



Full wwPDB X-ray Structure Validation Report

Sep 17, 2023 – 12:11 AM EDT

PDB ID : 4X0U
Title : Structure ALDH7A1 inactivated by 4-diethylaminobenzaldehyde
Authors : Luo, M.; Tanner, J.J.
Deposited on : 2014-11-23
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 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 : 2.35.1
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

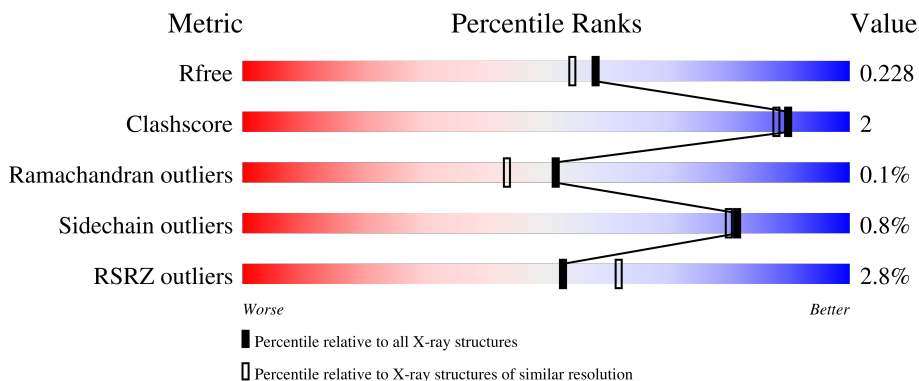
1 Overall quality at a glance

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 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	513	 89% 7%
1	B	513	 90% 6%
1	C	513	 88% 6% 5%
1	D	513	 88% 6% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15034 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.

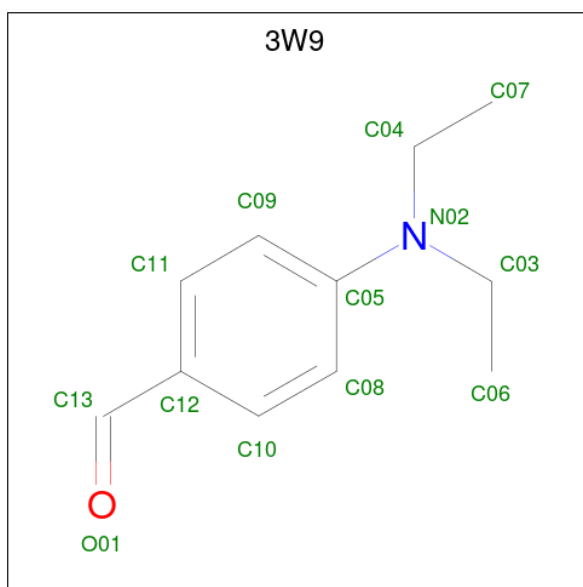
- Molecule 1 is a protein called Alpha-aminoadipic semialdehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	477	3588	2297	618	656	17	0	0	0
1	B	484	3629	2316	626	671	16	0	0	0
1	C	485	3613	2307	622	667	17	0	0	0
1	D	487	3635	2318	632	668	17	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P49419
A	0	HIS	-	expression tag	UNP P49419
B	-1	GLY	-	expression tag	UNP P49419
B	0	HIS	-	expression tag	UNP P49419
C	-1	GLY	-	expression tag	UNP P49419
C	0	HIS	-	expression tag	UNP P49419
D	-1	GLY	-	expression tag	UNP P49419
D	0	HIS	-	expression tag	UNP P49419

- Molecule 2 is 4-(diethylamino)benzaldehyde (three-letter code: 3W9) (formula: C₁₁H₁₅NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	13	11	1	1	0	0
2	B	1	13	11	1	1	0	0
2	C	1	13	11	1	1	0	0
2	D	1	13	11	1	1	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	D	1	1	1	0	0

- Molecule 4 is water.

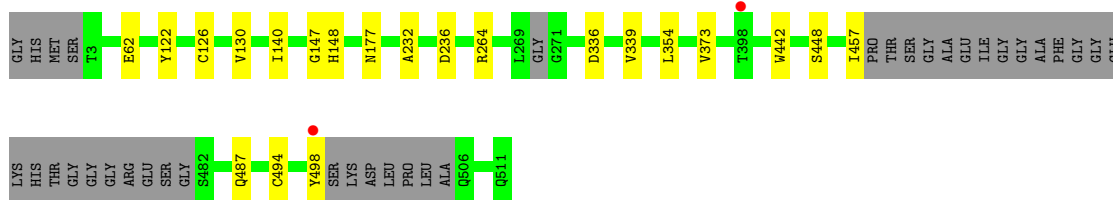
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	143	143	143	0	0
4	B	125	125	125	0	0
4	C	101	101	101	0	0
4	D	147	147	147	0	0

