



wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 08:08 PM GMT

PDB ID : 4BC9
Title : MAMMALIAN ALKYLDIHYDROXYACETONEPHOSPHATESYN-
THASE: WILD-TYPE, ADDUCT WITH CYANOETHYL
Authors : Nenci, S.; Piano, V.; Rosati, S.; Aliverti, A.; Pandini, V.; Fraaije, M.W.; Heck,
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Deposited on : 2012-10-01
Resolution : 2.41 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

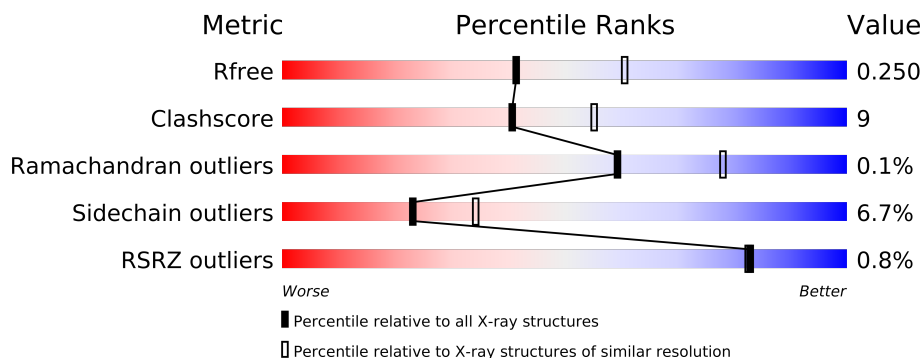
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.41 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}	66092	2496 (2.44-2.40)
Clashscore	79885	3124 (2.44-2.40)
Ramachandran outliers	78287	3067 (2.44-2.40)
Sidechain outliers	78261	3068 (2.44-2.40)
RSRZ outliers	66119	2499 (2.44-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	658	
1	B	658	
1	C	658	
1	D	658	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	CNV	B	998	-	X

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 17839 atoms, of which 0 are hydrogen and 0 are deuterium.

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 ALKYLDIHYDROXYACETONEPHOSPHATESYNTHASE, PEROXISOMAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	555	Total	C	N	O	S	0	1	0
			4365	2773	754	813	25			
1	B	542	Total	C	N	O	S	0	0	0
			4259	2705	737	793	24			
1	C	552	Total	C	N	O	S	0	1	0
			4331	2745	750	812	24			
1	D	550	Total	C	N	O	S	0	1	0
			4321	2739	752	806	24			

- Molecule 2 is PROPANENITRILE (three-letter code: CNV) (formula: C₃H₅N).



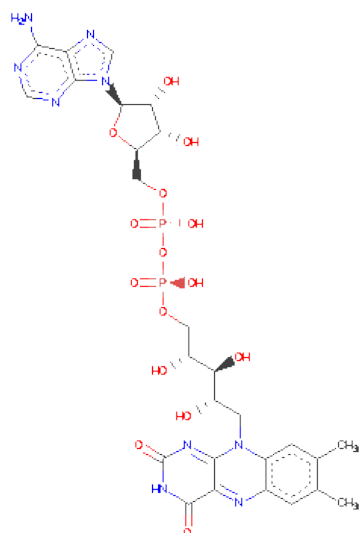
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			4	3	1		
2	B	1	Total	C	N	0	0
			4	3	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	N	0	0
			4	3	1		
2	D	1	Total	C	N	0	0
			4	3	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

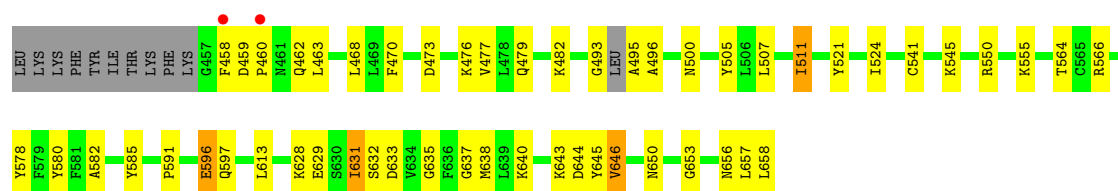
- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

