Full wwPDB X-ray Structure Validation Report (i)

Sep 24, 2023 – 06:06 AM EDT

PDB ID	:	5UA0
Title	:	Dimeric crystal structure of HTPA reductase from arabidopsis thaliana
Authors	:	Keown, J.K.; Pearce, F.G.; Goldstone, D.C.
Deposited on	:	2016-12-18
Resolution	:	2.30 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 (i)) were used in the production of this report:

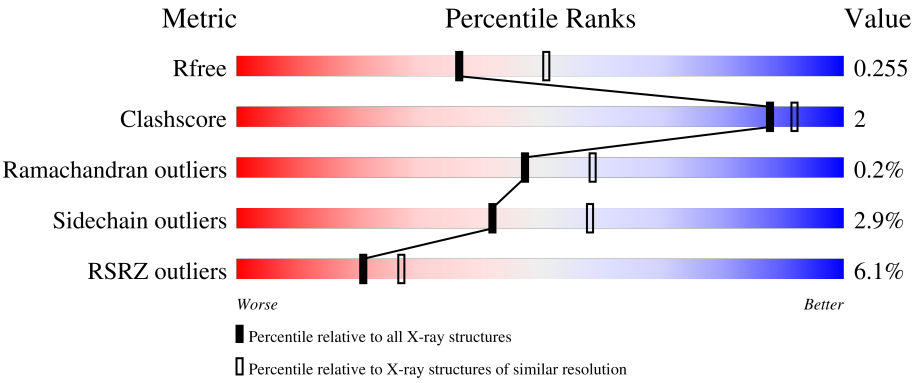
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	329	7% 78% · 18%
1	B	329	2% 77% 5% 18%
1	C	329	6% 76% 6% · 17%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6022 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 4-hydroxy-tetrahydrodipicolinate reductase 2, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	S	0	0	0
			1994	1269	334	378	13			
1	B	270	Total	C	N	O	S	0	0	0
			1988	1262	328	384	14			
1	C	274	Total	C	N	O	S	0	0	0
			1991	1263	331	383	14			

There are 99 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-32	MET	-	initiating methionine	UNP Q8LB01
A	-31	HIS	-	expression tag	UNP Q8LB01
A	-30	HIS	-	expression tag	UNP Q8LB01
A	-29	HIS	-	expression tag	UNP Q8LB01
A	-28	HIS	-	expression tag	UNP Q8LB01
A	-27	HIS	-	expression tag	UNP Q8LB01
A	-26	HIS	-	expression tag	UNP Q8LB01
A	-25	GLY	-	expression tag	UNP Q8LB01
A	-24	LEU	-	expression tag	UNP Q8LB01
A	-23	PRO	-	expression tag	UNP Q8LB01
A	-22	ILE	-	expression tag	UNP Q8LB01
A	-21	PRO	-	expression tag	UNP Q8LB01
A	-20	ASN	-	expression tag	UNP Q8LB01
A	-19	PRO	-	expression tag	UNP Q8LB01
A	-18	LEU	-	expression tag	UNP Q8LB01
A	-17	LEU	-	expression tag	UNP Q8LB01
A	-16	GLY	-	expression tag	UNP Q8LB01
A	-15	LEU	-	expression tag	UNP Q8LB01
A	-14	ASP	-	expression tag	UNP Q8LB01
A	-13	SER	-	expression tag	UNP Q8LB01
A	-12	THR	-	expression tag	UNP Q8LB01
A	-11	GLU	-	expression tag	UNP Q8LB01
A	-10	ASN	-	expression tag	UNP Q8LB01

