



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2023 – 05:28 AM EDT

PDB ID : 2PNF
Title : Structure of Aquifex Aeolicus FabG 3-oxoacyl-(acyl-carrier protein) reductase
Authors : Mao, Q.; Umland, T.C.
Deposited on : 2007-04-24
Resolution : 1.80 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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

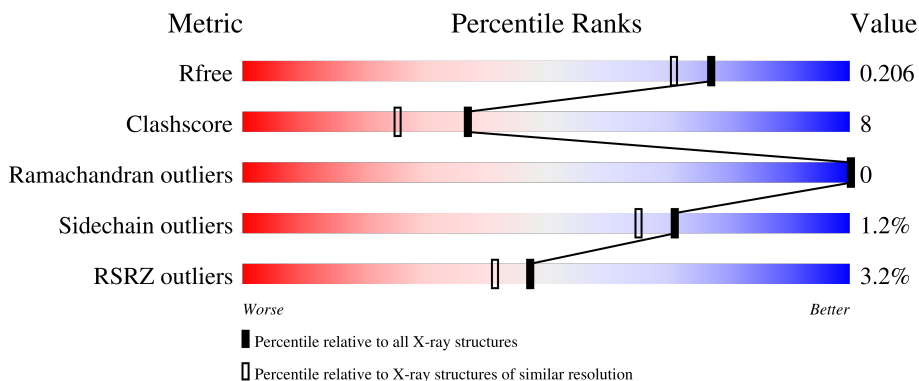
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

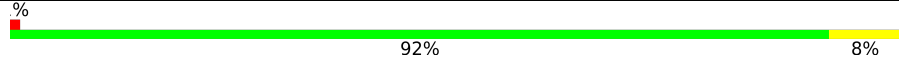
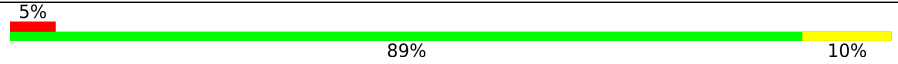
The reported resolution of this entry is 1.80 Å.

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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 $\leq 5\%$. 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	248	 92% 8%
1	B	248	 89% 10% 5% 5%

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
2	1PE	A	401	-	-	X	-
2	1PE	B	501	-	-	X	-

2 Entry composition [i](#)

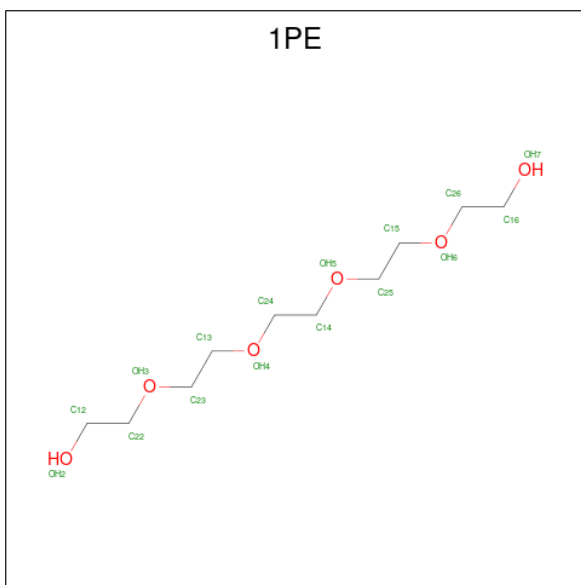
There are 4 unique types of molecules in this entry. The entry contains 4149 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 3-oxoacyl-[acyl-carrier-protein] reductase.