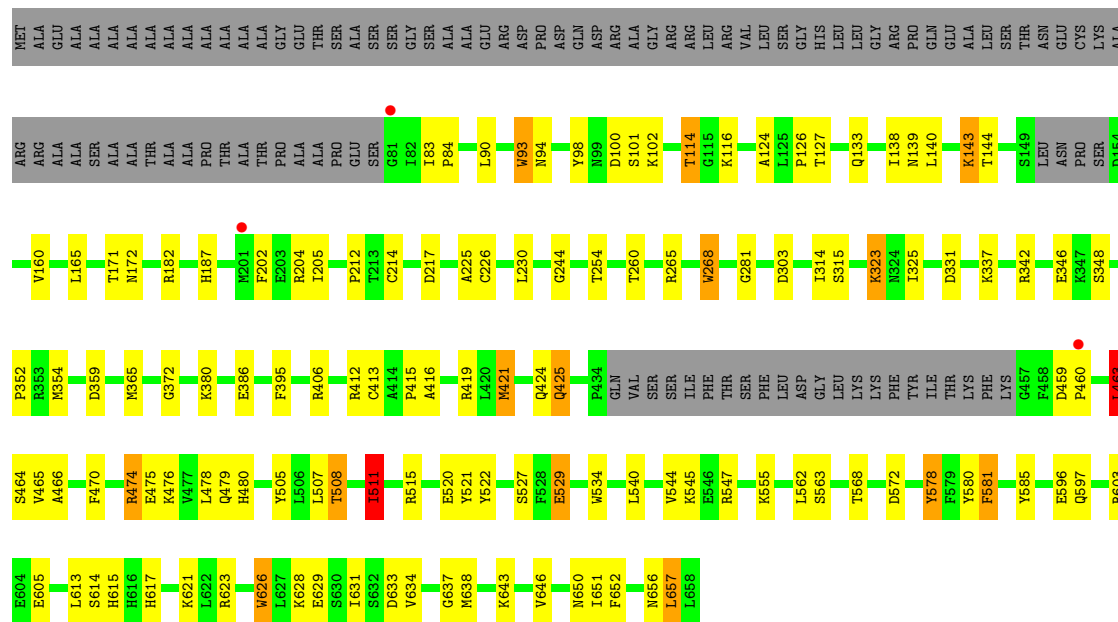
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	90	Total	O	0	0
			90	90		
5	B	73	Total	O	0	0
			73	73		
5	C	91	Total	O	0	0
			91	91		
5	D	66	Total	O	0	0
			66	66		



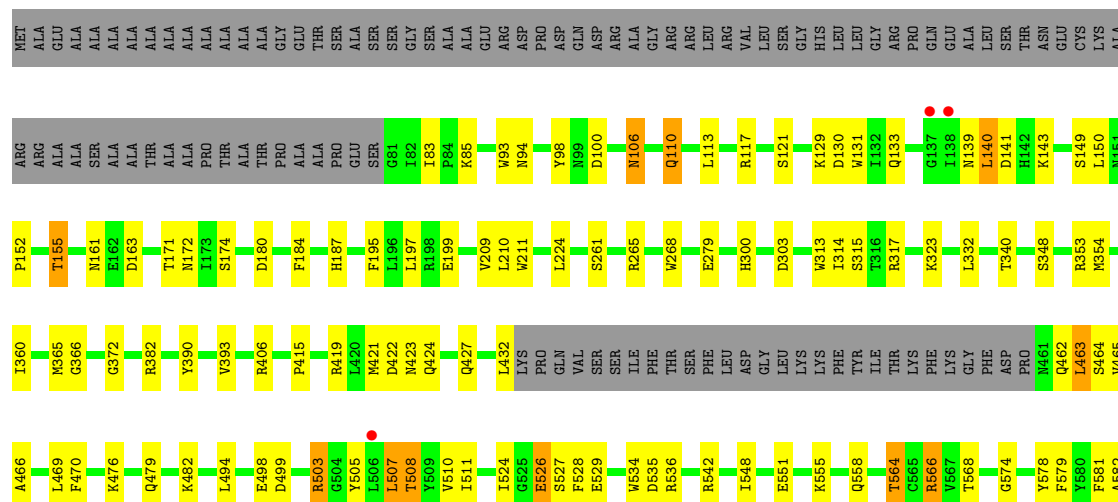
• Molecule 1: ALKYLDIHYDROXYACETONEPHOSPHATESYNTHASE, PEROXISOMAL

Chain C:



• Molecule 1: ALKYLDIHYDROXYACETONEPHOSPHATESYNTHASE, PEROXISOMAL

Chain D:



