Full wwPDB X-ray Structure Validation Report (i)

Nov 16, 2023 – 02:21 AM JST

PDB ID	:	6KOG
Title	:	Ketosynthase domain in tenuazonic acid synthetase 1 (TAS1).
Authors	:	Yun, C.S.; Nishimoto, K.; Motoyama, T.; Hino, T.; Nagano, S.; Osada, H.
Deposited on	:	2019-08-10
Resolution	:	1.68 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:

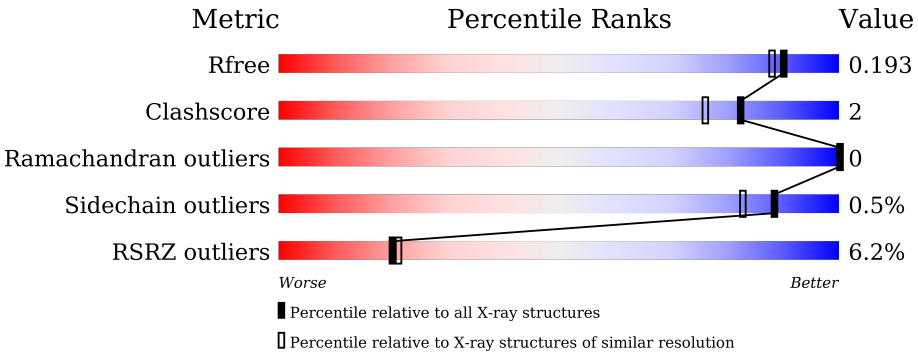
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.68 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	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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	463	2% 91% · 6%
1	B	463	10% 89% 5% 6%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6991 atoms, of which 8 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 Hybrid PKS-NRPS synthetase TAS1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	436	Total	C	N	O	S	0	5	0
			3154	1977	545	613	19			
1	B	433	Total	C	N	O	S	0	5	0
			3125	1964	544	599	18			

There are 62 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP G4N137
A	434	GLY	-	conflict	UNP G4N137
A	435	VAL	-	conflict	UNP G4N137
A	436	THR	-	conflict	UNP G4N137
A	437	SER	-	conflict	UNP G4N137
A	438	LEU	-	conflict	UNP G4N137
A	439	GLY	-	conflict	UNP G4N137
A	440	TYR	-	conflict	UNP G4N137
A	441	GLY	-	conflict	UNP G4N137
A	442	GLY	-	conflict	UNP G4N137
A	443	SER	-	conflict	UNP G4N137
A	444	ASN	-	conflict	UNP G4N137
A	445	ALA	-	conflict	UNP G4N137
A	446	HIS	-	conflict	UNP G4N137
A	447	VAL	-	conflict	UNP G4N137
A	448	VAL	-	conflict	UNP G4N137
A	449	LEU	-	conflict	UNP G4N137
A	450	ALA	-	conflict	UNP G4N137
A	451	SER	-	conflict	UNP G4N137
A	452	ALA	-	conflict	UNP G4N137
A	453	GLN	-	conflict	UNP G4N137
A	454	LEU	-	conflict	UNP G4N137
A	455	PHE	-	conflict	UNP G4N137
A	456	GLY	-	conflict	UNP G4N137
A	457	VAL	-	conflict	UNP G4N137

