



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 01:32 am BST

PDB ID : 2VOB
Title : TRYPANOTHIONE SYNTHETASE
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Deposited on : 2008-02-13
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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

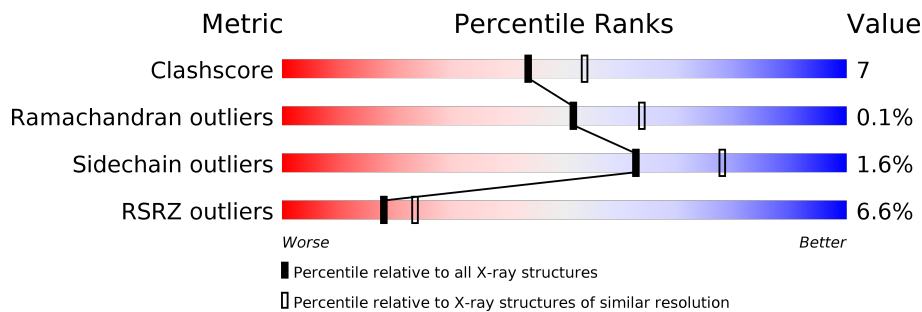
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
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 on 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	652	 5% 80% 11% 8%
1	B	652	 7% 76% 15% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10464 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 TRYPANOTHIONE SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	598	4948	3165	846	914	23	0	12	0
1	B	591	4911	3142	841	906	22	0	16	0

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total 1	Cl 1	0	0
2	A	1	Total 1	Cl 1	0	0

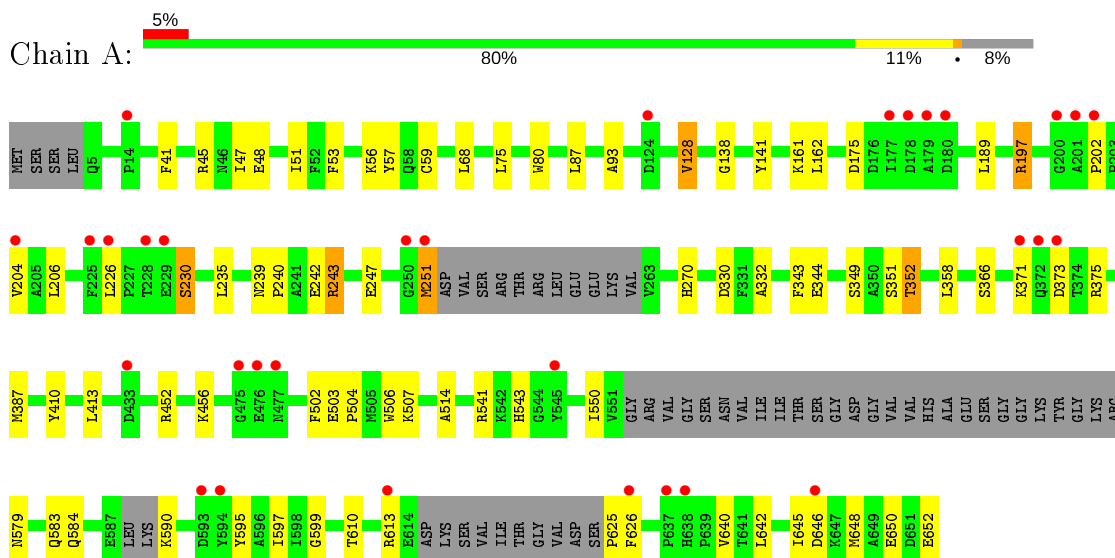
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	359	Total 359	O 359	0	0
3	B	244	Total 244	O 244	0	0

