Full wwPDB X-ray Structure Validation Report ⓘ

Jan 18, 2022 – 02:09 PM EST

PDB ID	:	7TKV
Title	:	Crystal Structure of the Thioredox_DsbH Domain-Containing Uncharacterized Protein Bab1_2064 from Brucella abortus
Authors	:	Kim, Y.; Crawford, M.; Endres, M.; Babnigg, G.; Crosson, S.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2022-01-17
Resolution	:	2.80 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:

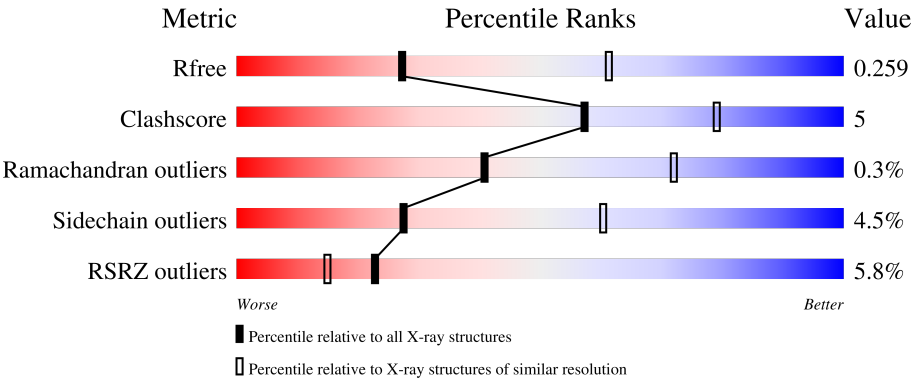
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.25
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.25

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 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	668	5% 83% 12%
1	B	668	6% 74% 17% 8%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 10046 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.

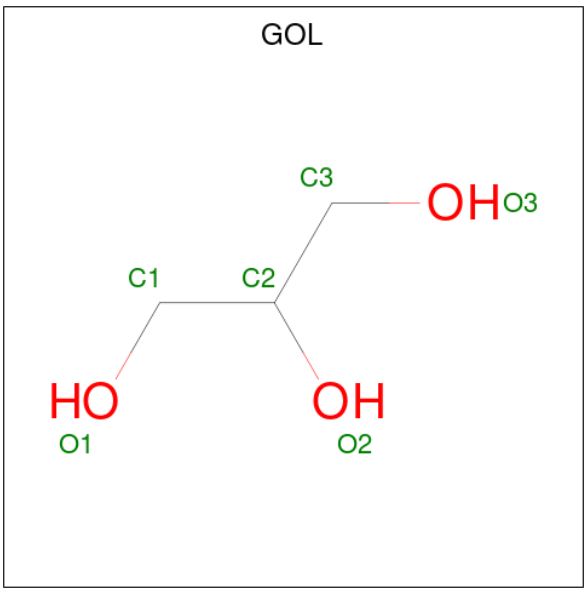
- Molecule 1 is a protein called Thioredox_DsbH domain-containing protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	642	Total	C	N	O	S	Se	0	4	0
			5114	3234	908	952	9	11			
1	B	612	Total	C	N	O	S	Se	0	1	0
			4852	3068	856	911	6	11			

There are 6 discrepancies between the modelled and reference sequences:

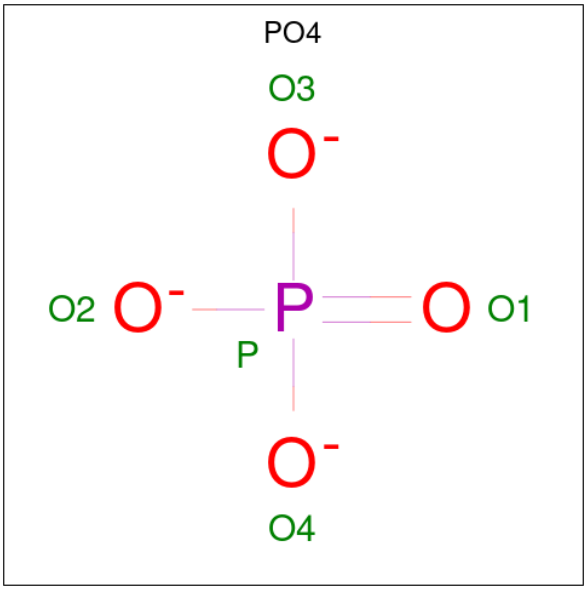
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q2YR10
A	-1	ASN	-	expression tag	UNP Q2YR10
A	0	ALA	-	expression tag	UNP Q2YR10
B	-2	SER	-	expression tag	UNP Q2YR10
B	-1	ASN	-	expression tag	UNP Q2YR10
B	0	ALA	-	expression tag	UNP Q2YR10