F583	N584	S589	L592	Q597	R603	L613	Y619	G620	K621	K624	Q625	K626	L627	K628	E629	S630	I631	S632	D633	V634	G635	F636	G637	K638	L639	K640	S641	Y642	K643	D644	Y645	Y646	N650	L651	F652	G653	L657	L658
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.91Å 98.62Å 106.28Å 90.92° 89.84° 95.66°	Depositor
Resolution (Å)	54.06 – 2.41 54.00 – 2.41	Depositor EDS
% Data completeness (in resolution range)	97.6 (54.06-2.41) 97.7 (54.00-2.41)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.7.0027	Depositor
R, R_{free}	0.186 , 0.248 0.187 , 0.250	Depositor DCC
R_{free} test set	1014 reflections (1.10%)	DCC
Wilson B-factor (Å ²)	31.1	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 18.7	EDS
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 92832 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17839	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CNV, SO4, FAD

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	0.73	2/4465 (0.0%)	0.82	2/6038 (0.0%)
1	B	0.75	5/4354 (0.1%)	0.82	2/5888 (0.0%)
1	C	0.73	4/4430 (0.1%)	0.82	4/5993 (0.1%)
1	D	0.73	6/4420 (0.1%)	0.79	1/5981 (0.0%)
All	All	0.74	17/17669 (0.1%)	0.81	9/23900 (0.0%)

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	626	TRP	CD2-CE2	7.13	1.50	1.41
1	B	268	TRP	CD2-CE2	6.93	1.49	1.41
1	B	313	TRP	CD2-CE2	6.31	1.49	1.41
1	B	96	TRP	CD2-CE2	6.29	1.48	1.41
1	C	534	TRP	CD2-CE2	6.18	1.48	1.41

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	603	ARG	NE-CZ-NH2	-7.01	116.79	120.30
1	C	623	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	C	463	LEU	CA-CB-CG	6.47	130.19	115.30
1	B	317	ARG	NE-CZ-NH2	-5.33	117.64	120.30
1	D	631	ILE	N-CA-C	-5.23	96.89	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4365	0	4289	85	0
1	B	4259	0	4174	84	0
1	C	4331	0	4236	89	0
1	D	4321	0	4239	81	0
2	A	4	0	3	0	0
2	B	4	0	3	2	0
2	C	4	0	3	5	0
2	D	4	0	3	1	0
3	A	53	0	31	1	0
3	B	53	0	31	2	0
3	C	53	0	31	0	0
3	D	53	0	31	0	0
4	A	5	0	0	1	0
4	B	5	0	0	0	0
4	D	5	0	0	0	0
5	A	90	0	0	5	0
5	B	73	0	0	3	0
5	C	91	0	0	3	0
5	D	66	0	0	0	0
All	All	17839	0	17074	322	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

The worst 5 of 322 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:615:HIS:HD2	1:A:616:HIS:CD2	1.77	1.03
1:D:503:ARG:HH11	1:D:503:ARG:HG3	1.23	1.01
1:A:615:HIS:CD2	1:A:616:HIS:HD2	1.82	0.97
1:C:144:THR:HG22	1:C:520:GLU:HA	1.48	0.94
1:C:505:TYR:O	1:C:508:THR:HG23	1.68	0.93

There are no symmetry-related clashes.

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	550/658 (84%)	527 (96%)	23 (4%)	0	100	100
1	B	534/658 (81%)	509 (95%)	24 (4%)	1 (0%)	56	74
1	C	547/658 (83%)	527 (96%)	19 (4%)	1 (0%)	56	74
1	D	547/658 (83%)	529 (97%)	17 (3%)	1 (0%)	56	74
All	All	2178/2632 (83%)	2092 (96%)	83 (4%)	3 (0%)	59	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	558	GLN
1	B	460	PRO
1	C	511	ILE

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	469/545 (86%)	439 (94%)	30 (6%)	25	37
1	B	456/545 (84%)	431 (94%)	25 (6%)	30	45
1	C	464/545 (85%)	435 (94%)	29 (6%)	25	38
1	D	463/545 (85%)	423 (91%)	40 (9%)	15	22
All	All	1852/2180 (85%)	1728 (93%)	124 (7%)	23	34

5 of 124 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	114	THR

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Mol	Chain	Res	Type
1	C	474	ARG
1	D	566	ARG
1	C	116	LYS
1	C	354	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	362	HIS
1	B	656	ASN
1	D	479	GLN
1	B	597	GLN
1	C	139	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