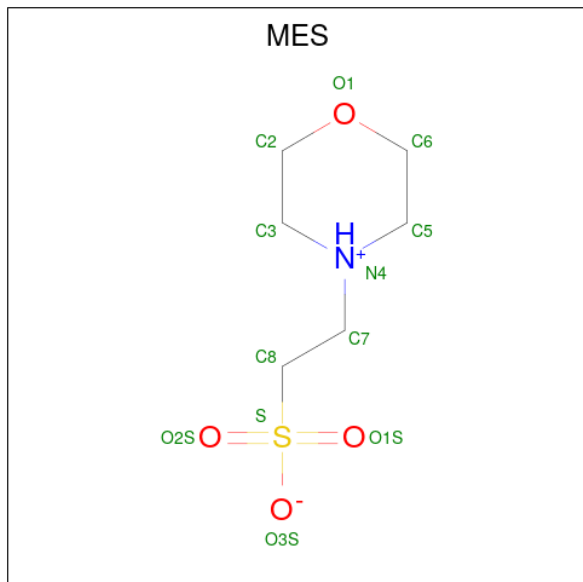
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	248	Total 1888	C 1199	N 322	O 360	S 7	0	0	0
1	B	248	Total 1888	C 1199	N 322	O 360	S 7	0	0	0

- Molecule 2 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	Total 16	C 10	O 6	0	0
2	A	1	Total 16	C 10	O 6	0	0
2	B	1	Total 16	C 10	O 6	0	0
2	B	1	Total 16	C 10	O 6	0	0

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	B	1	12	6	1	4	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	157	Total	O	0	0
			157	157		
4	B	140	Total	O	0	0
			140	140		

3 Residue-property plots [i](#)


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: 3-oxoacyl-[acyl-carrier-protein] reductase

Chain A:  92% 8%



- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] reductase

Chain B:  5% 89% 10%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	105.60Å 63.60Å 73.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.80 – 1.80 36.80 – 1.80	Depositor EDS
% Data completeness (in resolution range)	93.7 (36.80-1.80) 93.6 (36.80-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.06 (at 1.79Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.176 , 0.214 0.169 , 0.206	Depositor DCC
R_{free} test set	2294 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	22.2	Xtrriage
Anisotropy	0.678	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 58.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4149	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 1PE, MES

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	0.69	0/1911	0.77	0/2577
1	B	0.69	0/1911	0.80	0/2577
All	All	0.69	0/3822	0.79	0/5154

There are no bond length outliers.

There are no bond angle outliers.

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	1888	0	1957	25	0
1	B	1888	0	1957	35	0
2	A	32	0	44	12	0
2	B	32	0	44	16	0
3	B	12	0	13	2	0
4	A	157	0	0	6	0
4	B	140	0	0	3	0
All	All	4149	0	4015	60	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 8.

