Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 10:20 AM EDT

PDB ID	:	2OZ8
Title	:	Crystal structure of putative mandelate racemase from Mesorhizobium loti
Authors	:	Bonanno, J.B.; Freeman, J.; Bain, K.T.; Wu, B.; Sridhar, V.; Smith, D.; Wasserman, S.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on	:	2007-02-25
Resolution	:	2.48 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:

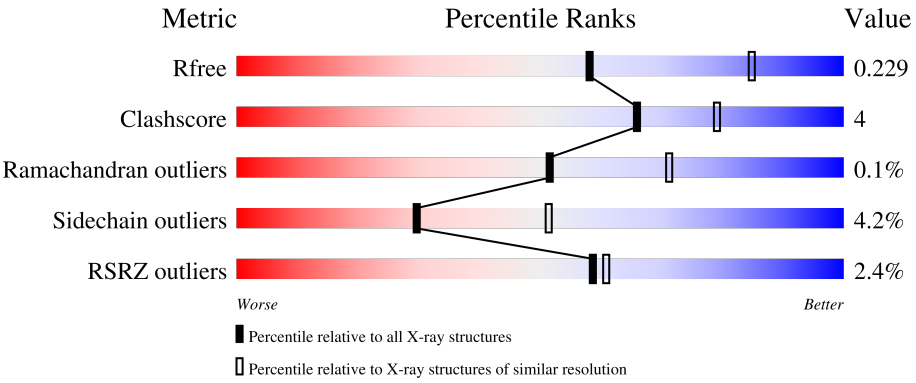
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.48 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	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (2.50-2.46)

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	389	3% 81% 13% • 5%
1	B	389	2% 85% 9% • 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6286 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.

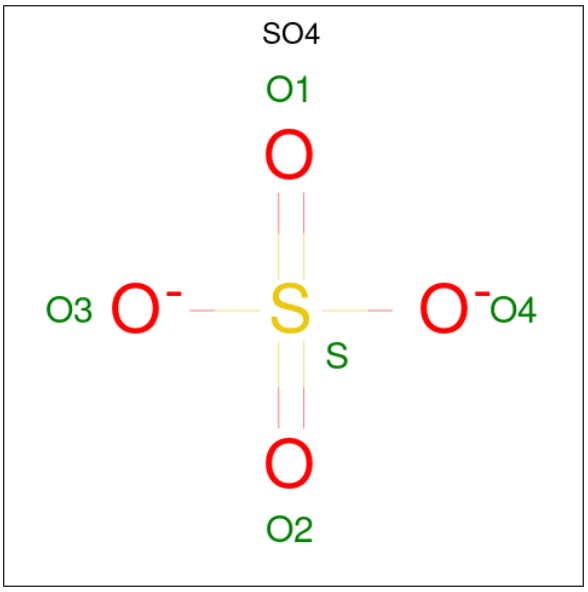
- Molecule 1 is a protein called Mll7089 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	371	Total	C	N	O	S	0	4	0
			2973	1891	541	537	4			
1	B	371	Total	C	N	O	S	0	3	0
			2969	1887	541	537	4			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	cloning artifact	UNP Q987E0
A	0	SER	-	cloning artifact	UNP Q987E0
A	1	LEU	-	cloning artifact	UNP Q987E0
A	380	GLU	-	cloning artifact	UNP Q987E0
A	381	GLY	-	cloning artifact	UNP Q987E0
A	382	HIS	-	cloning artifact	UNP Q987E0
A	383	HIS	-	cloning artifact	UNP Q987E0
A	384	HIS	-	cloning artifact	UNP Q987E0
A	385	HIS	-	cloning artifact	UNP Q987E0
A	386	HIS	-	cloning artifact	UNP Q987E0
A	387	HIS	-	cloning artifact	UNP Q987E0
B	-1	MET	-	cloning artifact	UNP Q987E0
B	0	SER	-	cloning artifact	UNP Q987E0
B	1	LEU	-	cloning artifact	UNP Q987E0
B	380	GLU	-	cloning artifact	UNP Q987E0
B	381	GLY	-	cloning artifact	UNP Q987E0
B	382	HIS	-	cloning artifact	UNP Q987E0
B	383	HIS	-	cloning artifact	UNP Q987E0
B	384	HIS	-	cloning artifact	UNP Q987E0
B	385	HIS	-	cloning artifact	UNP Q987E0
B	386	HIS	-	cloning artifact	UNP Q987E0
B	387	HIS	-	cloning artifact	UNP Q987E0

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



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

- Molecule 3 is water.