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



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

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cl 1 1	0	0

- Molecule 5 is water.

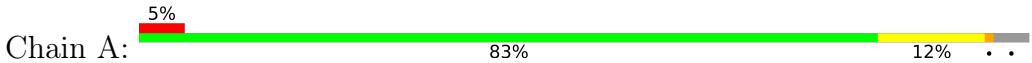
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	20	Total O 20 20	0	0
5	B	11	Total O 11 11	0	0

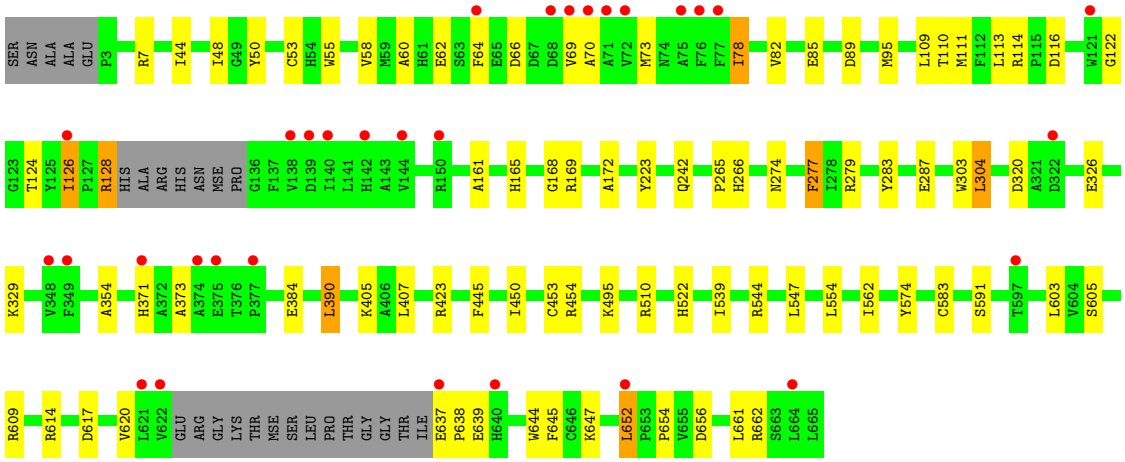
3 Residue-property plots (i)

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: Thioredox_DsbH domain-containing protein

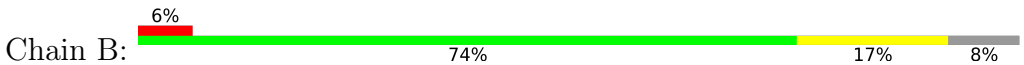
Chain A:

