	A	855	HIS
1	A	881	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 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 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
5	FES	A	908	1	0,4,4	0.00	-	0,4,4	0.00	-
5	FES	A	909	1	0,4,4	0.00	-	0,4,4	0.00	-
6	IPA	A	914	-	3,3,3	1.41	1 (33%)	3,3,3	0.82	0
6	IPA	A	915	-	3,3,3	3.31	3 (100%)	3,3,3	2.04	1 (33%)
4	PCD	A	921	-	40,53,53	2.52	12 (30%)	36,86,86	2.69	10 (27%)

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
5	FES	A	908	1	-	0/0/4/4	0/1/1/1
5	FES	A	909	1	-	0/0/4/4	0/1/1/1
6	IPA	A	914	-	-	0/0/0/0	0/0/0/0
6	IPA	A	915	-	-	0/0/0/0	0/0/0/0
4	PCD	A	921	-	-	0/18/78/78	0/6/6/6

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	921	PCD	C4-N3	-4.21	1.28	1.35
6	A	915	IPA	O2-C2	-3.39	1.20	1.42
6	A	914	IPA	C1-C2	2.10	1.63	1.48
6	A	915	IPA	C3-C2	2.29	1.64	1.48
4	A	921	PCD	O5'-C5'	2.37	1.54	1.44
4	A	921	PCD	C2'-N2'	2.47	1.39	1.34
4	A	921	PCD	C2D-C1'	2.60	1.57	1.53
4	A	921	PCD	C4B-N1'	2.69	1.39	1.34
4	A	921	PCD	C3'-C4D	2.99	1.60	1.53
4	A	921	PCD	O4D-C1'	3.82	1.46	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	915	IPA	C1-C2	4.02	1.76	1.48
4	A	921	PCD	C10-C9'	4.44	1.58	1.52
4	A	921	PCD	C5-C4	4.56	1.52	1.41
4	A	921	PCD	C2'-N3'	4.96	1.44	1.35
4	A	921	PCD	C4A-N5'	5.22	1.48	1.38
4	A	921	PCD	C7-C6'	7.56	1.59	1.53

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	921	PCD	C5-C4-N4	-5.18	111.95	121.26
4	A	921	PCD	N3'-C2'-N1'	-4.70	117.83	125.45
4	A	921	PCD	C4B-N8'-C7	-3.27	117.27	123.67
4	A	921	PCD	N2'-C2'-N3'	-2.58	113.11	117.24
4	A	921	PCD	C8'-C7'-S7'	2.47	121.55	120.15
4	A	921	PCD	O9'-C7'-C6'	2.98	110.95	108.96
4	A	921	PCD	C2'-N1'-C4B	2.99	121.25	114.51
6	A	915	IPA	O2-C2-C3	3.27	132.62	110.40
4	A	921	PCD	N4-C4-N3	5.25	125.48	116.64
4	A	921	PCD	C4A-C4B-N8'	7.21	124.65	118.17
4	A	921	PCD	N2'-C2'-N1'	7.38	129.05	117.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	915	IPA	2	0
4	A	921	PCD	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 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.