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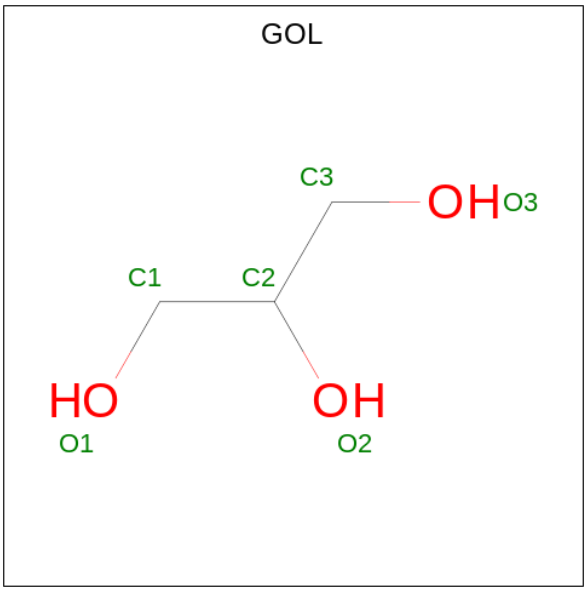
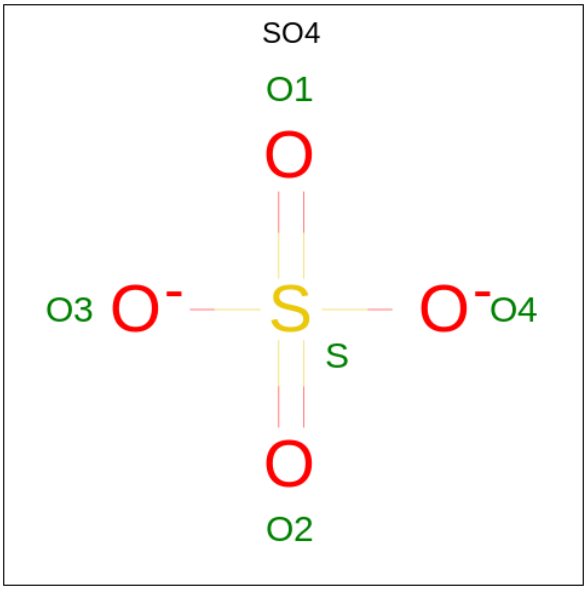
Chain	Residue	Modelled	Actual	Comment	Reference
A	458	GLU	-	conflict	UNP G4N137
A	459	GLN	-	conflict	UNP G4N137
A	460	LYS	-	conflict	UNP G4N137
A	461	ALA	-	conflict	UNP G4N137
A	462	PHE	-	conflict	UNP G4N137
A	463	PHE	-	conflict	UNP G4N137
B	1	MET	-	initiating methionine	UNP G4N137
B	434	GLY	-	conflict	UNP G4N137
B	435	VAL	-	conflict	UNP G4N137
B	436	THR	-	conflict	UNP G4N137
B	437	SER	-	conflict	UNP G4N137
B	438	LEU	-	conflict	UNP G4N137
B	439	GLY	-	conflict	UNP G4N137
B	440	TYR	-	conflict	UNP G4N137
B	441	GLY	-	conflict	UNP G4N137
B	442	GLY	-	conflict	UNP G4N137
B	443	SER	-	conflict	UNP G4N137
B	444	ASN	-	conflict	UNP G4N137
B	445	ALA	-	conflict	UNP G4N137
B	446	HIS	-	conflict	UNP G4N137
B	447	VAL	-	conflict	UNP G4N137
B	448	VAL	-	conflict	UNP G4N137
B	449	LEU	-	conflict	UNP G4N137
B	450	ALA	-	conflict	UNP G4N137
B	451	SER	-	conflict	UNP G4N137
B	452	ALA	-	conflict	UNP G4N137
B	453	GLN	-	conflict	UNP G4N137
B	454	LEU	-	conflict	UNP G4N137
B	455	PHE	-	conflict	UNP G4N137
B	456	GLY	-	conflict	UNP G4N137
B	457	VAL	-	conflict	UNP G4N137
B	458	GLU	-	conflict	UNP G4N137
B	459	GLN	-	conflict	UNP G4N137
B	460	LYS	-	conflict	UNP G4N137
B	461	ALA	-	conflict	UNP G4N137
B	462	PHE	-	conflict	UNP G4N137
B	463	PHE	-	conflict	UNP G4N137

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

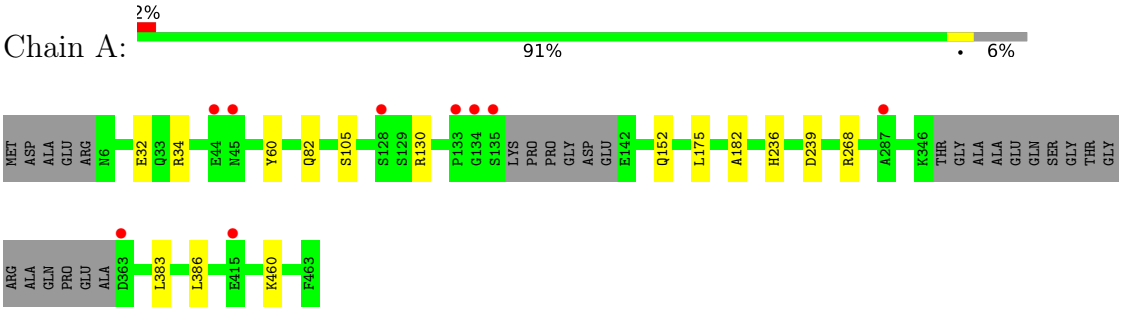
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	386	Total O 386 386	0	0
4	B	307	Total O 307 307	0	0