3 Residue-property plots [i](#)

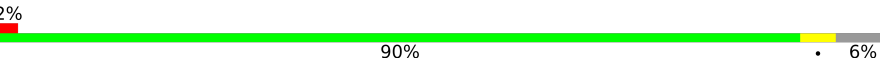
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

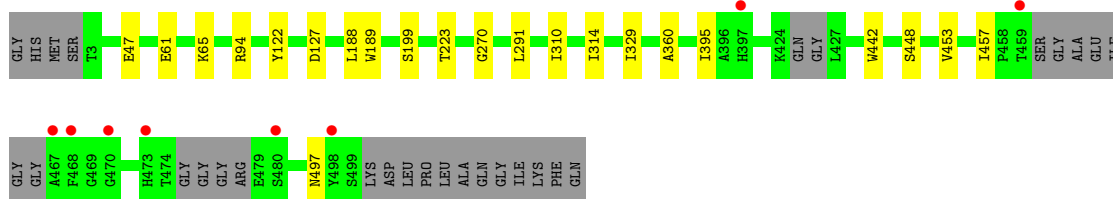
- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase

Chain A: 




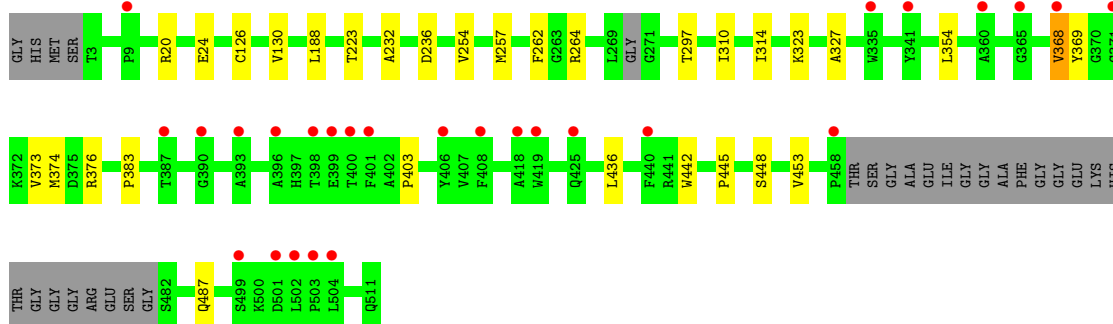
- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase

Chain B: 

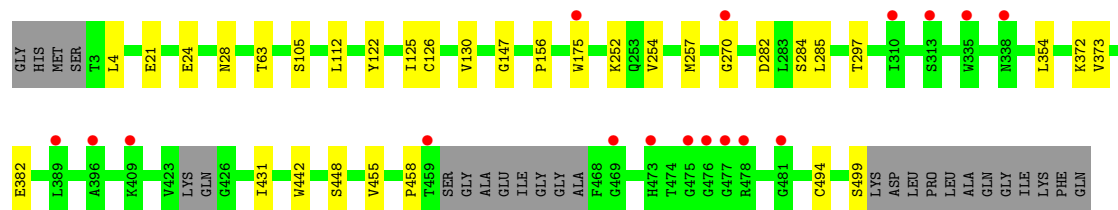
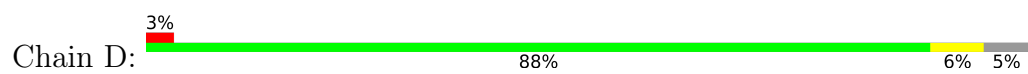


- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase

Chain C: 



- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	161.54Å 219.41Å 233.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.49 – 1.95 51.49 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.7 (51.49-1.95) 99.7 (51.49-1.95)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 1.95Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.188 , 0.227 0.189 , 0.228	Depositor DCC
R_{free} test set	7464 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	25.6	Xtrriage
Anisotropy	0.393	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.7	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	0.95	EDS
Total number of atoms	15034	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.36% 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: MG, 3W9

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	0.37	0/3660	0.50	0/4974
1	B	0.37	0/3703	0.49	0/5036
1	C	0.36	0/3687	0.48	0/5022
1	D	0.37	0/3708	0.48	0/5038
All	All	0.37	0/14758	0.49	0/20070

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	3588	0	3549	11	0
1	B	3629	0	3566	11	0
1	C	3613	0	3525	19	0
1	D	3635	0	3595	17	0
2	A	13	0	14	0	0
2	B	13	0	14	0	0
2	C	13	0	14	0	0
2	D	13	0	14	0	0
3	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	143	0	0	1	0
4	B	125	0	0	1	0
4	C	101	0	0	0	0
4	D	147	0	0	0	0
All	All	15034	0	14291	53	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 2.