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	LEU	-	expression tag	UNP Q8LB01
A	-8	TYR	-	expression tag	UNP Q8LB01
A	-7	PHE	-	expression tag	UNP Q8LB01
A	-6	GLN	-	expression tag	UNP Q8LB01
A	-5	GLY	-	expression tag	UNP Q8LB01
A	-4	ILE	-	expression tag	UNP Q8LB01
A	-3	ASP	-	expression tag	UNP Q8LB01
A	-2	PRO	-	expression tag	UNP Q8LB01
A	-1	PHE	-	expression tag	UNP Q8LB01
A	0	THR	-	expression tag	UNP Q8LB01
B	-32	MET	-	initiating methionine	UNP Q8LB01
B	-31	HIS	-	expression tag	UNP Q8LB01
B	-30	HIS	-	expression tag	UNP Q8LB01
B	-29	HIS	-	expression tag	UNP Q8LB01
B	-28	HIS	-	expression tag	UNP Q8LB01
B	-27	HIS	-	expression tag	UNP Q8LB01
B	-26	HIS	-	expression tag	UNP Q8LB01
B	-25	GLY	-	expression tag	UNP Q8LB01
B	-24	LEU	-	expression tag	UNP Q8LB01
B	-23	PRO	-	expression tag	UNP Q8LB01
B	-22	ILE	-	expression tag	UNP Q8LB01
B	-21	PRO	-	expression tag	UNP Q8LB01
B	-20	ASN	-	expression tag	UNP Q8LB01
B	-19	PRO	-	expression tag	UNP Q8LB01
B	-18	LEU	-	expression tag	UNP Q8LB01
B	-17	LEU	-	expression tag	UNP Q8LB01
B	-16	GLY	-	expression tag	UNP Q8LB01
B	-15	LEU	-	expression tag	UNP Q8LB01
B	-14	ASP	-	expression tag	UNP Q8LB01
B	-13	SER	-	expression tag	UNP Q8LB01
B	-12	THR	-	expression tag	UNP Q8LB01
B	-11	GLU	-	expression tag	UNP Q8LB01
B	-10	ASN	-	expression tag	UNP Q8LB01
B	-9	LEU	-	expression tag	UNP Q8LB01
B	-8	TYR	-	expression tag	UNP Q8LB01
B	-7	PHE	-	expression tag	UNP Q8LB01
B	-6	GLN	-	expression tag	UNP Q8LB01
B	-5	GLY	-	expression tag	UNP Q8LB01
B	-4	ILE	-	expression tag	UNP Q8LB01
B	-3	ASP	-	expression tag	UNP Q8LB01
B	-2	PRO	-	expression tag	UNP Q8LB01
B	-1	PHE	-	expression tag	UNP Q8LB01

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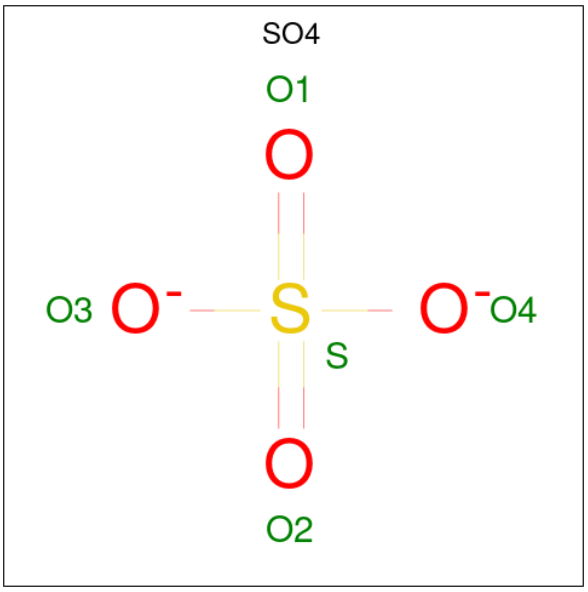
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	THR	-	expression tag	UNP Q8LB01
C	-32	MET	-	initiating methionine	UNP Q8LB01
C	-31	HIS	-	expression tag	UNP Q8LB01
C	-30	HIS	-	expression tag	UNP Q8LB01
C	-29	HIS	-	expression tag	UNP Q8LB01
C	-28	HIS	-	expression tag	UNP Q8LB01
C	-27	HIS	-	expression tag	UNP Q8LB01
C	-26	HIS	-	expression tag	UNP Q8LB01
C	-25	GLY	-	expression tag	UNP Q8LB01
C	-24	LEU	-	expression tag	UNP Q8LB01
C	-23	PRO	-	expression tag	UNP Q8LB01
C	-22	ILE	-	expression tag	UNP Q8LB01
C	-21	PRO	-	expression tag	UNP Q8LB01
C	-20	ASN	-	expression tag	UNP Q8LB01
C	-19	PRO	-	expression tag	UNP Q8LB01
C	-18	LEU	-	expression tag	UNP Q8LB01
C	-17	LEU	-	expression tag	UNP Q8LB01
C	-16	GLY	-	expression tag	UNP Q8LB01
C	-15	LEU	-	expression tag	UNP Q8LB01
C	-14	ASP	-	expression tag	UNP Q8LB01
C	-13	SER	-	expression tag	UNP Q8LB01
C	-12	THR	-	expression tag	UNP Q8LB01
C	-11	GLU	-	expression tag	UNP Q8LB01
C	-10	ASN	-	expression tag	UNP Q8LB01
C	-9	LEU	-	expression tag	UNP Q8LB01
C	-8	TYR	-	expression tag	UNP Q8LB01
C	-7	PHE	-	expression tag	UNP Q8LB01
C	-6	GLN	-	expression tag	UNP Q8LB01
C	-5	GLY	-	expression tag	UNP Q8LB01
C	-4	ILE	-	expression tag	UNP Q8LB01
C	-3	ASP	-	expression tag	UNP Q8LB01
C	-2	PRO	-	expression tag	UNP Q8LB01
C	-1	PHE	-	expression tag	UNP Q8LB01
C	0	THR	-	expression tag	UNP Q8LB01

