



Full wwPDB X-ray Structure Validation Report i

Jan 30, 2024 – 06:09 PM JST

PDB ID : 8I78
Title : Meso-Diaminopimelate dehydrogenase
Authors : Wei, S.; Wu, T.F.
Deposited on : 2023-01-31
Resolution : 2.64 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 i 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](#) ①) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
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)	:	2.36

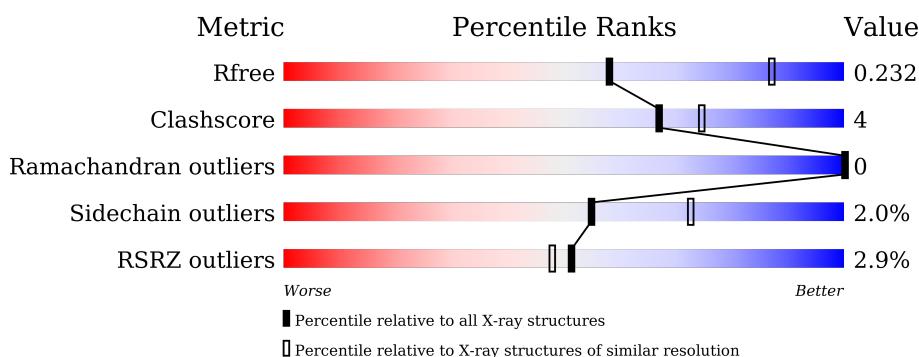
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

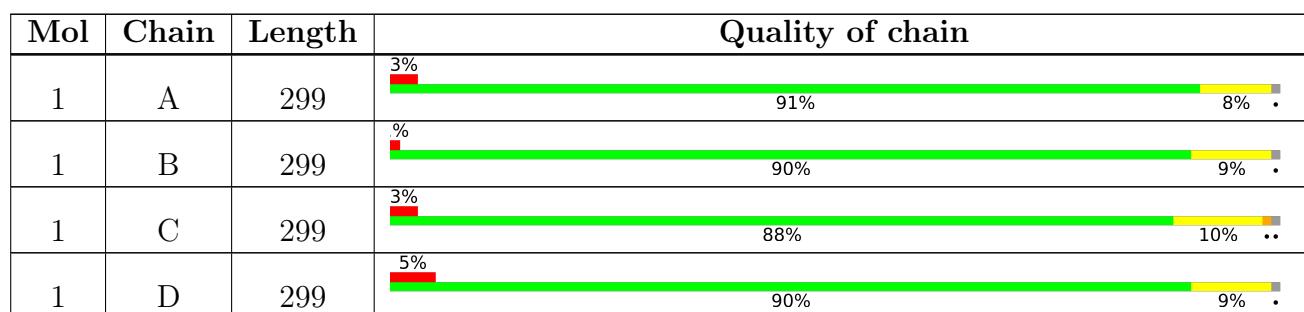
The reported resolution of this entry is 2.64 Å.

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	1426 (2.66-2.62)
Clashscore	141614	1472 (2.66-2.62)
Ramachandran outliers	138981	1446 (2.66-2.62)
Sidechain outliers	138945	1446 (2.66-2.62)
RSRZ outliers	127900	1408 (2.66-2.62)

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.



2 Entry composition [\(i\)](#)

There are 2 unique types of molecules in this entry. The entry contains 9445 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 Meso-diaminopimelate D-dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	297	Total 2245	C 1411	N 389	O 434	S 11	0	0	0
1	B	297	Total 2253	C 1416	N 392	O 434	S 11	0	1	0
1	C	297	Total 2245	C 1411	N 389	O 434	S 11	0	0	0
1	D	297	Total 2245	C 1411	N 389	O 434	S 11	0	0	0