All (53) 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:C:323:LYS:HD3	1:C:368:VAL:HG12	1.79	0.65
1:C:354:LEU:HD21	1:C:373:VAL:HG23	1.79	0.63
1:D:285:LEU:HD22	1:D:458:PRO:HB3	1.81	0.61
1:D:442:TRP:CZ2	1:D:448:SER:HB2	2.35	0.61
1:B:442:TRP:CZ2	1:B:448:SER:HB2	2.37	0.60
1:D:28:ASN:HB3	1:D:63:THR:HG23	1.85	0.57
1:D:354:LEU:HD21	1:D:373:VAL:HG23	1.86	0.57
1:A:442:TRP:CE2	1:A:448:SER:HB2	2.42	0.55
1:A:177:ASN:ND2	4:A:789:HOH:O	2.25	0.54
1:D:147:GLY:HA3	1:D:499:SER:HB3	1.89	0.53
1:A:147:GLY:O	1:A:498:TYR:N	2.41	0.53
1:C:20:ARG:NH2	1:C:24:GLU:OE1	2.33	0.53
1:A:442:TRP:CZ2	1:A:448:SER:HB2	2.43	0.52
1:C:442:TRP:CE2	1:C:448:SER:HB2	2.46	0.51
1:D:125:ILE:HG21	1:D:175:TRP:HA	1.94	0.50
1:D:442:TRP:CE2	1:D:448:SER:HB2	2.47	0.50
1:B:94:ARG:NH2	1:B:127:ASP:OD2	2.44	0.49
1:C:188:LEU:HD11	1:C:223:THR:HG23	1.93	0.49
1:A:126:CYS:O	1:A:130:VAL:HG23	2.13	0.48
1:A:336:ASP:HB2	1:A:339:VAL:HG21	1.96	0.47
1:B:291:LEU:HD11	1:B:329:ILE:HD11	1.97	0.47
1:A:264:ARG:NH1	1:A:487:GLN:O	2.47	0.47
1:C:383:PRO:HA	1:C:403:PRO:HB2	1.98	0.46
1:B:310:ILE:HG22	1:B:314:ILE:HG13	1.96	0.46
1:A:354:LEU:HD21	1:A:373:VAL:HG23	1.98	0.46
1:B:61:GLU:HG3	1:B:65:LYS:HE3	1.98	0.46
1:C:310:ILE:HG22	1:C:314:ILE:HG13	1.98	0.46
1:B:188:LEU:HD11	1:B:223:THR:HG23	1.99	0.44
1:C:264:ARG:NH2	1:C:487:GLN:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:126:CYS:O	1:C:130:VAL:HG23	2.18	0.44
1:A:494:CYS:HA	1:B:453:VAL:O	2.17	0.44
1:C:327:ALA:HA	1:C:369:TYR:OH	2.17	0.43
1:D:254:VAL:HA	1:D:257:MET:HE2	2.01	0.43
1:C:354:LEU:HD23	1:C:354:LEU:HA	1.89	0.42
1:C:254:VAL:HA	1:C:257:MET:HE3	2.01	0.42
1:D:126:CYS:O	1:D:130:VAL:HG23	2.20	0.42
1:B:360:ALA:HA	1:B:395:ILE:HG21	2.01	0.41
1:D:4:LEU:CD1	1:D:21:GLU:HG3	2.50	0.41
1:D:372:LYS:HE3	1:D:382:GLU:OE1	2.20	0.41
1:B:457:ILE:HB	4:B:817:HOH:O	2.20	0.41
1:A:457:ILE:HD13	1:B:497:ASN:HB2	2.02	0.41
1:C:262:PHE:CZ	1:D:252:LYS:HB2	2.56	0.41
1:C:374:MET:O	1:C:376:ARG:N	2.54	0.41
1:D:431:ILE:HD11	1:D:455:VAL:HG22	2.03	0.41
1:C:453:VAL:O	1:D:494:CYS:HA	2.21	0.41
1:C:232:ALA:O	1:C:236:ASP:HB2	2.20	0.41
1:D:282:ASP:OD1	1:D:284:SER:HB3	2.21	0.40
1:C:436:LEU:HD12	1:C:436:LEU:HA	1.90	0.40
1:D:105:SER:OG	1:D:112:LEU:HA	2.22	0.40
1:B:189:TRP:CH2	1:B:199:SER:HA	2.57	0.40
1:C:445:PRO:HB3	1:D:156:PRO:HD2	2.03	0.40
1:C:442:TRP:CZ2	1:C:448:SER:HB2	2.56	0.40
1:A:232:ALA:O	1:A:236:ASP:HB2	2.22	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	469/513 (91%)	460 (98%)	9 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	476/513 (93%)	465 (98%)	10 (2%)	1 (0%)	47	38
1	C	479/513 (93%)	471 (98%)	8 (2%)	0	100	100
1	D	481/513 (94%)	471 (98%)	9 (2%)	1 (0%)	47	38
All	All	1905/2052 (93%)	1867 (98%)	36 (2%)	2 (0%)	51	43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	270	GLY
1	B	270	GLY