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0

- Molecule 3 is water.

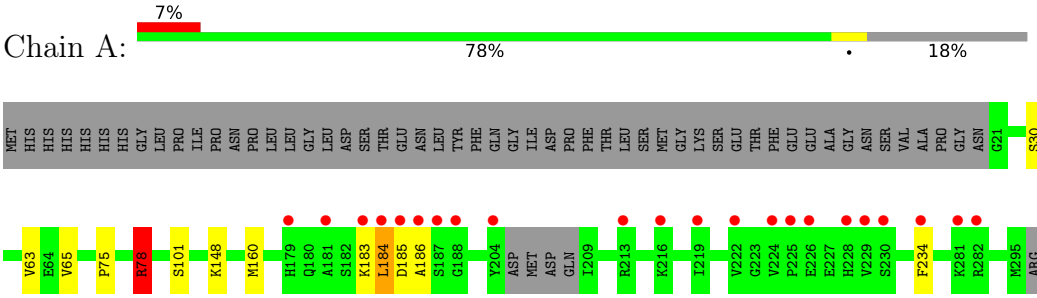
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	10	Total O 10 10	0	0
3	B	18	Total O 18 18	0	0
3	C	11	Total O 11 11	0	0

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.

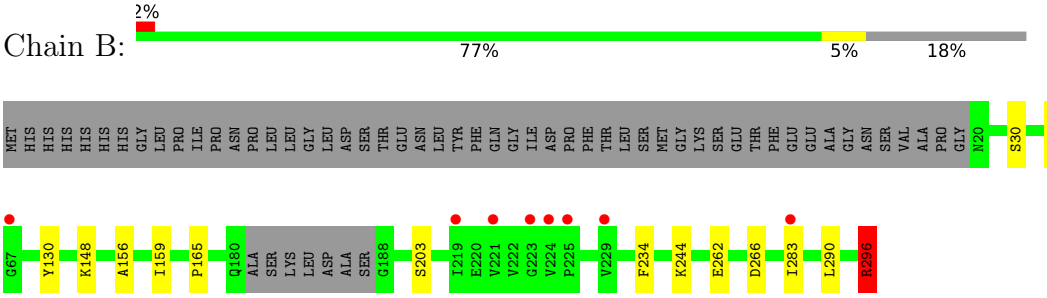
• Molecule 1: 4-hydroxy-tetrahydrodipicolinate reductase 2, chloroplastic

Chain A:



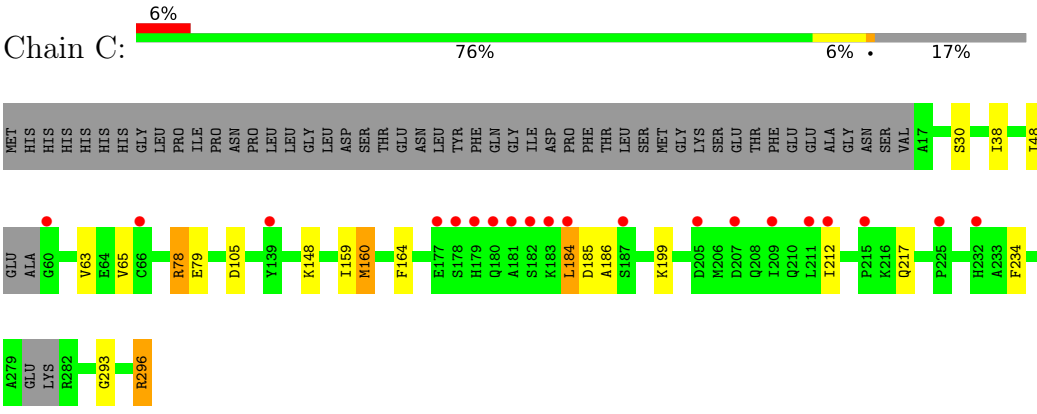
• Molecule 1: 4-hydroxy-tetrahydrodipicolinate reductase 2, chloroplastic

