



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 04:46 am BST

PDB ID : 3T4C
Title : Crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from Burkholderia ambifaria
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2011-07-25
Resolution : 1.95 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

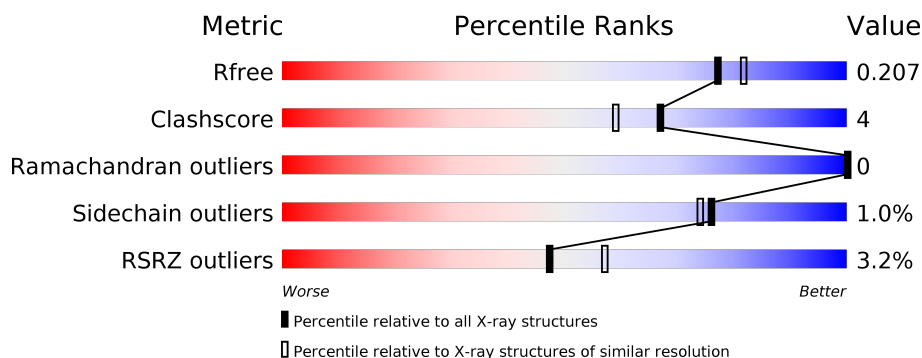
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 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	288	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>11%</div> <div>8%</div> </div> </div>
1	B	288	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>8%</div> <div>9%</div> </div> </div>
1	C	288	<div> <div>3%</div> <div> <div></div> <div>83%</div> <div>7%</div> <div>9%</div> </div> </div>
1	D	288	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>7%</div> <div>10%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8565 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 2-dehydro-3-deoxyphosphooctonate aldolase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	8	0
			2033	1286	350	383	14			
1	B	262	Total	C	N	O	S	0	4	0
			2004	1269	345	377	13			
1	C	262	Total	C	N	O	S	0	4	0
			1998	1260	347	377	14			
1	D	259	Total	C	N	O	S	0	5	0
			1969	1245	337	373	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	EXPRESSION TAG	UNP B1YT10
A	-2	PRO	-	EXPRESSION TAG	UNP B1YT10
A	-1	GLY	-	EXPRESSION TAG	UNP B1YT10
A	0	SER	-	EXPRESSION TAG	UNP B1YT10
B	-3	GLY	-	EXPRESSION TAG	UNP B1YT10
B	-2	PRO	-	EXPRESSION TAG	UNP B1YT10
B	-1	GLY	-	EXPRESSION TAG	UNP B1YT10
B	0	SER	-	EXPRESSION TAG	UNP B1YT10
C	-3	GLY	-	EXPRESSION TAG	UNP B1YT10
C	-2	PRO	-	EXPRESSION TAG	UNP B1YT10
C	-1	GLY	-	EXPRESSION TAG	UNP B1YT10
C	0	SER	-	EXPRESSION TAG	UNP B1YT10
D	-3	GLY	-	EXPRESSION TAG	UNP B1YT10
D	-2	PRO	-	EXPRESSION TAG	UNP B1YT10
D	-1	GLY	-	EXPRESSION TAG	UNP B1YT10
D	0	SER	-	EXPRESSION TAG	UNP B1YT10

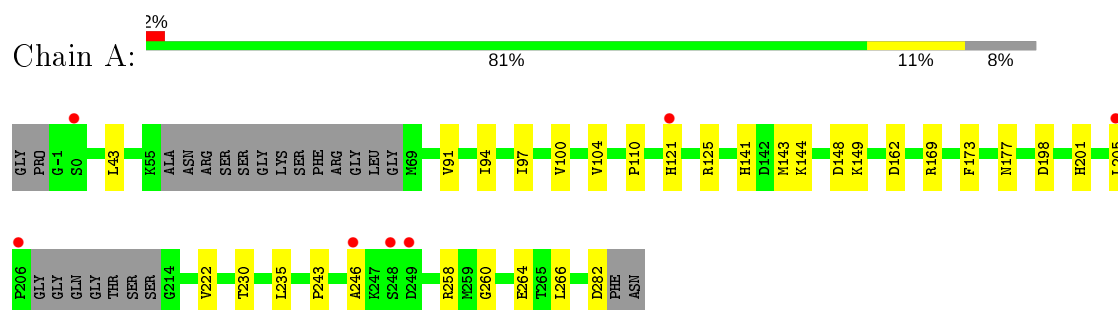
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	149	Total 149	O 149	0	0
2	B	140	Total 140	O 140	0	0
2	C	160	Total 160	O 160	0	0
2	D	112	Total 112	O 112	0	0