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	364/410 (89%)	360 (99%)	4 (1%)	73	71
1	B	369/410 (90%)	367 (100%)	2 (0%)	88	88
1	C	363/410 (88%)	361 (99%)	2 (1%)	86	85
1	D	369/410 (90%)	366 (99%)	3 (1%)	81	80
All	All	1465/1640 (89%)	1454 (99%)	11 (1%)	81	80

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	GLU
1	A	122	TYR
1	A	140	ILE
1	A	148	HIS
1	B	47	GLU
1	B	122	TYR
1	C	297	THR
1	C	368	VAL
1	D	24	GLU

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Mol	Chain	Res	Type
1	D	122	TYR
1	D	297	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	177	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](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\# Z > 2$
2	3W9	A	601	1	13,13,13	0.55	0	16,16,16	0.85	1 (6%)
2	3W9	C	601	1	13,13,13	0.60	0	16,16,16	0.73	0
2	3W9	D	601	1	13,13,13	0.63	0	16,16,16	0.72	0
2	3W9	B	601	1	13,13,13	0.64	0	16,16,16	0.64	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	3W9	A	601	1	-	2/10/10/10	0/1/1/1
2	3W9	C	601	1	-	2/10/10/10	0/1/1/1
2	3W9	D	601	1	-	0/10/10/10	0/1/1/1
2	3W9	B	601	1	-	2/10/10/10	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	3W9	O01-C13-C12	-2.08	117.85	124.59

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	3W9	C11-C12-C13-O01
2	A	601	3W9	C10-C12-C13-O01
2	B	601	3W9	C11-C12-C13-O01
2	B	601	3W9	C10-C12-C13-O01
2	C	601	3W9	C11-C12-C13-O01
2	C	601	3W9	C10-C12-C13-O01

There are no ring outliers.

No monomer is involved in short contacts.

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	477/513 (92%)	-0.16	2 (0%) 92 95	15, 28, 51, 67	0
1	B	484/513 (94%)	-0.00	8 (1%) 70 77	17, 31, 54, 68	0
1	C	485/513 (94%)	0.18	27 (5%) 24 33	18, 34, 61, 72	0
1	D	487/513 (94%)	0.15	17 (3%) 44 53	15, 31, 58, 68	0
All	All	1933/2052 (94%)	0.04	54 (2%) 53 62	15, 31, 57, 72	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	476	GLY	4.6
1	B	467	ALA	4.4
1	C	360	ALA	4.3
1	C	335	TRP	3.5
1	D	481	GLY	3.4
1	B	473	HIS	3.4
1	C	458	PRO	3.4
1	C	504	LEU	3.3
1	B	468	PHE	3.3
1	C	503	PRO	3.1
1	B	480	SER	3.1
1	D	459	THR	2.9
1	B	470	GLY	2.8
1	C	393	ALA	2.8
1	C	400	THR	2.8
1	A	398	THR	2.8
1	D	335	TRP	2.8
1	B	459	THR	2.7
1	C	341	TYR	2.7
1	C	501	ASP	2.7
1	C	396	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	399	GLU	2.6
1	D	396	ALA	2.6
1	C	499	SER	2.5
1	C	419	TRP	2.5
1	D	389	LEU	2.5
1	D	313	SER	2.4
1	C	398	THR	2.4
1	D	409	LYS	2.4
1	D	175	TRP	2.4
1	C	401	PHE	2.4
1	D	310	ILE	2.4
1	C	406	TYR	2.3
1	C	440	PHE	2.3
1	D	477	GLY	2.3
1	C	365	GLY	2.3
1	C	418	ALA	2.2
1	B	397	HIS	2.2
1	C	502	LEU	2.2
1	D	270	GLY	2.2
1	D	475	GLY	2.2
1	D	478	ARG	2.2
1	C	9	PRO	2.1
1	A	498	TYR	2.1
1	C	408	PHE	2.1
1	C	425	GLN	2.1
1	B	498	TYR	2.1
1	D	338	ASN	2.1
1	D	469	GLY	2.1
1	C	390	GLY	2.1
1	C	368	VAL	2.0
1	C	371	GLY	2.0
1	D	473	HIS	2.0
1	C	387	THR	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](#)

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	3W9	B	601	13/13	0.78	0.20	31,44,52,56	0
2	3W9	D	601	13/13	0.85	0.16	30,38,43,47	0
2	3W9	C	601	13/13	0.86	0.22	41,43,49,54	0
2	3W9	A	601	13/13	0.91	0.16	36,42,46,47	0
3	MG	D	602	1/1	0.96	0.13	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.