



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 30, 2021 – 04:04 AM EDT

PDB ID : 7JZ7
Title : Dihydrodipicolinate synthase mutant S48F
Authors : Board, A.J.; Dobson, R.C.J.
Deposited on : 2020-09-01
Resolution : 1.74 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
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) : 2.23.2

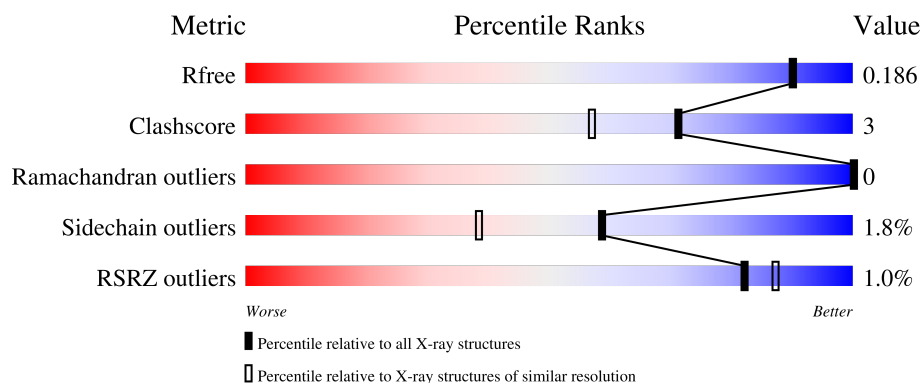
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.74 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	3764 (1.76-1.72)
Clashscore	141614	3923 (1.76-1.72)
Ramachandran outliers	138981	3878 (1.76-1.72)
Sidechain outliers	138945	3878 (1.76-1.72)
RSRZ outliers	127900	3705 (1.76-1.72)

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	292	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>8%</div> </div> </div>
1	B	292	<div> <div>88%</div> <div>11%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5063 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 synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	4	0
			2186	1382	381	408	15			
1	B	292	Total	C	N	O	S	0	8	0
			2224	1402	392	415	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	PHE	SER	engineered mutation	UNP A0A066Q637
B	48	PHE	SER	engineered mutation	UNP A0A066Q637

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	K	0	0
			2	2		
2	B	2	Total	K	0	0
			2	2		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

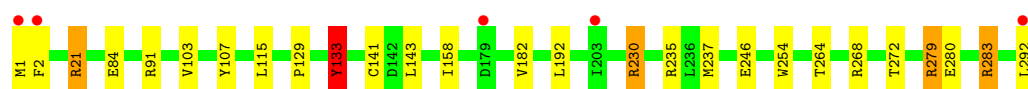
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	305	Total	O	0	0
			305	305		
4	B	314	Total	O	0	0
			314	314		

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.

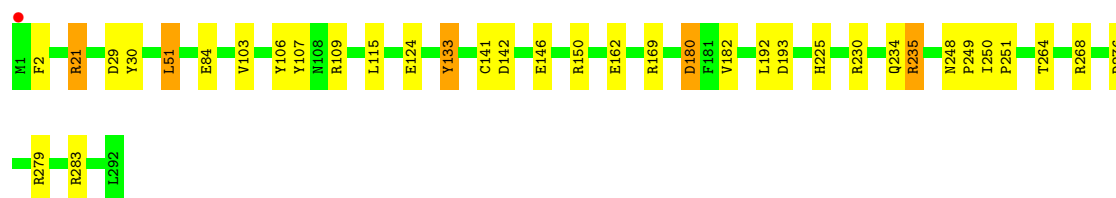
- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain A:  2% 91% 8%



- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain B:  88% 11%



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	120.73Å 120.73Å 110.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.17 – 1.74 32.17 – 1.74	Depositor EDS
% Data completeness (in resolution range)	99.9 (32.17-1.74) 100.0 (32.17-1.74)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 1.74Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.149 , 0.172 0.163 , 0.186	Depositor DCC
R_{free} test set	4777 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	19.0	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 44.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5063	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% 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: GOL, K

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	1.29	4/2234 (0.2%)	1.21	14/3037 (0.5%)
1	B	1.21	6/2278 (0.3%)	1.19	19/3095 (0.6%)
All	All	1.25	10/4512 (0.2%)	1.20	33/6132 (0.5%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	84	GLU	CG-CD	7.61	1.63	1.51
1	A	84	GLU	CD-OE2	6.55	1.32	1.25
1	B	84	GLU	CD-OE1	6.50	1.32	1.25
1	B	84	GLU	CD-OE2	6.33	1.32	1.25
1	B	180	ASP	CB-CG	-5.65	1.39	1.51
1	A	246	GLU	CD-OE2	5.56	1.31	1.25
1	B	106	TYR	CE1-CZ	-5.42	1.31	1.38
1	A	133	TYR	CE2-CZ	-5.34	1.31	1.38
1	A	84	GLU	CG-CD	5.18	1.59	1.51
1	B	30	TYR	CG-CD1	-5.10	1.32	1.39