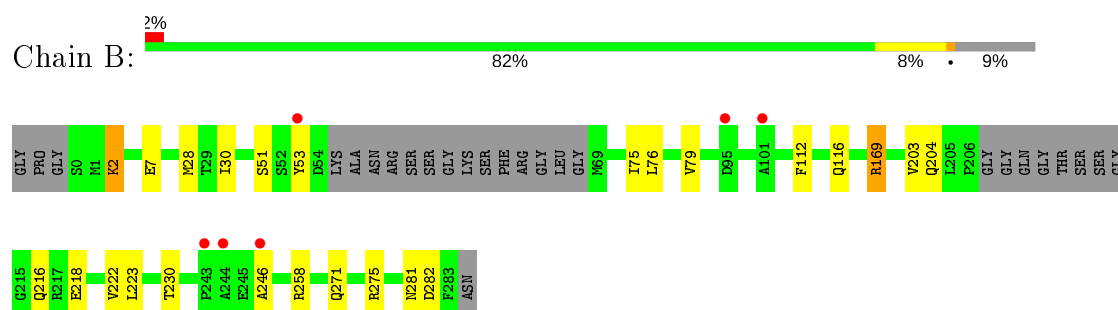
3 Residue-property plots [i](#)

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.

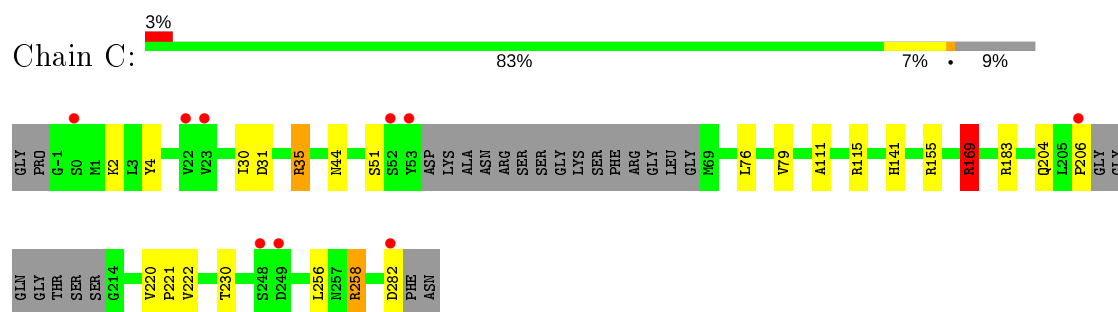
- Molecule 1: 2-dehydro-3-deoxyphosphooctonate aldolase 1



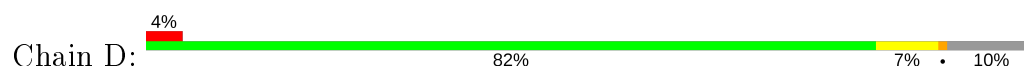
- Molecule 1: 2-dehydro-3-deoxyphosphooctonate aldolase 1

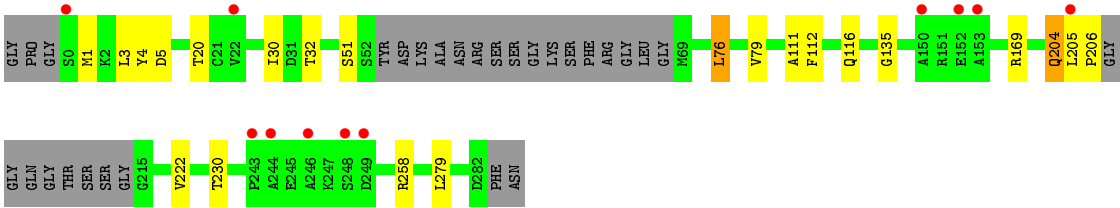


- Molecule 1: 2-dehydro-3-deoxyphosphooctonate aldolase 1



- Molecule 1: 2-dehydro-3-deoxyphosphooctonate aldolase 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.13Å 129.50Å 169.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.33 – 1.95 44.33 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.6 (44.33-1.95) 98.6 (44.33-1.95)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 1.95Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.170 , 0.203 0.174 , 0.207	Depositor DCC
R_{free} test set	3951 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	24.6	Xtriage
Anisotropy	0.202	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8565	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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](#)