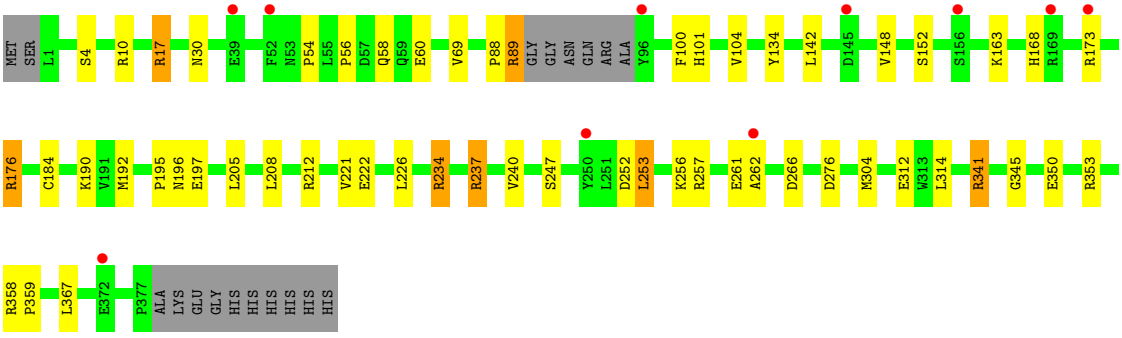
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	151	Total O 151 151	0	0
3	B	153	Total O 153 153	0	0

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.

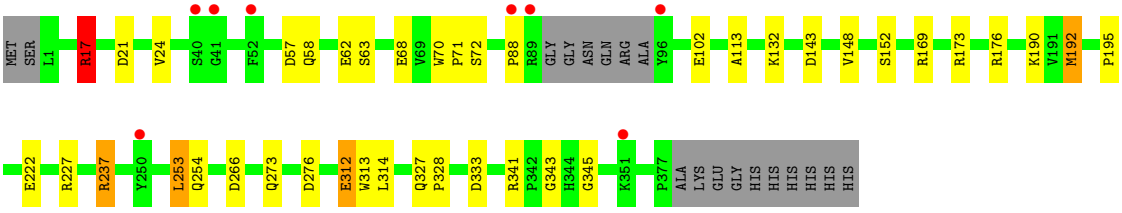
• Molecule 1: Mll7089 protein

Chain A:



• Molecule 1: Mll7089 protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α, β, γ	160.18Å 160.18Å 82.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.48 29.87 – 2.48	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.48) 100.0 (29.87-2.48)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	0.18	Depositor
$< I/\sigma(I) >$ [1]	3.16 (at 2.48Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.174 , 0.229 0.178 , 0.229	Depositor DCC
R_{free} test set	1946 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	28.6	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 45.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6286	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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	0.89	3/3054 (0.1%)	0.91	9/4148 (0.2%)
1	B	0.90	0/3047	0.86	6/4138 (0.1%)
All	All	0.90	3/6101 (0.0%)	0.88	15/8286 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	197	GLU	CG-CD	5.54	1.60	1.51
1	A	190	LYS	CE-NZ	5.38	1.62	1.49
1	A	190	LYS	CD-CE	5.05	1.63	1.51