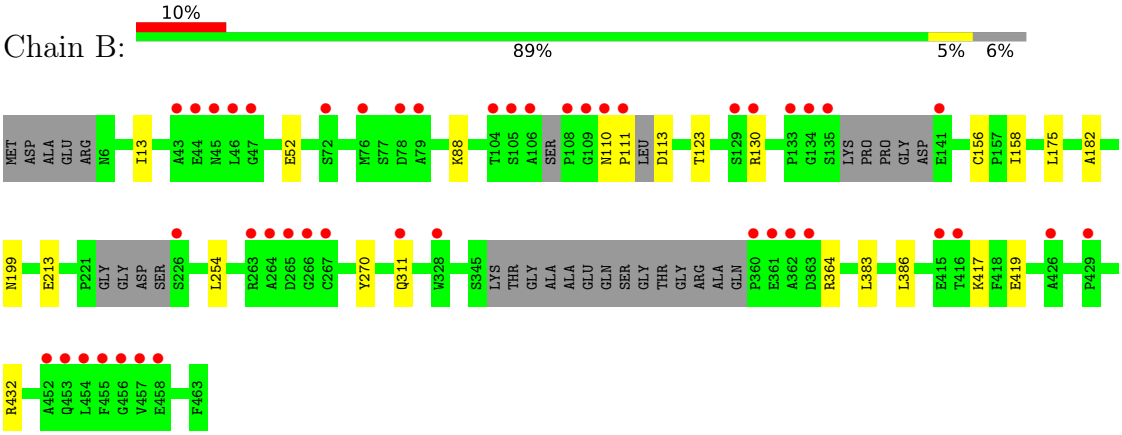
3 Residue-property plots (i)

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: Hybrid PKS-NRPS synthetase TAS1



• Molecule 1: Hybrid PKS-NRPS synthetase TAS1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	79.63Å 99.14Å 127.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.57 – 1.68 49.57 – 1.68	Depositor EDS
% Data completeness (in resolution range)	98.7 (49.57-1.68) 98.7 (49.57-1.68)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.70 (at 1.68Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.165 , 0.192 0.165 , 0.193	Depositor DCC
R_{free} test set	5763 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	20.6	Xtriage
Anisotropy	0.402	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 53.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	6991	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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, GOL

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	0.76	1/3231 (0.0%)	0.82	0/4398
1	B	0.68	1/3200 (0.0%)	0.75	0/4352
All	All	0.72	2/6431 (0.0%)	0.79	0/8750

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	460	LYS	CE-NZ	5.14	1.61	1.49
1	B	156	CYS	CB-SG	-5.06	1.73	1.81

There are no bond angle outliers.

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	3154	0	3072	12	0
1	B	3125	0	3036	19	0
2	A	6	8	8	1	0
3	B	5	0	0	0	0
4	A	386	0	0	5	0
4	B	307	0	0	7	0
All	All	6983	8	6116	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 2.