Chain B:



• Molecule 1: 4-hydroxy-tetrahydrodipicolinate reductase 2, chloroplastic

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	124.55Å 80.62Å 92.79Å 90.00° 95.84° 90.00°	Depositor
Resolution (Å)	61.95 – 2.30 54.05 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (61.95-2.30) 100.0 (54.05-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.46 (at 2.29Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.226 , 0.258 0.228 , 0.255	Depositor DCC
R_{free} test set	2012 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	50.0	Xtriage
Anisotropy	0.368	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 41.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	6022	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.09% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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

5.1 Standard geometry

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

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	0.60	0/2030	0.72	3/2751 (0.1%)
1	B	0.59	0/2024	0.73	2/2745 (0.1%)
1	C	0.64	1/2026 (0.0%)	0.81	7/2752 (0.3%)
All	All	0.61	1/6080 (0.0%)	0.75	12/8248 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	79	GLU	CG-CD	5.12	1.59	1.51

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	296	ARG	NE-CZ-NH1	-8.67	115.96	120.30
1	C	296	ARG	NE-CZ-NH2	8.63	124.61	120.30
1	B	296	ARG	NE-CZ-NH1	7.41	124.01	120.30
1	B	296	ARG	NE-CZ-NH2	-7.24	116.68	120.30
1	C	78	ARG	NE-CZ-NH2	-7.20	116.70	120.30
1	C	78	ARG	NE-CZ-NH1	6.78	123.69	120.30
1	A	78	ARG	NE-CZ-NH2	-6.16	117.22	120.30
1	C	105	ASP	CB-CG-OD2	-6.06	112.84	118.30
1	A	160	MET	CG-SD-CE	5.89	109.62	100.20
1	C	160	MET	CG-SD-CE	5.58	109.13	100.20
1	C	79	GLU	OE1-CD-OE2	-5.47	116.73	123.30
1	A	78	ARG	NE-CZ-NH1	5.25	122.93	120.30

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	1994	0	1948	6	0
1	B	1988	0	1914	10	0
1	C	1991	0	1905	13	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
3	A	10	0	0	0	0
3	B	18	0	0	0	0
3	C	11	0	0	0	0
All	All	6022	0	5767	24	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 (24) 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:262:GLU:OE1	1:C:296:ARG:NH1	2.19	0.74
1:C:63:VAL:HG12	1:C:65:VAL:HG23	1.77	0.67
1:A:63:VAL:HG12	1:A:65:VAL:HG23	1.78	0.65
1:B:130:TYR:CE1	1:B:283:ILE:HD11	2.38	0.58
1:C:212:ILE:HD11	1:C:217:GLN:CG	2.39	0.53
1:A:75:PRO:HA	1:A:78:ARG:HG3	1.94	0.49
1:B:266:ASP:OD1	1:B:296:ARG:NE	2.45	0.49
1:C:184:LEU:O	1:C:186:ALA:N	2.45	0.49
1:C:212:ILE:CD1	1:C:217:GLN:HG2	2.43	0.48
1:B:156:ALA:HB2	1:C:160:MET:HB2	1.96	0.47
1:C:212:ILE:HD11	1:C:217:GLN:HG2	1.96	0.47
1:B:159:ILE:HG22	1:C:159:ILE:HD13	1.96	0.46
1:B:130:TYR:CD1	1:B:283:ILE:HD11	2.51	0.45
1:A:184:LEU:O	1:A:186:ALA:N	2.50	0.45
1:A:38:ILE:HG23	1:A:48:ILE:HD13	2.00	0.44
1:B:38:ILE:HG23	1:B:48:ILE:HD13	2.00	0.44
1:C:38:ILE:HG23	1:C:48:ILE:HD13	1.99	0.44
1:B:290:LEU:HB3	1:C:164:PHE:CD1	2.52	0.44
1:B:262:GLU:OE1	1:B:296:ARG:NH2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:PRO:O	1:C:293:GLY:HA2	2.18	0.43
1:C:38:ILE:HG23	1:C:48:ILE:CD1	2.50	0.41
1:A:38:ILE:HG23	1:A:48:ILE:CD1	2.50	0.41
1:A:101:SER:O	1:C:199:LYS:HD2	2.20	0.41
1:B:38:ILE:HG23	1:B:48:ILE:CD1	2.51	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	267/329 (81%)	255 (96%)	11 (4%)	1 (0%)	34	42
1	B	266/329 (81%)	257 (97%)	9 (3%)	0	100	100
1	C	268/329 (82%)	257 (96%)	10 (4%)	1 (0%)	34	42
All	All	801/987 (81%)	769 (96%)	30 (4%)	2 (0%)	47	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	185	ASP
1	C	185	ASP