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	17	ARG	NE-CZ-NH1	8.83	124.72	120.30
1	B	17	ARG	NE-CZ-NH2	-7.99	116.31	120.30
1	A	212	ARG	NE-CZ-NH1	-7.49	116.56	120.30
1	A	17	ARG	NE-CZ-NH2	-7.38	116.61	120.30
1	B	17	ARG	NE-CZ-NH1	7.14	123.87	120.30
1	A	237	ARG	NE-CZ-NH2	-6.52	117.04	120.30
1	A	197	GLU	OE1-CD-OE2	-6.45	115.56	123.30
1	A	234	ARG	NE-CZ-NH2	-6.16	117.22	120.30
1	B	57	ASP	CB-CG-OD1	6.08	123.77	118.30
1	B	192	MET	CB-CG-SD	5.65	129.35	112.40
1	A	341	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	B	237	ARG	NE-CZ-NH2	-5.48	117.56	120.30
1	A	237	ARG	NE-CZ-NH1	5.41	123.01	120.30
1	B	192	MET	CA-CB-CG	5.12	122.01	113.30
1	A	304	MET	CG-SD-CE	-5.07	92.09	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	2973	0	2946	29	0
1	B	2969	0	2937	19	0
2	A	15	0	0	3	0
2	B	25	0	0	0	0
3	A	151	0	0	1	0
3	B	153	0	0	4	0
All	All	6286	0	5883	48	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 (48) 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:173:ARG:NH1	1:B:176:ARG:HH11	1.71	0.88
1:B:17:ARG:HD2	3:B:456:HOH:O	1.71	0.88
1:B:58[B]:GLN:NE2	1:B:62:GLU:OE2	2.12	0.83
1:A:176:ARG:HH11	1:A:176:ARG:HG2	1.55	0.71
1:B:173:ARG:NH1	1:B:176:ARG:NH1	2.40	0.69
1:A:234:ARG:NH2	2:A:388:SO4:O4	2.25	0.69
1:A:253:LEU:HG	1:A:276:ASP:HB3	1.76	0.68
1:A:237:ARG:HD2	1:A:266:ASP:OD1	1.96	0.65
1:B:341:ARG:NH1	1:B:345:GLY:O	2.32	0.63
1:B:132:LYS:NZ	3:B:512:HOH:O	2.33	0.62
1:B:312:GLU:HG2	1:B:313:TRP:CD1	2.36	0.61
1:A:134:TYR:HE1	1:A:163:LYS:HE3	1.68	0.58
1:A:350:GLU:OE1	1:A:353:ARG:NH1	2.38	0.57
1:A:176:ARG:HG2	1:A:176:ARG:NH1	2.20	0.56
1:B:237:ARG:HD2	1:B:266:ASP:OD1	2.05	0.56
1:A:208:LEU:CD2	1:A:221[B]:VAL:HG21	2.35	0.56
1:A:208:LEU:HD21	1:A:221[B]:VAL:HG21	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:HIS:HE1	2:A:390:SO4:O3	1.89	0.55
1:B:72:SER:HB3	3:B:464:HOH:O	2.07	0.54
1:B:173:ARG:HH12	1:B:176:ARG:HH11	1.52	0.52
1:A:341:ARG:NH2	3:A:448:HOH:O	2.14	0.52
1:A:134:TYR:CE1	1:A:163:LYS:HE3	2.45	0.52
1:A:314:LEU:C	1:A:314:LEU:HD23	2.31	0.51
1:A:10:ARG:HD3	1:A:358:ARG:O	2.11	0.50
1:A:152:SER:HB3	1:A:184:CYS:HB2	1.96	0.47
1:B:253:LEU:HG	1:B:276:ASP:HB3	1.97	0.47
1:A:30:ASN:CG	1:A:54:PRO:HA	2.36	0.46
1:B:195:PRO:HD2	1:B:222:GLU:O	2.16	0.46
1:A:195:PRO:HD2	1:A:222:GLU:O	2.17	0.45
1:A:56:PRO:HB2	1:A:60:GLU:HB3	2.00	0.44
1:B:21:ASP:OD1	1:B:24:VAL:HG12	2.17	0.44
1:A:58:GLN:HB2	1:A:359:PRO:HA	2.00	0.43
1:B:327:GLN:HA	1:B:328:PRO:HD2	1.87	0.43
1:A:88:PRO:O	1:A:89:ARG:C	2.57	0.43
1:A:168:HIS:ND1	2:A:389:SO4:O4	2.52	0.42
1:B:227:ARG:HB3	3:B:489:HOH:O	2.18	0.42
1:B:70:TRP:N	1:B:71:PRO:CD	2.83	0.42
1:A:341:ARG:NH1	1:A:345:GLY:O	2.52	0.42
1:B:113:ALA:HB3	1:B:343:GLY:HA2	2.02	0.42
1:A:168:HIS:CD2	1:A:173:ARG:HG2	2.56	0.41
1:A:100:PHE:O	1:A:104:VAL:HG23	2.21	0.41
1:A:226:LEU:HD12	1:A:226:LEU:HA	1.89	0.41
1:A:257:ARG:NH1	1:A:261:GLU:OE2	2.53	0.41
1:A:205:LEU:HD13	1:A:240:VAL:HG22	2.03	0.41
1:A:252:ASP:O	1:A:256:LYS:HG3	2.21	0.41
1:B:102:GLU:HB2	1:B:273:GLN:HG3	2.02	0.41
1:B:254:GLN:H	1:B:254:GLN:CD	2.24	0.40
1:A:234:ARG:HH21	1:A:262:ALA:HB1	1.85	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	371/389 (95%)	364 (98%)	7 (2%)	0	100	100
1	B	370/389 (95%)	363 (98%)	6 (2%)	1 (0%)	41	59
All	All	741/778 (95%)	727 (98%)	13 (2%)	1 (0%)	51	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	88	PRO