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:113:ASP:HA	1:B:199:ASN:HD22	1.43	0.83
1:B:311:GLN:HE21	1:B:432:ARG:HH22	1.26	0.82
1:B:364:ARG:HD3	1:B:419:GLU:OE2	1.82	0.80
1:B:130:ARG:NH2	4:B:601:HOH:O	2.10	0.79
1:A:82[B]:GLN:NE2	4:A:601:HOH:O	2.03	0.79
1:B:182:ALA:HB1	1:B:383:LEU:HG	1.69	0.74
1:A:82[A]:GLN:NE2	4:A:602:HOH:O	2.07	0.71
1:B:123[B]:THR:HG21	4:B:667:HOH:O	1.90	0.70
1:B:113:ASP:HA	1:B:199:ASN:ND2	2.07	0.70
1:B:123[B]:THR:HG22	4:B:817:HOH:O	1.92	0.69
1:B:123[B]:THR:HG23	4:B:813:HOH:O	2.04	0.58
1:A:34:ARG:NH2	4:A:605:HOH:O	2.38	0.56
1:A:182:ALA:HB1	1:A:383:LEU:HG	1.90	0.54
1:A:60:TYR:CE1	2:A:501:GOL:H31	2.46	0.49
1:B:213:GLU:OE2	4:B:601:HOH:O	2.20	0.48
1:A:236:HIS:HE1	4:A:641:HOH:O	1.96	0.48
1:B:254:LEU:HD11	1:B:386:LEU:HD23	1.94	0.48
1:A:383:LEU:HD23	1:A:386:LEU:HD12	1.96	0.47
1:B:383:LEU:HD23	1:B:383:LEU:HA	1.66	0.47
1:A:383:LEU:HD23	1:A:383:LEU:HA	1.68	0.47
1:B:417:LYS:CE	4:B:618:HOH:O	2.63	0.47
1:B:88:LYS:HG3	1:B:158:ILE:HG12	1.98	0.45
1:A:236:HIS:HB3	1:A:239:ASP:HB3	1.99	0.45
1:B:52:GLU:H	1:B:52:GLU:CD	2.20	0.45
1:B:417:LYS:HE3	4:B:618:HOH:O	2.16	0.45
1:B:110:ASN:HA	1:B:111:PRO:HD3	1.84	0.44
1:B:13:ILE:HG22	1:B:270:TYR:CE2	2.52	0.43
1:B:254:LEU:CD1	1:B:386:LEU:HD23	2.49	0.42
1:A:105:SER:HB3	1:A:268:ARG:HD2	2.00	0.42
1:A:152:GLN:NE2	4:A:612:HOH:O	2.48	0.41
1:A:32:GLU:HB2	1:A:34:ARG:HD3	2.02	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	435/463 (94%)	426 (98%)	9 (2%)	0	100	100
1	B	426/463 (92%)	418 (98%)	8 (2%)	0	100	100
All	All	861/926 (93%)	844 (98%)	17 (2%)	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	326/350 (93%)	324 (99%)	2 (1%)	86	79
1	B	317/350 (91%)	316 (100%)	1 (0%)	92	89
All	All	643/700 (92%)	640 (100%)	3 (0%)	88	83

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	ARG
1	A	175	LEU
1	B	175	LEU

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	311	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

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	GOL	A	501	-	5,5,5	1.20	0	5,5,5	1.24	1 (20%)
3	SO4	B	501	-	4,4,4	0.15	0	6,6,6	0.37	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	GOL	A	501	-	-	2/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	GOL	C3-C2-C1	-2.36	102.51	111.70

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	O1-C1-C2-C3
2	A	501	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	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

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	436/463 (94%)	0.11	9 (2%) 63 67	13, 19, 38, 55	0
1	B	433/463 (93%)	0.33	45 (10%) 6 6	16, 24, 48, 71	0
All	All	869/926 (93%)	0.22	54 (6%) 20 21	13, 21, 43, 71	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	109	GLY	8.8
1	B	108	PRO	7.7
1	B	110	ASN	7.4
1	B	362	ALA	6.0
1	B	106	ALA	5.8
1	B	105	SER	5.7
1	B	135	SER	5.6
1	B	267	CYS	5.2
1	B	360	PRO	5.0
1	A	135	SER	4.7
1	A	415	GLU	4.3
1	B	111	PRO	4.3
1	B	104	THR	4.3
1	B	456	GLY	4.3
1	A	287	ALA	4.2
1	B	264	ALA	3.9
1	B	133	PRO	3.8
1	B	78	ASP	3.7
1	B	79	ALA	3.7
1	B	453	GLN	3.6
1	B	361	GLU	3.6
1	A	133	PRO	3.5
1	B	134	GLY	3.4
1	B	45	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	455	PHE	3.2
1	B	429	PRO	3.0
1	B	415	GLU	3.0
1	A	134	GLY	2.9
1	B	457	VAL	2.9
1	B	47	GLY	2.9
1	B	130	ARG	2.8
1	B	328	TRP	2.8
1	B	454	LEU	2.8
1	B	43	ALA	2.8
1	B	226	SER	2.7
1	B	141	GLU	2.7
1	B	265	ASP	2.7
1	B	266	GLY	2.5
1	B	416	THR	2.5
1	B	46	LEU	2.4
1	B	311	GLN	2.4
1	B	426	ALA	2.4
1	B	263	ARG	2.3
1	B	363	ASP	2.3
1	B	129	SER	2.3
1	A	45	ASN	2.3
1	A	363	ASP	2.2
1	A	44	GLU	2.2
1	B	44	GLU	2.2
1	B	452	ALA	2.2
1	A	128	SER	2.1
1	B	76	MET	2.1
1	B	72	SER	2.0
1	B	458	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

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	GOL	A	501	6/6	0.92	0.12	23,35,44,49	0
3	SO4	B	501	5/5	0.97	0.23	40,42,47,59	0

6.5 Other polymers

There are no such residues in this entry.