All (60) 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:B:8:LYS:HZ2	2:B:501:1PE:H242	1.28	0.96
1:B:206:TYR:CE2	2:B:601:1PE:H131	2.17	0.80
1:B:205:LYS:O	1:B:208:GLU:HB3	1.85	0.76
1:B:8:LYS:NZ	2:B:501:1PE:H242	2.01	0.75
1:B:8:LYS:HD3	2:B:501:1PE:H132	1.72	0.71
1:A:195:THR:HG23	2:A:701:1PE:H162	1.73	0.69
2:A:701:1PE:H252	4:A:1188:HOH:O	1.94	0.67
1:B:128:LEU:HD21	1:B:139:ILE:HD11	1.79	0.64
1:B:8:LYS:NZ	2:B:501:1PE:H251	2.13	0.62
1:A:8:LYS:NZ	2:A:401:1PE:H141	2.15	0.61
1:B:199:SER:O	1:B:203:LYS:HG3	2.01	0.60
1:A:195:THR:HG23	2:A:701:1PE:C16	2.32	0.58
1:A:169:LYS:NZ	4:A:1261:HOH:O	2.30	0.58
1:B:8:LYS:CE	2:B:501:1PE:H251	2.34	0.57
1:B:8:LYS:CE	2:B:501:1PE:H242	2.36	0.56
1:B:244:ASN:HB2	1:B:247:MET:HG2	1.90	0.54
4:A:1291:HOH:O	1:B:106:LEU:HD21	2.07	0.54
1:B:4:LYS:HD3	4:B:1282:HOH:O	2.08	0.53
1:B:206:TYR:CD2	2:B:601:1PE:H131	2.43	0.53
1:A:43:ARG:HG3	1:A:43:ARG:NH1	2.22	0.52
1:A:4:LYS:O	2:A:401:1PE:H162	2.09	0.52
1:A:114:LYS:NZ	4:A:1291:HOH:O	2.42	0.52
1:B:199:SER:HB2	1:B:202:ILE:H	1.75	0.52
1:A:102:LEU:HD11	1:B:132:ILE:CD1	2.40	0.51
1:A:232:LEU:HD12	1:A:232:LEU:N	2.25	0.51
1:B:201:GLU:HG2	4:B:1297:HOH:O	2.10	0.50
1:A:136:TRP:CD1	2:A:401:1PE:H242	2.46	0.50
1:A:169:LYS:CE	4:A:1261:HOH:O	2.60	0.50
1:A:102:LEU:HD21	1:B:132:ILE:HD12	1.93	0.50
1:B:8:LYS:NZ	2:B:501:1PE:C25	2.76	0.49
1:A:8:LYS:HZ1	2:A:401:1PE:H141	1.77	0.49
1:A:43:ARG:HG3	1:A:43:ARG:HH11	1.78	0.48
1:A:174:GLU:HG2	1:B:152:VAL:HG13	1.94	0.48
1:B:8:LYS:HZ2	2:B:501:1PE:C25	2.28	0.47
1:B:8:LYS:HE3	2:B:501:1PE:H251	1.96	0.46
1:A:8:LYS:HZ1	2:A:401:1PE:C14	2.28	0.46
1:B:102:LEU:O	3:B:801:MES:H82	2.15	0.46
1:A:41:GLY:CA	1:A:63:GLU:HB2	2.46	0.45
2:B:601:1PE:H232	2:B:601:1PE:H122	1.37	0.45
1:A:128:LEU:HD21	1:A:139:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:MET:HA	4:A:1264:HOH:O	2.18	0.44
1:A:102:LEU:HD11	1:B:132:ILE:HD11	1.99	0.44
1:B:195:THR:HG23	2:B:601:1PE:OH2	2.18	0.44
1:A:132:ILE:HD13	1:B:102:LEU:HD11	2.00	0.43
1:A:8:LYS:CE	2:A:401:1PE:H141	2.48	0.43
2:A:701:1PE:H252	2:A:701:1PE:H261	1.48	0.43
1:B:8:LYS:HZ2	2:B:501:1PE:H251	1.81	0.43
1:B:199:SER:C	1:B:201:GLU:N	2.71	0.43
1:B:199:SER:HB2	1:B:201:GLU:HB3	2.01	0.43
1:A:202:ILE:HD13	1:A:205:LYS:NZ	2.34	0.42
1:A:161:LYS:HD3	1:A:161:LYS:HA	1.86	0.42
1:B:195:THR:CG2	2:B:601:1PE:OH2	2.68	0.42
2:A:401:1PE:H141	2:A:401:1PE:H132	1.92	0.42
3:B:801:MES:H81	3:B:801:MES:H31	1.85	0.41
1:A:8:LYS:NZ	2:A:401:1PE:C14	2.83	0.41
1:B:144:SER:HB3	1:B:161:LYS:HG3	2.01	0.41
1:B:8:LYS:HE3	2:B:501:1PE:H242	2.03	0.41
1:B:96:THR:HG22	1:B:157:TYR:CD1	2.56	0.41
1:B:143:SER:HA	1:B:161:LYS:HD2	2.02	0.41
1:B:130:LYS:N	4:B:1275:HOH:O	2.53	0.41

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	246/248 (99%)	240 (98%)	6 (2%)	0	100	100
1	B	246/248 (99%)	241 (98%)	5 (2%)	0	100	100
All	All	492/496 (99%)	481 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	205/205 (100%)	204 (100%)	1 (0%)	88	87
1	B	205/205 (100%)	201 (98%)	4 (2%)	55	44
All	All	410/410 (100%)	405 (99%)	5 (1%)	71	65

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	GLU
1	B	83	VAL
1	B	193	ASP
1	B	197	VAL
1	B	208	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
2	1PE	B	601	1	15,15,15	0.54	0	14,14,14	0.88	0
2	1PE	A	401	-	15,15,15	0.53	0	14,14,14	0.75	0
3	MES	B	801	-	12,12,12	1.50	1 (8%)	14,16,16	3.00	6 (42%)
2	1PE	B	501	-	15,15,15	0.53	0	14,14,14	1.18	2 (14%)
2	1PE	A	701	-	15,15,15	0.56	0	14,14,14	0.59	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	1PE	B	601	1	-	6/13/13/13	-
2	1PE	A	401	-	-	7/13/13/13	-
3	MES	B	801	-	-	3/6/14/14	0/1/1/1
2	1PE	B	501	-	-	4/13/13/13	-
2	1PE	A	701	-	-	9/13/13/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	801	MES	C8-S	4.18	1.83	1.77