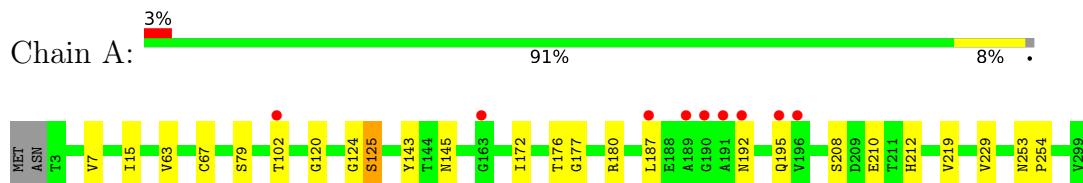
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	141	Total 141 O 141 141	0	0
2	B	119	Total 119 O 119 119	0	0
2	C	102	Total 102 O 102 102	0	0
2	D	95	Total 95 O 95 95	0	0

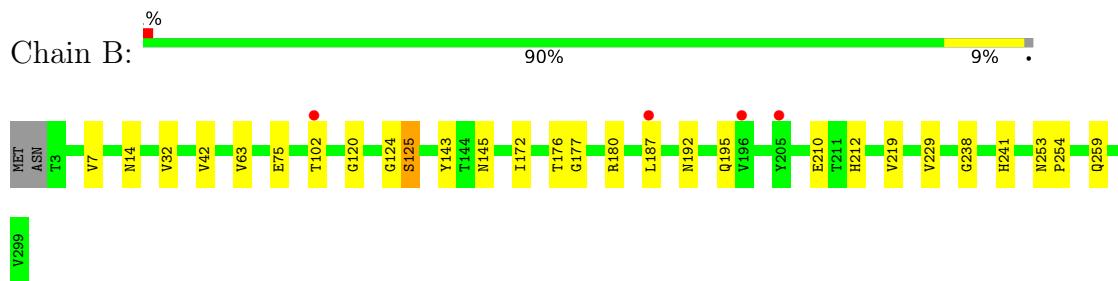
3 Residue-property plots

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.

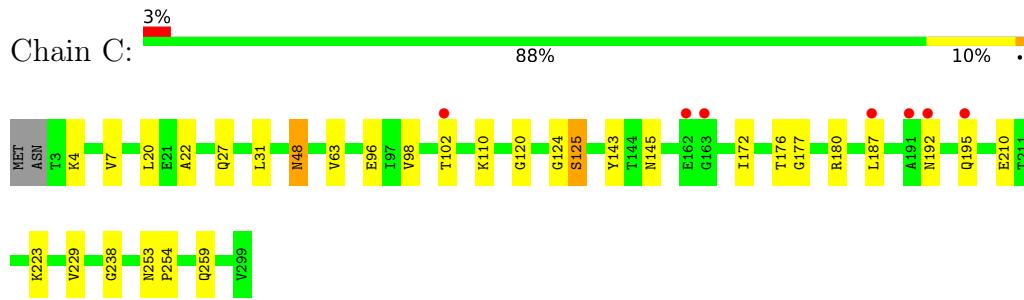
- Molecule 1: Meso-diaminopimelate D-dehydrogenase



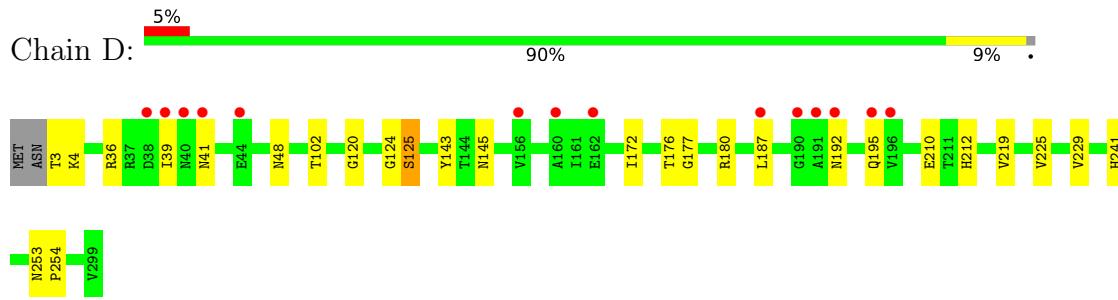
- Molecule 1: Meso-diaminopimelate D-dehydrogenase