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	0.71	0/2092	0.79	2/2835 (0.1%)
1	B	0.68	0/2052	0.76	0/2782
1	C	0.75	0/2044	0.84	7/2768 (0.3%)
1	D	0.64	0/2018	0.75	0/2738
All	All	0.70	0/8206	0.79	9/11123 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	169	ARG	NE-CZ-NH1	-6.71	116.94	120.30
1	A	162	ASP	CB-CG-OD1	6.17	123.85	118.30
1	C	155	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	C	258	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	C	258	ARG	NE-CZ-NH1	5.65	123.12	120.30
1	C	115	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	C	35	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	C	183	ARG	NE-CZ-NH1	5.05	122.82	120.30
1	A	143	MET	CG-SD-CE	-5.03	92.15	100.20

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	2033	0	2017	20	0
1	B	2004	0	1979	22	0
1	C	1998	0	1987	16	0
1	D	1969	0	1943	17	0
2	A	149	0	0	3	0
2	B	140	0	0	3	0
2	C	160	0	0	1	0
2	D	112	0	0	1	0
All	All	8565	0	7926	62	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 4.

All (62) 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:205:LEU:HD23	2:A:459:HOH:O	1.91	0.69
1:B:116:GLN:OE1	1:D:112:PHE:HZ	1.76	0.68
1:B:116:GLN:OE1	1:D:112:PHE:CZ	2.50	0.65
1:A:125:ARG:HD3	2:A:457:HOH:O	1.98	0.64
1:D:205:LEU:HD23	2:D:522:HOH:O	1.99	0.63
1:D:111:ALA:HB1	1:D:135:GLY:HA2	1.79	0.62
1:B:281:ASN:ND2	2:B:339:HOH:O	2.34	0.60
1:A:258[B]:ARG:HB3	1:D:279:LEU:HD11	1.84	0.59
1:A:222:VAL:HG13	1:D:230:THR:HG23	1.85	0.59
1:A:230:THR:HG23	1:D:222:VAL:HG13	1.86	0.58
1:B:218[B]:GLU:H	1:B:218[B]:GLU:CD	2.10	0.55
1:B:282:ASP:OD2	1:C:258:ARG:NH2	2.40	0.55
1:B:112:PHE:HD2	2:B:521:HOH:O	1.90	0.54
1:B:169:ARG:HH12	1:B:204:GLN:HE22	1.54	0.54
1:C:204:GLN:O	1:C:206:PRO:HD3	2.08	0.54
1:C:169:ARG:NH1	1:C:204:GLN:HE21	2.06	0.54
1:B:30:ILE:HD13	1:B:79:VAL:HG22	1.90	0.52
1:C:169:ARG:NH1	1:C:204:GLN:NE2	2.57	0.52
1:C:30:ILE:HD13	1:C:79:VAL:HG22	1.90	0.52
1:B:230:THR:HG23	1:C:222:VAL:HG13	1.92	0.52
1:B:222:VAL:HG13	1:C:230:THR:HG23	1.92	0.51
1:B:2:LYS:HE2	1:B:7:GLU:HG2	1.92	0.51
1:C:51:SER:HB2	1:C:76:LEU:HD11	1.93	0.50
1:B:271:GLN:O	1:B:275:ARG:HG3	2.11	0.50
1:A:243:PRO:HA	1:A:246:ALA:HB3	1.93	0.50
1:A:43:LEU:HD22	1:A:264[B]:GLU:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:GLN:HA	1:B:218[B]:GLU:OE1	2.13	0.49
1:A:91:VAL:O	1:A:110:PRO:HD3	2.14	0.48
1:A:121:HIS:NE2	1:A:149:LYS:HB3	2.28	0.47
1:A:94:ILE:HA	1:A:97:ILE:HD12	1.95	0.47
1:C:31:ASP:HB3	1:C:35:ARG:NH2	2.28	0.47
1:B:112:PHE:HZ	1:D:116:GLN:OE1	1.97	0.47
1:D:51:SER:HB3	1:D:76:LEU:HG	1.97	0.47
1:A:258[A]:ARG:HB3	1:D:279:LEU:HD11	1.97	0.46
1:A:260:GLY:O	1:A:264[B]:GLU:HG3	2.15	0.46
1:A:282:ASP:CB	1:D:258:ARG:HH22	2.28	0.46
1:B:169:ARG:NH1	1:B:204:GLN:HE22	2.14	0.45
1:D:204:GLN:O	1:D:206:PRO:HD3	2.17	0.45
1:A:144:LYS:NZ	1:A:148:ASP:OD2	2.46	0.45
1:C:220:VAL:HB	1:C:221:PRO:HD3	1.97	0.45
1:A:198:ASP:OD2	1:A:201:HIS:HD2	1.99	0.44
1:B:51:SER:HB2	1:B:76:LEU:HD11	1.99	0.44
1:C:169:ARG:HH12	1:C:204:GLN:NE2	2.16	0.44
1:A:235:LEU:CD2	1:A:266:LEU:HD13	2.48	0.44
1:B:28:MET:CE	1:B:28:MET:HA	2.48	0.44
1:B:53:TYR:OH	1:B:75:ILE:HG21	2.18	0.44
1:D:30:ILE:HD13	1:D:79:VAL:HG22	2.00	0.43
1:C:2:LYS:HE2	1:C:4:TYR:O	2.19	0.43
1:B:112:PHE:CZ	1:D:116:GLN:OE1	2.71	0.43
1:B:203:VAL:HG12	1:B:223:LEU:HD12	2.00	0.43
1:C:111:ALA:CB	1:C:169:ARG:HD2	2.49	0.43
1:C:35:ARG:HD2	1:C:256:LEU:HD21	2.01	0.43
1:A:100:VAL:O	1:A:104:VAL:HG22	2.19	0.42
1:C:141[B]:HIS:CD2	2:C:319:HOH:O	2.72	0.42
1:D:1:MET:CE	1:D:3:LEU:HD13	2.50	0.42
1:A:173:PHE:HD2	1:A:177[B]:ASN:HD22	1.68	0.41
1:B:258:ARG:NH2	1:C:282:ASP:O	2.51	0.41
1:D:20:THR:CG2	1:D:32:THR:HG21	2.51	0.41
1:A:141[B]:HIS:HD2	2:A:305:HOH:O	2.02	0.41
1:D:4:TYR:CD2	1:D:5:ASP:HB2	2.57	0.40
1:B:246:ALA:HB3	2:B:557:HOH:O	2.21	0.40