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	313/322 (97%)	300 (96%)	13 (4%)	30	51
1	B	312/322 (97%)	299 (96%)	13 (4%)	30	51
All	All	625/644 (97%)	599 (96%)	26 (4%)	30	51

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	17	ARG
1	A	69	VAL
1	A	89	ARG
1	A	142	LEU
1	A	148	VAL
1	A	176	ARG
1	A	192	MET
1	A	196	ASN
1	A	247	SER
1	A	253	LEU
1	A	312	GLU

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Mol	Chain	Res	Type
1	A	367	LEU
1	B	17	ARG
1	B	63	SER
1	B	68	GLU
1	B	143	ASP
1	B	148	VAL
1	B	152	SER
1	B	169	ARG
1	B	190	LYS
1	B	192	MET
1	B	253	LEU
1	B	312	GLU
1	B	314	LEU
1	B	333	ASP

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	295	ASN
1	B	295	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)

8 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	A	389	-	4,4,4	0.35	0	6,6,6	0.66	0
2	SO4	B	391	-	4,4,4	0.57	0	6,6,6	0.41	0
2	SO4	B	392	-	4,4,4	0.41	0	6,6,6	0.66	0
2	SO4	B	390	-	4,4,4	0.80	0	6,6,6	0.83	0
2	SO4	A	390	-	4,4,4	0.71	0	6,6,6	0.71	0
2	SO4	A	388	-	4,4,4	0.27	0	6,6,6	0.40	0
2	SO4	B	389	-	4,4,4	0.54	0	6,6,6	0.63	0
2	SO4	B	388	-	4,4,4	0.41	0	6,6,6	0.37	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.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	389	SO4	1	0
2	A	390	SO4	1	0
2	A	388	SO4	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

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	371/389 (95%)	-0.14	10 (2%) 54 56	30, 41, 58, 69	0
1	B	371/389 (95%)	-0.12	8 (2%) 62 64	31, 42, 56, 75	0
All	All	742/778 (95%)	-0.13	18 (2%) 59 61	30, 42, 57, 75	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	96	TYR	6.1
1	B	88	PRO	4.2
1	B	52	PHE	3.3
1	B	351	LYS	3.1
1	B	89	ARG	2.8
1	B	250	TYR	2.7
1	A	39	GLU	2.6
1	A	96	TYR	2.5
1	A	262	ALA	2.4
1	A	52	PHE	2.3
1	A	169	ARG	2.3
1	B	40	SER	2.2
1	A	145	ASP	2.2
1	A	156	SER	2.1
1	B	41	GLY	2.1
1	A	173	ARG	2.1
1	A	372	GLU	2.0
1	A	250	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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	389	5/5	0.90	0.44	60,63,67,68	0
2	SO4	B	391	5/5	0.90	0.35	69,69,70,71	0
2	SO4	A	390	5/5	0.91	0.42	59,62,65,67	0
2	SO4	B	390	5/5	0.94	0.32	54,55,59,64	0
2	SO4	B	392	5/5	0.94	0.44	56,57,60,60	0
2	SO4	B	388	5/5	0.95	0.23	56,59,61,61	0
2	SO4	A	388	5/5	0.96	0.29	57,57,58,59	0
2	SO4	A	389	5/5	0.96	0.48	57,58,60,61	0

6.5 Other polymers (i)

There are no such residues in this entry.