- Molecule 1: Meso-diaminopimelate D-dehydrogenase



- Molecule 1: Meso-diaminopimelate D-dehydrogenase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	211.91Å 211.91Å 245.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.52 – 2.64 47.48 – 2.64	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.52-2.64) 100.0 (47.48-2.64)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ ¹	2.28 (at 2.65Å)	Xtriage
Refinement program	PHENIX V1.0	Depositor
R , R_{free}	0.183 , 0.214 0.198 , 0.232	Depositor DCC
R_{free} test set	3204 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	32.8	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.1	EDS
L-test for twinning ²	$< L > = 0.53$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.013 for -2/3*h-1/3*k+2/3*l,-1/3*h-2/3*k- 2/3*l,1/2/3*h-2/3*k+1/3*l 0.003 for -h,1/3*h-1/3*k+2/3*l,1/2/3*h+4/3*k+1/3*l 0.000 for -1/3*h+1/3*k-2/3*l,-k,-4/3*h-2/3*k+1/3*l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9445	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $< |L| >$, $< L^2 >$ 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	0.68	0/2279	0.81	0/3086
1	B	0.67	0/2290	0.81	0/3100
1	C	0.68	0/2279	0.80	0/3086
1	D	0.67	0/2279	0.81	0/3086
All	All	0.68	0/9127	0.81	0/12358

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	2245	0	2273	14	0
1	B	2253	0	2286	21	0
1	C	2245	0	2273	24	0
1	D	2245	0	2273	18	0
2	A	141	0	0	3	1
2	B	119	0	0	2	0
2	C	102	0	0	8	0
2	D	95	0	0	3	0
All	All	9445	0	9105	71	1