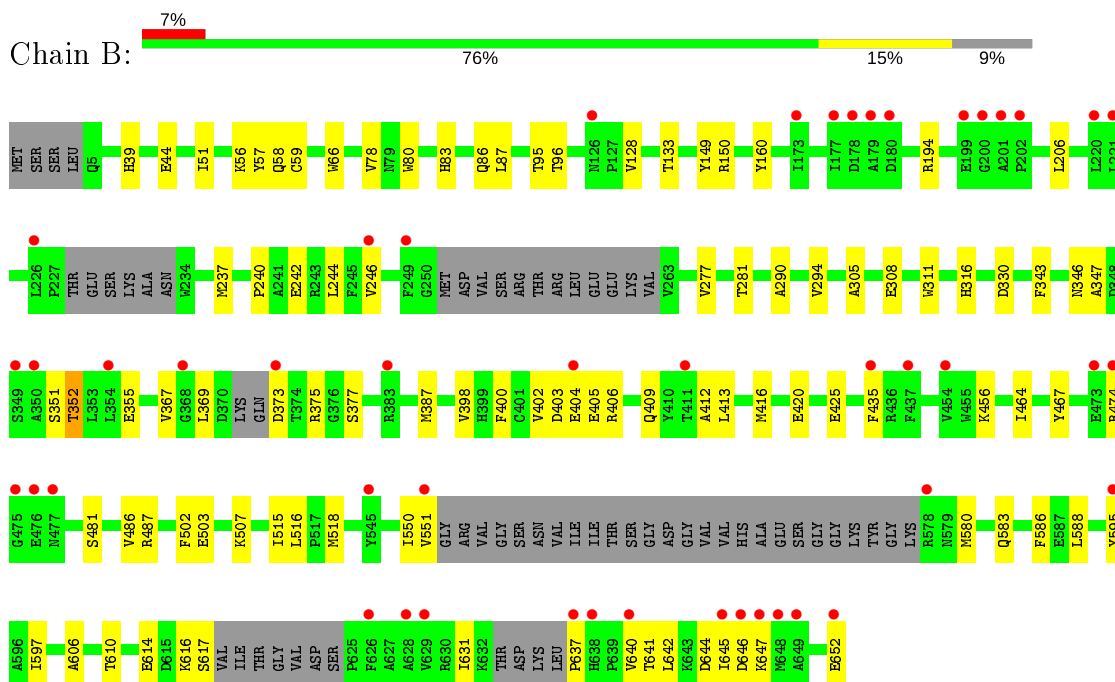
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: TRYPANOTHIONE SYNTHETASE



- Molecule 1: TRYPANOTHIONE SYNTHETASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.12Å 127.71Å 88.79Å 90.00° 94.56° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 20.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.30) 99.9 (20.00-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.57 (at 2.30Å)	Xtrriage
Refinement program	REFMAC 5.3.0027	Depositor
R, R_{free}	0.190 , 0.251 0.196 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	31.9	Xtrriage
Anisotropy	0.182	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.6	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	0.93	EDS
Total number of atoms	10464	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% 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

5.1 Standard geometry

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

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	0.72	3/5093 (0.1%)	0.72	5/6903 (0.1%)
1	B	0.61	0/5048	0.68	4/6840 (0.1%)
All	All	0.67	3/10141 (0.0%)	0.70	9/13743 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	4
All	All	0	8

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	243[A]	ARG	CD-NE	15.92	1.73	1.46
1	A	243[B]	ARG	CD-NE	15.92	1.73	1.46
1	A	48	GLU	CB-CG	5.11	1.61	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	503	GLU	N-CA-C	-6.88	92.42	111.00
1	B	637	PRO	N-CA-CB	6.07	110.59	103.30
1	A	57	TYR	N-CA-C	5.54	125.95	111.00
1	A	197	ARG	NE-CZ-NH1	5.45	123.02	120.30
1	A	503	GLU	N-CA-C	-5.18	97.00	111.00
1	A	452	ARG	NE-CZ-NH1	5.15	122.88	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	194	ARG	NE-CZ-NH2	5.07	122.83	120.30
1	A	45	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	B	57	TYR	N-CA-C	5.00	124.50	111.00

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	502	PHE	Mainchain,Peptide
1	A	56	LYS	Mainchain,Peptide
1	B	502	PHE	Mainchain,Peptide
1	B	56	LYS	Mainchain,Peptide

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	4948	0	4707	53	0
1	B	4911	0	4668	75	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	359	0	0	7	0
3	B	244	0	0	4	0
All	All	10464	0	9375	127	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 7.