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	266/288 (92%)	263 (99%)	3 (1%)	0	100	100
1	B	260/288 (90%)	255 (98%)	5 (2%)	0	100	100
1	C	260/288 (90%)	260 (100%)	0	0	100	100
1	D	258/288 (90%)	257 (100%)	1 (0%)	0	100	100
All	All	1044/1152 (91%)	1035 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	218/236 (92%)	217 (100%)	1 (0%)	88	88
1	B	214/236 (91%)	212 (99%)	2 (1%)	78	77
1	C	215/236 (91%)	213 (99%)	2 (1%)	78	77
1	D	211/236 (89%)	208 (99%)	3 (1%)	67	62
All	All	858/944 (91%)	850 (99%)	8 (1%)	76	77

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	169	ARG
1	B	2	LYS

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Mol	Chain	Res	Type
1	B	169	ARG
1	C	44	ASN
1	C	169	ARG
1	D	76	LEU
1	D	169	ARG
1	D	204	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	145	ASN
1	B	204	GLN
1	C	204	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 ⓘ

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	264/288 (91%)	0.08	7 (2%) 54 63	14, 25, 45, 63	0
1	B	262/288 (90%)	0.15	6 (2%) 60 69	14, 26, 47, 64	0
1	C	262/288 (90%)	0.04	9 (3%) 45 55	12, 22, 46, 62	0
1	D	259/288 (89%)	0.10	11 (4%) 36 45	15, 30, 50, 70	0
All	All	1047/1152 (90%)	0.09	33 (3%) 47 57	12, 26, 48, 70	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	205	LEU	5.1
1	D	246	ALA	4.6
1	D	244	ALA	4.5
1	B	53	TYR	4.3
1	A	248	SER	3.8
1	D	0	SER	3.8
1	D	243	PRO	3.6
1	A	246	ALA	3.6
1	C	23	VAL	3.3
1	D	205	LEU	2.9
1	D	248	SER	2.9
1	B	244	ALA	2.9
1	A	0	SER	2.8
1	C	249	ASP	2.8
1	D	153	ALA	2.7
1	C	0	SER	2.7
1	A	121	HIS	2.6
1	B	243	PRO	2.6
1	A	206	PRO	2.6
1	D	22	VAL	2.6
1	C	206	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	101	ALA	2.3
1	D	150	ALA	2.3
1	C	53	TYR	2.3
1	D	249	ASP	2.3
1	C	52	SER	2.3
1	C	248	SER	2.2
1	C	22	VAL	2.2
1	A	249	ASP	2.1
1	C	282	ASP	2.1
1	B	95	ASP	2.1
1	B	246	ALA	2.0
1	D	152	GLU	2.0

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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.