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 (71) 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:D:125:SER:HB2	2:D:327:HOH:O	1.81	0.79
1:C:192:ASN:HD22	1:C:195:GLN:HG2	1.47	0.78
1:B:192:ASN:HD22	1:B:195:GLN:HG2	1.50	0.77
1:A:192:ASN:HD22	1:A:195:GLN:HG2	1.53	0.74
1:C:192:ASN:ND2	1:C:195:GLN:HG2	2.03	0.73
1:D:192:ASN:HD22	1:D:195:GLN:HG2	1.54	0.72
1:B:125:SER:HB2	2:B:312:HOH:O	1.89	0.71
1:B:259:GLN:HE21	1:C:238:GLY:H	1.37	0.71
1:D:192:ASN:ND2	1:D:195:GLN:HG2	2.06	0.70
1:A:192:ASN:ND2	1:A:195:GLN:HG2	2.06	0.69
1:B:238:GLY:H	1:C:259:GLN:HE21	1.40	0.69
1:B:192:ASN:ND2	1:B:195:GLN:HG2	2.07	0.68
1:A:125:SER:HB2	2:A:311:HOH:O	1.94	0.67
1:C:125:SER:HB2	2:C:316:HOH:O	1.95	0.67
1:D:3:THR:HG23	1:D:4:LYS:H	1.62	0.65
1:B:14:ASN:HB2	2:B:322:HOH:O	1.98	0.63
1:C:102:THR:HG23	2:C:351:HOH:O	1.98	0.63
1:C:4:LYS:HE3	1:C:27:GLN:O	1.99	0.61
1:D:39:ILE:HG22	1:D:39:ILE:O	2.01	0.60
1:D:102:THR:HG23	2:D:330:HOH:O	2.01	0.59
1:D:145:ASN:HD21	1:D:177:GLY:H	1.51	0.58
1:A:102:THR:HG23	2:A:372:HOH:O	2.04	0.58
1:C:145:ASN:HD21	1:C:177:GLY:H	1.52	0.57
1:B:145:ASN:HD21	1:B:177:GLY:H	1.52	0.57
1:B:241:HIS:HD2	1:D:225:VAL:H	1.52	0.57
1:A:145:ASN:HD21	1:A:177:GLY:H	1.53	0.57
1:B:102:THR:CG2	2:C:350:HOH:O	2.53	0.55
1:B:102:THR:HG21	2:C:350:HOH:O	2.09	0.52
1:A:210:GLU:OE2	1:A:212:HIS:HE1	1.93	0.51
1:B:210:GLU:OE2	1:B:212:HIS:HE1	1.94	0.50
1:C:210:GLU:OE2	1:C:212:HIS:HE1	1.93	0.50
1:D:210:GLU:OE2	1:D:212:HIS:HE1	1.93	0.50
1:A:143:TYR:CG	1:A:176:THR:HA	2.47	0.49
1:C:223:LYS:HE2	2:C:377:HOH:O	2.13	0.49
1:C:143:TYR:CG	1:C:176:THR:HA	2.47	0.49
1:C:253:ASN:HB3	1:C:254:PRO:CD	2.43	0.48
1:B:259:GLN:HE21	1:C:238:GLY:N	2.09	0.48
1:D:36:ARG:NH1	1:D:41:ASN:O	2.46	0.48
1:C:110:LYS:HD2	2:C:383:HOH:O	2.13	0.48
1:A:145:ASN:ND2	1:A:177:GLY:H	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:143:TYR:CG	1:D:176:THR:HA	2.48	0.48
1:B:145:ASN:ND2	1:B:177:GLY:H	2.12	0.47
1:B:253:ASN:HB3	1:B:254:PRO:CD	2.44	0.47
1:D:145:ASN:ND2	1:D:177:GLY:H	2.12	0.47
1:B:42:VAL:O	1:B:42:VAL:HG23	2.15	0.47
1:C:145:ASN:ND2	1:C:177:GLY:H	2.13	0.47
1:D:39:ILE:O	1:D:39:ILE:CG2	2.62	0.47
1:B:143:TYR:CG	1:B:176:THR:HA	2.50	0.47
1:C:48:ASN:HD22	1:C:48:ASN:N	2.12	0.47
1:A:253:ASN:HB3	1:A:254:PRO:CD	2.45	0.46
1:C:98:VAL:HG23	2:C:333:HOH:O	2.15	0.46
1:A:172:ILE:HB	1:A:180:ARG:HB3	1.99	0.44
1:A:208:SER:HB2	2:A:334:HOH:O	2.18	0.44
1:B:172:ILE:HB	1:B:180:ARG:HB3	2.00	0.44
1:D:48:ASN:HD22	1:D:48:ASN:N	2.16	0.43
1:C:96:GLU:HG2	2:C:349:HOH:O	2.18	0.43
1:A:120:GLY:O	1:A:124:GLY:HA3	2.18	0.43
1:B:238:GLY:N	1:C:259:GLN:HE21	2.14	0.43
1:D:253:ASN:HB3	1:D:254:PRO:CD	2.48	0.43
1:C:172:ILE:HB	1:C:180:ARG:HB3	2.00	0.43
1:B:238:GLY:HA2	1:C:22:ALA:HA	2.00	0.43
1:D:120:GLY:O	1:D:124:GLY:HA3	2.19	0.42
1:C:120:GLY:O	1:C:124:GLY:HA3	2.19	0.42
1:B:120:GLY:O	1:B:124:GLY:HA3	2.20	0.42
1:D:172:ILE:HB	1:D:180:ARG:HB3	2.01	0.41
1:C:7:VAL:HA	1:C:63:VAL:O	2.21	0.41
1:A:15:ILE:HD11	1:A:67:CYS:HA	2.02	0.41
1:A:7:VAL:HA	1:A:63:VAL:O	2.22	0.40
1:B:7:VAL:HA	1:B:63:VAL:O	2.21	0.40
1:D:241:HIS:HE1	2:D:379:HOH:O	2.04	0.40
1:C:20:LEU:HD12	1:C:31:LEU:CD2	2.51	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:395:HOH:O	2:A:415:HOH:O[11_445]	2.03	0.17