All (127) 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:367:VAL:HG23	1:B:369:LEU:HD13	1.48	0.96
1:B:474:ARG:NH2	1:B:487:ARG:CD	2.29	0.95
1:B:474:ARG:NH2	1:B:487:ARG:HG3	1.80	0.95
1:B:550:ILE:O	1:B:551:VAL:HG22	1.66	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:ASP:HB3	1:A:597:ILE:HD11	1.54	0.87
1:B:474:ARG:NH2	1:B:487:ARG:CG	2.37	0.86
1:B:95:THR:O	1:B:96:THR:HB	1.78	0.81
1:B:367:VAL:CG2	1:B:369:LEU:HD13	2.10	0.81
1:A:51:ILE:HG12	1:A:206:LEU:HD22	1.63	0.80
1:A:235:LEU:HD12	1:A:251:MET:HE3	1.64	0.80
1:B:642:LEU:O	1:B:645:ILE:HG22	1.83	0.79
1:A:239:ASN:HD22	1:A:242:GLU:HG3	1.49	0.78
1:A:332:ALA:HB2	1:A:343:PHE:HE2	1.48	0.77
1:B:474:ARG:HH21	1:B:487:ARG:CD	2.02	0.72
1:B:435:PHE:HB2	1:B:486:VAL:HG11	1.72	0.72
1:B:367:VAL:HG23	1:B:369:LEU:CD1	2.20	0.72
1:B:474:ARG:HH21	1:B:487:ARG:HG3	1.56	0.70
1:B:244:LEU:HD22	1:B:406:ARG:HG2	1.74	0.69
1:B:39:HIS:HB2	1:B:387:MET:HE1	1.74	0.69
1:B:646:ASP:OD1	1:B:647:LYS:NZ	2.22	0.67
1:A:75:LEU:HD11	1:A:87[B]:LEU:HD21	1.75	0.67
1:B:474:ARG:HH22	1:B:487:ARG:HG3	1.56	0.67
1:B:83:HIS:ND1	1:B:644:ASP:OD1	2.19	0.66
1:B:83:HIS:O	1:B:640:VAL:HG21	1.96	0.66
1:B:474:ARG:NH2	1:B:487:ARG:HD2	2.12	0.65
1:B:346:ASN:OD1	3:B:2181:HOH:O	2.14	0.64
1:B:351:SER:C	1:B:352:THR:HG23	2.18	0.64
1:B:474:ARG:HH22	1:B:487:ARG:CG	2.10	0.63
1:B:474:ARG:HH21	1:B:487:ARG:HD2	1.61	0.63
1:B:86[B]:GLN:NE2	1:B:641:THR:HG21	2.13	0.63
1:A:648:MET:HE3	1:A:650:GLU:CD	2.19	0.63
1:A:75:LEU:CD1	1:A:87[B]:LEU:HD21	2.30	0.62
1:B:242:GLU:O	1:B:246:VAL:HG23	1.99	0.62
1:A:80:TRP:CD1	1:A:128:VAL:HG22	2.34	0.62
1:A:351:SER:O	1:A:352:THR:HB	2.01	0.61
1:B:474:ARG:NH2	1:B:487:ARG:HD3	2.13	0.61
1:A:543[A]:HIS:CE1	1:A:584:GLN:HE21	2.19	0.60
1:B:51:ILE:HG12	1:B:206:LEU:HD22	1.83	0.60
1:B:66:TRP:CE2	1:B:133:THR:HG21	2.36	0.60
1:A:239:ASN:ND2	3:A:2178:HOH:O	2.33	0.60
1:B:606:ALA:HB2	3:B:2239:HOH:O	2.01	0.60
1:B:78:VAL:HG23	1:B:640:VAL:HG11	1.85	0.59