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	207/275 (75%)	201 (97%)	6 (3%)	42	58
1	B	207/275 (75%)	201 (97%)	6 (3%)	42	58
1	C	204/275 (74%)	198 (97%)	6 (3%)	42	58
All	All	618/825 (75%)	600 (97%)	18 (3%)	42	58

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	SER
1	A	78	ARG
1	A	148	LYS
1	A	183	LYS
1	A	184	LEU
1	A	234	PHE
1	B	30	SER
1	B	148	LYS
1	B	203	SER
1	B	234	PHE
1	B	244	LYS
1	B	296	ARG
1	C	30	SER
1	C	78	ARG
1	C	148	LYS
1	C	184	LEU
1	C	234	PHE
1	C	244	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	179	HIS
1	C	217	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	SO4	C	301	-	4,4,4	0.38	0	6,6,6	0.51	0
2	SO4	B	301	-	4,4,4	0.33	0	6,6,6	0.22	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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, 95^{th} 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	271/329 (82%)	0.50	22 (8%) 12 16	39, 59, 92, 116	0
1	B	270/329 (82%)	0.30	8 (2%) 50 57	40, 58, 83, 103	0
1	C	274/329 (83%)	0.60	20 (7%) 15 20	41, 62, 104, 131	0
All	All	815/987 (82%)	0.47	50 (6%) 21 27	39, 59, 94, 131	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	181	ALA	6.2
1	C	207	ASP	6.1
1	C	184	LEU	6.0
1	C	182	SER	5.1
1	A	187	SER	4.4
1	B	224	VAL	4.4
1	C	209	ILE	4.0
1	C	187	SER	4.0
1	A	224	VAL	3.9
1	C	66	CYS	3.6
1	C	180	GLN	3.5
1	C	211	LEU	3.4
1	A	222	VAL	3.3
1	C	60	GLY	3.3
1	A	216	LYS	3.2
1	A	225	PRO	3.2
1	A	186	ALA	3.2
1	A	179	HIS	3.0
1	C	179	HIS	3.0
1	A	184	LEU	2.8
1	A	219	ILE	2.8
1	A	213	ARG	2.7
1	B	223	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	219	ILE	2.6
1	B	225	PRO	2.5
1	A	183	LYS	2.5
1	A	181	ALA	2.5
1	A	229	VAL	2.5
1	A	282	ARG	2.5
1	A	204	TYR	2.5
1	C	232	HIS	2.4
1	A	230	SER	2.3
1	B	283	ILE	2.3
1	C	225	PRO	2.3
1	A	281	LYS	2.2
1	C	205	ASP	2.2
1	C	215	PRO	2.2
1	B	67	GLY	2.2
1	C	139	TYR	2.1
1	C	212	ILE	2.1
1	A	226	GLU	2.1
1	C	183	LYS	2.1
1	C	177	GLU	2.1
1	C	178	SER	2.1
1	A	234	PHE	2.1
1	A	228	HIS	2.0
1	A	188	GLY	2.0
1	A	185	ASP	2.0
1	B	221	VAL	2.0
1	B	229	VAL	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, 95^{th} 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	SO4	B	301	5/5	0.94	0.12	72,77,81,87	0
2	SO4	C	301	5/5	0.94	0.17	65,70,72,74	0

6.5 Other polymers (i)

There are no such residues in this entry.