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	295/299 (99%)	284 (96%)	11 (4%)	0	100 100
1	B	296/299 (99%)	284 (96%)	12 (4%)	0	100 100
1	C	295/299 (99%)	282 (96%)	13 (4%)	0	100 100
1	D	295/299 (99%)	283 (96%)	12 (4%)	0	100 100
All	All	1181/1196 (99%)	1133 (96%)	48 (4%)	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	246/248 (99%)	241 (98%)	5 (2%)	55 72
1	B	247/248 (100%)	241 (98%)	6 (2%)	49 67
1	C	246/248 (99%)	241 (98%)	5 (2%)	55 72
1	D	246/248 (99%)	242 (98%)	4 (2%)	62 78
All	All	985/992 (99%)	965 (98%)	20 (2%)	55 72

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	SER
1	A	125	SER

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Mol	Chain	Res	Type
1	A	187	LEU
1	A	219	VAL
1	A	229	VAL
1	B	32	VAL
1	B	75	GLU
1	B	125	SER
1	B	187	LEU
1	B	219	VAL
1	B	229	VAL
1	C	48	ASN
1	C	125	SER
1	C	187	LEU
1	C	219	VAL
1	C	229	VAL
1	D	125	SER
1	D	187	LEU
1	D	219	VAL
1	D	229	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	145	ASN
1	A	192	ASN
1	A	212	HIS
1	A	242	ASN
1	B	145	ASN
1	B	192	ASN
1	B	212	HIS
1	B	241	HIS
1	B	259	GLN
1	C	40	ASN
1	C	48	ASN
1	C	145	ASN
1	C	192	ASN
1	C	212	HIS
1	C	241	HIS
1	C	259	GLN
1	D	40	ASN
1	D	48	ASN
1	D	145	ASN

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Mol	Chain	Res	Type
1	D	192	ASN
1	D	212	HIS
1	D	241	HIS
1	D	242	ASN

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 [\(i\)](#)

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 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	297/299 (99%)	-0.32	9 (3%) 50 46	21, 32, 68, 87	0
1	B	297/299 (99%)	-0.22	4 (1%) 77 75	25, 36, 66, 91	0
1	C	297/299 (99%)	-0.17	8 (2%) 54 50	25, 36, 68, 99	0
1	D	297/299 (99%)	-0.10	14 (4%) 31 27	23, 35, 78, 157	0
All	All	1188/1196 (99%)	-0.20	35 (2%) 51 48	21, 35, 71, 157	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	40	ASN	6.3
1	D	41	ASN	5.1
1	D	44	GLU	3.5
1	D	39	ILE	3.4
1	C	102	THR	3.3
1	D	196	VAL	3.3
1	D	195	GLN	2.9
1	C	187	LEU	2.9
1	A	191	ALA	2.9
1	D	190	GLY	2.9
1	A	190	GLY	2.8
1	D	160	ALA	2.8
1	C	195	GLN	2.7
1	A	196	VAL	2.7
1	A	163	GLY	2.6
1	C	191	ALA	2.6
1	D	191	ALA	2.5
1	A	192	ASN	2.4
1	A	189	ALA	2.3
1	A	102	THR	2.3
1	D	192	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	187	LEU	2.2
1	D	156	VAL	2.2
1	D	187	LEU	2.2
1	A	187	LEU	2.2
1	B	205	TYR	2.1
1	A	195	GLN	2.1
1	B	196	VAL	2.1
1	D	162	GLU	2.1
1	D	38	ASP	2.1
1	B	102	THR	2.1
1	C	217	ASP	2.1
1	C	192	ASN	2.1
1	C	163	GLY	2.1
1	C	162	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 monosaccharides 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.