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	235	ARG	NE-CZ-NH1	9.04	124.82	120.30
1	B	235	ARG	CG-CD-NE	8.64	129.95	111.80
1	B	21[A]	ARG	NE-CZ-NH1	8.35	124.48	120.30
1	B	21[B]	ARG	NE-CZ-NH1	8.35	124.48	120.30
1	B	150	ARG	NE-CZ-NH1	7.61	124.10	120.30
1	A	21	ARG	NE-CZ-NH2	-7.49	116.56	120.30
1	A	133	TYR	CB-CG-CD1	7.33	125.40	121.00
1	B	268	ARG	NE-CZ-NH1	6.70	123.65	120.30
1	B	21[A]	ARG	NE-CZ-NH2	-6.65	116.98	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	21[B]	ARG	NE-CZ-NH2	-6.65	116.98	120.30
1	B	235	ARG	NE-CZ-NH1	-6.57	117.02	120.30
1	A	21	ARG	NE-CZ-NH1	6.53	123.56	120.30
1	B	29	ASP	CB-CG-OD2	-6.43	112.51	118.30
1	A	133	TYR	CB-CG-CD2	-6.30	117.22	121.00
1	B	133	TYR	CB-CG-CD2	-6.26	117.25	121.00
1	B	235	ARG	CA-CB-CG	6.22	127.08	113.40
1	B	276	ASP	CB-CG-OD1	6.18	123.86	118.30
1	B	279	ARG	NE-CZ-NH2	-6.06	117.27	120.30
1	A	143	LEU	CB-CG-CD2	-5.87	101.02	111.00
1	B	29	ASP	CB-CG-OD1	5.79	123.52	118.30
1	B	193	ASP	CB-CG-OD1	5.76	123.48	118.30
1	B	169	ARG	NE-CZ-NH2	-5.65	117.47	120.30
1	A	268	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	A	283[A]	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	A	283[B]	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	B	107	TYR	CB-CG-CD1	-5.51	117.69	121.00
1	A	279	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	A	235	ARG	NE-CZ-NH2	-5.40	117.60	120.30
1	A	107	TYR	CB-CG-CD1	-5.34	117.80	121.00
1	A	279	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	B	133	TYR	CB-CG-CD1	5.18	124.11	121.00
1	A	237	MET	CG-SD-CE	5.05	108.28	100.20
1	B	142	ASP	CB-CG-OD1	5.04	122.83	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	2186	0	2210	13	0
1	B	2224	0	2256	17	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	12	0	16	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	18	0	24	2	0
4	A	305	0	0	5	0
4	B	314	0	0	9	0
All	All	5063	0	4506	31	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 3.

All (31) 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:B:146:GLU:CG	4:B:714:HOH:O	2.18	0.91
1:A:230[A]:ARG:NH1	4:A:402:HOH:O	2.18	0.76
1:B:230[A]:ARG:NH1	4:B:402:HOH:O	2.18	0.72
1:A:2:PHE:O	1:A:182[A]:VAL:HG11	1.96	0.65
1:B:51:LEU:O	4:B:401:HOH:O	2.15	0.65
1:A:280:GLU:CG	4:A:405:HOH:O	2.45	0.63
1:A:272:THR:OG1	4:A:401:HOH:O	1.98	0.59
1:A:254:TRP:CE2	1:A:279:ARG:HG2	2.39	0.56
1:B:234[B]:GLN:CD	4:B:406:HOH:O	2.43	0.56
1:B:124:GLU:HG3	4:B:553:HOH:O	2.06	0.55
1:B:115:LEU:HD11	1:B:141[B]:CYS:SG	2.48	0.53
1:A:283[A]:ARG:NH1	4:A:405:HOH:O	2.44	0.51
1:A:91:ARG:NH1	4:A:404:HOH:O	2.36	0.51
1:A:21:ARG:HH22	3:A:303:GOL:H2	1.76	0.50
1:B:2:PHE:O	1:B:182[A]:VAL:HG11	2.11	0.50
1:B:192:LEU:HD23	1:B:230[A]:ARG:HG2	1.95	0.48
1:B:250:ILE:HB	1:B:251:PRO:HD3	1.96	0.48
1:A:129:PRO:HB3	1:A:158:ILE:HG12	1.97	0.47
1:B:248:ASN:ND2	1:B:249:PRO:HA	2.29	0.47
1:B:235:ARG:HG3	4:B:559:HOH:O	2.16	0.46
1:B:225:HIS:HE1	4:B:665:HOH:O	2.00	0.44
1:A:192:LEU:CD2	1:A:230[A]:ARG:HG3	2.48	0.43
1:A:103:VAL:HA	1:A:133:TYR:HB3	2.01	0.42
1:B:283[B]:ARG:HD3	4:B:562:HOH:O	2.20	0.42
1:B:192:LEU:CD2	1:B:230[A]:ARG:HG2	2.50	0.42
1:A:115:LEU:HD11	1:A:141[A]:CYS:SG	2.59	0.41
3:B:304:GOL:O3	3:B:304:GOL:O1	2.04	0.41
1:B:21[A]:ARG:HD2	4:B:634:HOH:O	2.21	0.41
1:A:292:LEU:HD12	1:A:292:LEU:HA	1.79	0.40
1:B:109:ARG:HH12	3:B:302:GOL:H2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:VAL:HA	1:B:133:TYR:HB3	2.04	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	294/292 (101%)	292 (99%)	2 (1%)	0	100	100
1	B	298/292 (102%)	296 (99%)	2 (1%)	0	100	100
All	All	592/584 (101%)	588 (99%)	4 (1%)	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	229/238 (96%)	224 (98%)	5 (2%)	52	29
1	B	237/238 (100%)	233 (98%)	4 (2%)	60	41
All	All	466/476 (98%)	457 (98%)	9 (2%)	59	36