1:B:435:PHE:CB	1:B:486:VAL:HG11	2.34	0.58
1:A:235:LEU:HG	1:A:251:MET:HE1	1.86	0.58
1:B:403:ASP:OD1	1:B:404:GLU:N	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:LEU:HD22	3:A:2178:HOH:O	2.03	0.58
1:B:86[B]:GLN:HE22	1:B:641:THR:HG21	1.70	0.56
1:B:44:GLU:OE1	3:B:2050:HOH:O	2.18	0.55
1:B:377:SER:OG	1:B:610:THR:O	2.18	0.55
1:B:128:VAL:HG21	1:B:652:GLU:HA	1.89	0.55
1:A:543[A]:HIS:CE1	1:A:584:GLN:NE2	2.74	0.54
1:A:332:ALA:CB	1:A:343:PHE:HE2	2.19	0.54
1:A:87[A]:LEU:HD23	1:A:189:LEU:HD13	1.90	0.54
1:A:247:GLU:OE1	3:A:2180:HOH:O	2.19	0.54
1:B:330:ASP:OD2	1:B:346:ASN:ND2	2.41	0.54
1:B:305:ALA:CB	1:B:551:VAL:HG12	2.37	0.53
1:B:80:TRP:CD1	1:B:647:LYS:HB3	2.44	0.53
1:A:270:HIS:NE2	1:A:650:GLU:OE2	2.34	0.53
1:A:59:CYS:SG	1:A:652:GLU:OE1	2.67	0.52
1:B:59:CYS:SG	1:B:652:GLU:OE1	2.67	0.52
1:A:358:LEU:CD2	3:A:2178:HOH:O	2.57	0.52
1:B:474:ARG:HH21	1:B:487:ARG:CG	2.09	0.52
1:B:586[A]:PHE:HE2	1:B:588:LEU:HD21	1.75	0.51
1:A:330:ASP:HB2	1:A:344:GLU:HG2	1.92	0.51
1:B:87[B]:LEU:HD23	1:B:640:VAL:HG23	1.92	0.51
1:B:305:ALA:HB2	1:B:551:VAL:CG1	2.39	0.51
1:B:87[B]:LEU:HD21	1:B:640:VAL:HB	1.92	0.51
1:A:504:PRO:O	1:A:507:LYS:HB2	2.11	0.51
1:B:316:HIS:HD2	3:B:2164:HOH:O	1.95	0.50
1:A:87[B]:LEU:HA	1:A:640:VAL:HG13	1.93	0.50
1:B:305:ALA:HB2	1:B:551:VAL:HG12	1.92	0.50
1:A:506:TRP:CZ3	1:A:507:LYS:HD2	2.47	0.49
1:A:240:PRO:HB2	1:A:413:LEU:HD13	1.94	0.49
1:A:626:PHE:O	1:A:626:PHE:CD2	2.65	0.49
1:B:240:PRO:HB2	1:B:413:LEU:HD13	1.95	0.49
1:B:550:ILE:O	1:B:551:VAL:CG2	2.51	0.49
1:A:375:ARG:HD3	1:A:648:MET:SD	2.53	0.49
1:B:150:ARG:HD3	1:B:160:TYR:CD1	2.47	0.49
1:A:583[A]:GLN:NE2	3:A:2336:HOH:O	2.47	0.48
1:A:541:ARG:NH2	1:B:425:GLU:OE1	2.47	0.48
1:A:235:LEU:HD12	1:A:251:MET:CE	2.39	0.47
1:B:464:ILE:O	1:B:467:TYR:HB3	2.14	0.47
1:A:162:LEU:HD22	1:A:175:ASP:HA	1.97	0.47
1:B:405:GLU:O	1:B:409:GLN:HG3	2.14	0.47
1:A:141:TYR:CD2	1:A:161:LYS:HD3	2.50	0.47