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	801	MES	O3S-S-C8	7.39	117.72	105.77
3	B	801	MES	O3S-S-O1S	-4.31	100.74	111.27
3	B	801	MES	O2S-S-O1S	-3.65	101.31	113.95
3	B	801	MES	O1S-S-C8	-3.63	102.55	106.92
3	B	801	MES	O3S-S-O2S	3.44	119.69	111.27
3	B	801	MES	O2S-S-C8	3.32	110.91	106.92
2	B	501	1PE	OH6-C15-C25	-2.18	100.58	110.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	1PE	OH6-C26-C16	-2.03	101.14	110.07

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	801	MES	C8-C7-N4-C3
2	B	601	1PE	C12-C22-OH3-C23
2	A	701	1PE	C25-C15-OH6-C26
2	B	601	1PE	OH5-C14-C24-OH4
2	A	701	1PE	OH6-C15-C25-OH5
2	A	401	1PE	OH4-C13-C23-OH3
2	B	501	1PE	OH7-C16-C26-OH6
2	A	701	1PE	OH7-C16-C26-OH6
2	B	601	1PE	OH2-C12-C22-OH3
2	A	701	1PE	OH2-C12-C22-OH3
2	B	501	1PE	C23-C13-OH4-C24
2	A	701	1PE	C15-C25-OH5-C14
2	B	501	1PE	C24-C14-OH5-C25
2	B	601	1PE	C15-C25-OH5-C14
2	A	701	1PE	C16-C26-OH6-C15
2	A	401	1PE	OH5-C14-C24-OH4
3	B	801	MES	C7-C8-S-O3S
2	A	701	1PE	C13-C23-OH3-C22
2	B	601	1PE	C23-C13-OH4-C24
2	A	701	1PE	C12-C22-OH3-C23
2	A	401	1PE	C15-C25-OH5-C14
2	A	401	1PE	C24-C14-OH5-C25
3	B	801	MES	C8-C7-N4-C5
2	A	401	1PE	C25-C15-OH6-C26
2	A	401	1PE	C14-C24-OH4-C13
2	A	401	1PE	C23-C13-OH4-C24
2	B	501	1PE	OH6-C15-C25-OH5
2	B	601	1PE	OH4-C13-C23-OH3
2	A	701	1PE	OH4-C13-C23-OH3

There are no ring outliers.

5 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	1PE	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	1PE	8	0
3	B	801	MES	2	0
2	B	501	1PE	11	0
2	A	701	1PE	4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	248/248 (100%)	-0.32	3 (1%) 79 76	16, 26, 48, 59	0
1	B	248/248 (100%)	-0.07	13 (5%) 27 22	17, 26, 51, 63	0
All	All	496/496 (100%)	-0.19	16 (3%) 47 41	16, 26, 49, 63	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	197	VAL	10.9
1	B	204	GLN	6.2
1	B	199	SER	5.2
1	B	196	ALA	5.1
1	A	202	ILE	4.4
1	B	202	ILE	4.2
1	B	206	TYR	4.2
1	B	198	LEU	4.1
1	B	201	GLU	3.7
1	B	200	GLU	3.4
1	A	205	LYS	3.3
1	B	193	ASP	3.0
1	B	194	MET	3.0
1	B	203	LYS	3.0
1	B	195	THR	2.4
1	A	201	GLU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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	1PE	A	701	16/16	0.74	0.20	47,57,60,64	0
2	1PE	A	401	16/16	0.83	0.16	32,41,47,49	0
2	1PE	B	601	16/16	0.84	0.24	49,56,62,62	0
2	1PE	B	501	16/16	0.88	0.16	34,45,53,53	0
3	MES	B	801	12/12	0.92	0.19	44,50,57,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.