11 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
4	SO4	A	1659	-	4,4,4	0.63	0	6,6,6	0.44	0
2	CNV	A	998	3	3,3,3	0.68	0	2,2,2	0.54	0
3	FAD	A	999	2	58,58,58	1.74	10 (17%)	85,89,89	2.11	19 (22%)
4	SO4	B	1659	-	4,4,4	0.87	0	6,6,6	0.43	0
2	CNV	B	998	3	3,3,3	1.45	1 (33%)	2,2,2	0.53	0
3	FAD	B	999	2	58,58,58	1.81	8 (13%)	85,89,89	1.96	17 (20%)
2	CNV	C	998	3	3,3,3	1.60	1 (33%)	2,2,2	0.50	0
3	FAD	C	999	2	58,58,58	1.51	9 (15%)	85,89,89	2.18	22 (25%)
4	SO4	D	1659	-	4,4,4	0.94	0	6,6,6	0.30	0
2	CNV	D	998	3	3,3,3	0.45	0	2,2,2	0.65	0
3	FAD	D	999	2	58,58,58	1.68	11 (18%)	85,89,89	2.04	16 (18%)

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
4	SO4	A	1659	-	-	0/0/0/0	0/0/0/0
2	CNV	A	998	3	-	0/1/1/1	0/0/0/0
3	FAD	A	999	2	-	0/34/50/50	0/1/6/6
4	SO4	B	1659	-	-	0/0/0/0	0/0/0/0
2	CNV	B	998	3	-	0/1/1/1	0/0/0/0
3	FAD	B	999	2	-	0/34/50/50	0/1/6/6
2	CNV	C	998	3	-	0/1/1/1	0/0/0/0
3	FAD	C	999	2	-	0/34/50/50	0/1/6/6
4	SO4	D	1659	-	-	0/0/0/0	0/0/0/0
2	CNV	D	998	3	-	0/1/1/1	0/0/0/0
3	FAD	D	999	2	-	0/34/50/50	0/1/6/6

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	999	FAD	C5X-N5	7.30	1.46	1.35
3	A	999	FAD	C5X-N5	6.14	1.44	1.35
3	D	999	FAD	C5X-N5	5.28	1.43	1.35
3	B	999	FAD	C4-C4X	5.05	1.49	1.41
3	B	999	FAD	C4X-C10	4.61	1.48	1.40

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	999	FAD	C2-N1-C10	8.47	123.52	114.98
3	D	999	FAD	C2-N1-C10	8.35	123.40	114.98
3	C	999	FAD	O4B-C1B-N9A	-8.02	100.98	108.44
3	A	999	FAD	C2-N1-C10	7.91	122.95	114.98
3	D	999	FAD	N3A-C2A-N1A	-7.29	122.61	128.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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

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	555/658 (84%)	-0.34	4 (0%) 84 84	17, 30, 58, 89	0
1	B	542/658 (82%)	-0.35	7 (1%) 74 73	15, 31, 60, 91	0
1	C	552/658 (83%)	-0.42	3 (0%) 88 88	16, 31, 59, 84	0
1	D	550/658 (83%)	-0.32	3 (0%) 88 88	16, 34, 61, 79	0
All	All	2199/2632 (83%)	-0.36	17 (0%) 83 82	15, 31, 60, 91	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	460	PRO	3.7
1	B	458	PHE	3.5
1	B	81	GLY	3.2
1	C	201	MET	2.6
1	C	81	GLY	2.5

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CNV	B	998	4/4	0.13	2.42	28,28,31,32	0
2	CNV	D	998	4/4	0.14	1.26	38,40,44,45	0
2	CNV	C	998	4/4	0.12	0.33	23,24,27,31	0
2	CNV	A	998	4/4	0.12	0.25	24,28,33,34	0
4	SO4	A	1659	5/5	0.14	0.19	50,51,62,63	0
4	SO4	B	1659	5/5	0.17	-0.04	53,57,61,63	0
3	FAD	A	999	53/53	0.11	-0.10	14,19,23,25	0
3	FAD	D	999	53/53	0.12	-0.11	15,22,26,27	0
3	FAD	C	999	53/53	0.11	-0.29	14,17,20,22	0
3	FAD	B	999	53/53	0.10	-0.33	16,21,27,30	0
4	SO4	D	1659	5/5	0.10	-0.85	40,46,53,54	0

6.5 Other polymers ⓘ

There are no such residues in this entry.