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	133	TYR
1	A	230[A]	ARG
1	A	230[B]	ARG
1	A	264	THR
1	B	51	LEU
1	B	162	GLU
1	B	180	ASP
1	B	264	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	GLN
1	A	233	ASN
1	A	248	ASN
1	B	90	GLN
1	B	225	HIS
1	B	233	ASN
1	B	248	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 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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
3	GOL	A	303	-	5,5,5	0.63	0	5,5,5	0.87	0
3	GOL	A	302	-	5,5,5	1.49	1 (20%)	5,5,5	1.16	0
3	GOL	B	302	-	5,5,5	0.37	0	5,5,5	0.77	0
3	GOL	B	304	-	5,5,5	1.16	1 (20%)	5,5,5	1.28	1 (20%)
3	GOL	B	303	-	5,5,5	0.45	0	5,5,5	0.77	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
3	GOL	A	303	-	-	4/4/4/4	-
3	GOL	A	302	-	-	0/4/4/4	-
3	GOL	B	302	-	-	4/4/4/4	-
3	GOL	B	304	-	-	1/4/4/4	-
3	GOL	B	303	-	-	2/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	304	GOL	O2-C2	2.39	1.50	1.43
3	A	302	GOL	O3-C3	2.19	1.51	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	304	GOL	C3-C2-C1	-2.16	103.29	111.70

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	GOL	O1-C1-C2-C3
3	A	303	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	A	303	GOL	O2-C2-C3-O3
3	B	302	GOL	C1-C2-C3-O3
3	B	303	GOL	C1-C2-C3-O3
3	B	302	GOL	O1-C1-C2-O2
3	B	302	GOL	O1-C1-C2-C3
3	B	304	GOL	O1-C1-C2-C3
3	A	303	GOL	O1-C1-C2-O2
3	B	303	GOL	O2-C2-C3-O3
3	B	302	GOL	O2-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	303	GOL	1	0
3	B	302	GOL	1	0
3	B	304	GOL	1	0

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	292/292 (100%)	-0.22	5 (1%) 70 76	13, 20, 33, 90	0
1	B	292/292 (100%)	-0.39	1 (0%) 94 95	11, 16, 33, 70	0
All	All	584/584 (100%)	-0.31	6 (1%) 82 87	11, 18, 33, 90	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	292	LEU	4.2
1	A	1	MET	2.7
1	B	1	MET	2.6
1	A	2	PHE	2.5
1	A	179	ASP	2.3
1	A	203	ILE	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(\AA^2)	Q<0.9
3	GOL	B	302	6/6	0.79	0.20	61,66,69,70	0
3	GOL	B	304	6/6	0.82	0.31	43,50,57,62	0
3	GOL	A	303	6/6	0.83	0.25	47,52,60,70	0
3	GOL	B	303	6/6	0.90	0.11	43,50,54,57	0
3	GOL	A	302	6/6	0.90	0.11	29,31,35,37	0
2	K	A	301	1/1	0.98	0.05	24,24,24,24	0
2	K	B	301	1/1	0.99	0.04	20,20,20,20	0
2	K	A	304	1/1	0.99	0.03	26,26,26,26	0
2	K	B	305	1/1	1.00	0.05	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.