1:A:599:GLY:O	1:A:610:THR:HA	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:MET:HE3	3:A:2246:HOH:O	2.14	0.47
1:A:590:LYS:HD3	1:A:595:TYR:CZ	2.50	0.47
1:A:59:CYS:HG	1:A:652:GLU:CD	2.18	0.46
1:B:377:SER:HA	1:B:631:ILE:HD11	1.97	0.46
1:A:41:PHE:CE2	1:A:650:GLU:HG3	2.50	0.46
1:B:616:LYS:O	1:B:617:SER:HB2	2.16	0.46
1:B:308:GLU:HA	1:B:311:TRP:CE2	2.51	0.46
1:A:645:ILE:O	1:A:646:ASP:HB2	2.16	0.46
1:B:290:ALA:O	1:B:294:VAL:HG23	2.16	0.45
1:B:373:ASP:CG	1:B:373:ASP:O	2.55	0.44
1:B:58:GLN:NE2	1:B:652:GLU:HB3	2.32	0.44
1:A:93:ALA:HB1	1:A:206:LEU:HD12	1.99	0.44
1:B:343:PHE:CZ	1:B:597:ILE:HD12	2.53	0.44
1:B:78:VAL:HG23	1:B:640:VAL:CG1	2.47	0.44
1:B:416:MET:O	1:B:420:GLU:HG3	2.18	0.44
1:A:613:ARG:HA	1:A:625:PRO:O	2.18	0.43
1:A:514:ALA:HB2	1:A:550:ILE:HD12	2.00	0.43
1:B:277:VAL:O	1:B:281:THR:HG23	2.19	0.43
1:B:347:ALA:HB1	1:B:507:LYS:HD2	2.00	0.43
1:A:387:MET:CE	3:A:2246:HOH:O	2.66	0.43
1:B:351:SER:O	1:B:352:THR:HG23	2.17	0.43
1:B:237:MET:CE	1:B:246:VAL:HG11	2.49	0.43
1:A:80:TRP:CG	1:A:128:VAL:HG22	2.54	0.42
1:B:515:ILE:O	1:B:518:MET:HB2	2.19	0.42
1:B:586[A]:PHE:CE2	1:B:588:LEU:HD21	2.55	0.42
1:A:68:LEU:O	1:A:204:VAL:HG21	2.20	0.42
1:B:237:MET:HE2	1:B:246:VAL:HG11	2.01	0.42
1:B:398[B]:VAL:HG13	1:B:400:PHE:HE2	1.85	0.42
1:B:59:CYS:HG	1:B:652:GLU:CD	2.23	0.42
1:A:197:ARG:NH2	1:A:202:PRO:O	2.53	0.41
1:B:516:LEU:HD13	1:B:583:GLN:NE2	2.35	0.41
1:A:47:ILE:HA	1:A:51:ILE:O	2.21	0.41
1:A:138:GLY:HA3	1:A:141:TYR:CE1	2.56	0.41
1:A:230:SER:HA	1:A:366:SER:O	2.21	0.41
1:A:53:PHE:HE1	1:A:68:LEU:HD23	1.85	0.40
1:B:595:TYR:O	1:B:614:GLU:HA	2.21	0.40
1:B:128:VAL:HG21	1:B:652:GLU:HG3	2.03	0.40
1:A:371:LYS:HB2	1:A:373:ASP:OD1	2.21	0.40
1:B:402:VAL:HG11	1:B:412:ALA:HB2	2.03	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	598/652 (92%)	580 (97%)	18 (3%)	0	100	100
1	B	589/652 (90%)	568 (96%)	20 (3%)	1 (0%)	47	58
All	All	1187/1304 (91%)	1148 (97%)	38 (3%)	1 (0%)	51	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	352	THR

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	521/556 (94%)	511 (98%)	10 (2%)	57	73
1	B	516/556 (93%)	510 (99%)	6 (1%)	71	84
All	All	1037/1112 (93%)	1021 (98%)	16 (2%)	62	79

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	128	VAL
1	A	226	LEU
1	A	230	SER
1	A	251	MET
1	A	349	SER

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Mol	Chain	Res	Type
1	A	352	THR
1	A	410	TYR
1	A	456	LYS
1	A	579	ASN
1	A	642	LEU
1	B	149	TYR
1	B	355	GLU
1	B	375	ARG
1	B	456	LYS
1	B	481	SER
1	B	580	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	152	HIS
1	A	211	HIS
1	A	239	ASN
1	A	417	GLN
1	B	152	HIS
1	B	224	ASN
1	B	316	HIS
1	B	583	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 [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	598/652 (91%)	0.16	31 (5%) 27 34	2, 14, 25, 31	28 (4%)
1	B	591/652 (90%)	0.31	47 (7%) 12 16	2, 15, 35, 41	46 (7%)
All	All	1189/1304 (91%)	0.23	78 (6%) 18 23	2, 14, 31, 41	74 (6%)

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	595	TYR	7.6
1	B	649	ALA	7.4
1	B	477	ASN	6.4
1	A	179	ALA	6.4
1	B	646	ASP	5.3
1	B	640	VAL	4.9
1	B	637	PRO	4.8
1	A	228	THR	4.6
1	A	477	ASN	4.6
1	A	372	GLN	4.5
1	B	179	ALA	4.4
1	B	173	ILE	4.3
1	B	178	ASP	4.2
1	B	645	ILE	4.1
1	A	226	LEU	4.1
1	B	373	ASP	3.9
1	B	578	ARG	3.8
1	A	476	GLU	3.7
1	B	246	VAL	3.6
1	B	249	PHE	3.3
1	B	545	TYR	3.3
1	A	180	ASP	3.3
1	B	474	ARG	3.3
1	A	229	GLU	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	476	GLU	3.2
1	B	354	LEU	3.2
1	B	638	HIS	3.2
1	A	475	GLY	3.1
1	A	204	VAL	3.1
1	B	629	VAL	3.1
1	B	202	PRO	3.1
1	A	124	ASP	3.0
1	B	350	ALA	3.0
1	B	177	ILE	3.0
1	B	551	VAL	3.0
1	A	638	HIS	3.0
1	B	220	LEU	2.9
1	A	433	ASP	2.9
1	B	404	GLU	2.9
1	A	250	GLY	2.8
1	B	473	GLU	2.8
1	B	200	GLY	2.7
1	A	626	PHE	2.7
1	B	628	ALA	2.7
1	B	180	ASP	2.6
1	B	475	GLY	2.6
1	B	201	ALA	2.6
1	B	199[A]	GLU	2.6
1	A	251	MET	2.6
1	A	371	LYS	2.5
1	A	178	ASP	2.5
1	A	594	TYR	2.5
1	A	202	PRO	2.4
1	B	652	GLU	2.4
1	A	200	GLY	2.4
1	A	201	ALA	2.4
1	A	225	PHE	2.4
1	A	646	ASP	2.4
1	B	437	PHE	2.4
1	A	637	PRO	2.4
1	A	177	ILE	2.3
1	B	648	MET	2.3
1	B	435	PHE	2.3
1	A	14	PRO	2.3
1	A	593	ASP	2.3
1	B	349	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	226	LEU	2.2
1	B	454	VAL	2.2
1	B	626	PHE	2.2
1	A	373	ASP	2.2
1	B	647	LYS	2.2
1	B	221	LEU	2.1
1	B	411	THR	2.1
1	A	545	TYR	2.1
1	A	613	ARG	2.1
1	B	126[A]	ASN	2.0
1	B	383	ARG	2.0
1	B	368	GLY	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 carbohydrates 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	CL	B	1653	1/1	0.97	0.18	15,15,15,15	0
2	CL	A	1653	1/1	0.98	0.15	11,11,11,11	0

6.5 Other polymers [i](#)

There are no such residues in this entry.