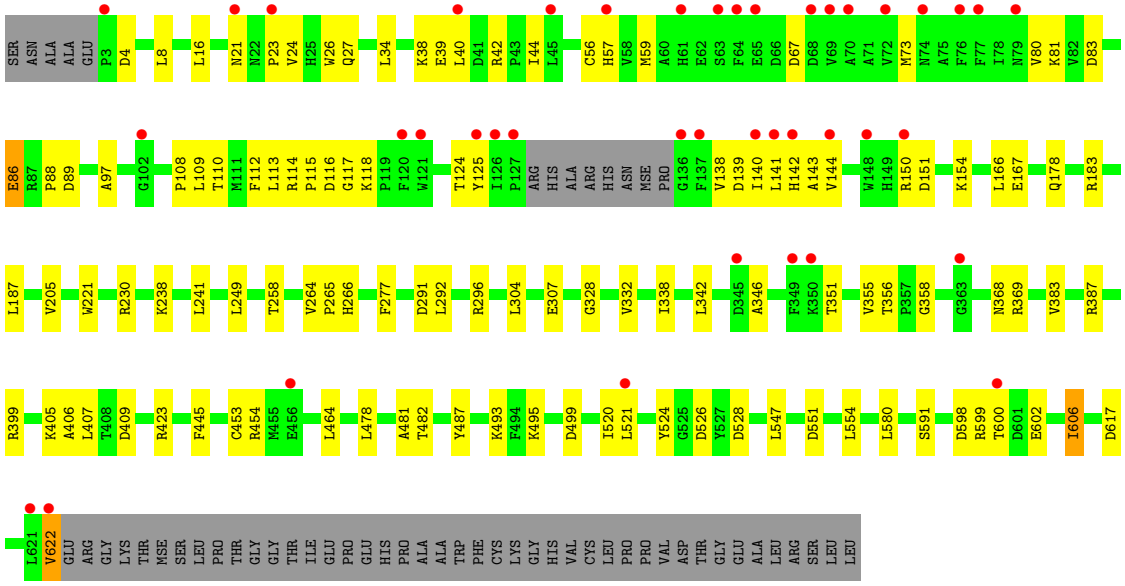




• Molecule 1: Thioredox_DsbH domain-containing protein

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	94.20Å 94.20Å 327.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.25 – 2.80 47.25 – 2.80	Depositor EDS
% Data completeness (in resolution range)	95.0 (47.25-2.80) 95.0 (47.25-2.80)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.19 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
R, R_{free}	0.225 , 0.262 0.223 , 0.259	Depositor DCC
R_{free} test set	1753 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å^2)	62.4	Xtriage
Anisotropy	0.334	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 41.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	10046	wwPDB-VP
Average B, all atoms (Å^2)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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: PO4, CL, 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	0.24	0/5235	0.47	0/7092
1	B	0.24	0/4963	0.47	0/6722
All	All	0.24	0/10198	0.47	0/13814

There are no bond length outliers.

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	5114	0	4898	46	0
1	B	4852	0	4649	52	0
2	A	12	0	16	0	0
2	B	6	0	8	0	0
3	A	10	0	0	0	0
3	B	20	0	0	0	0
4	A	1	0	0	0	0
5	A	20	0	0	1	0
5	B	11	0	0	0	0
All	All	10046	0	9571	95	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 5.

All (95) 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:A:169:ARG:NH2	1:A:574:TYR:OH	2.29	0.66
1:B:38:LYS:HD3	1:B:115:PRO:HB2	1.80	0.62
1:A:407:LEU:HD23	1:A:453:CYS:HB3	1.84	0.60
1:A:495:LYS:HE3	1:A:554:LEU:HD21	1.84	0.58
1:A:48:ILE:HD12	1:A:109:LEU:HD23	1.85	0.58
1:B:44:ILE:HB	1:B:113:LEU:HB2	1.85	0.58
1:A:544:ARG:NH2	5:A:801:HOH:O	2.34	0.57
1:A:605:SER:O	1:A:609:ARG:HG2	2.06	0.55
1:B:117:GLY:C	1:B:520:ILE:HD11	2.28	0.54
1:B:151:ASP:HB3	1:B:154:LYS:HB3	1.90	0.54
1:B:238:LYS:HG3	1:B:292:LEU:HD23	1.89	0.54
1:B:187:LEU:HD22	1:B:580:LEU:HD12	1.90	0.53
1:A:44:ILE:HB	1:A:113:LEU:HB2	1.91	0.53
1:A:645:PHE:HB3	1:A:652:LEU:HD11	1.90	0.53
1:B:406:ALA:HB3	1:B:454:ARG:HG3	1.91	0.53
1:A:639:GLU:HB2	1:B:622:VAL:HG13	1.90	0.52
1:B:24:VAL:HG21	1:B:73:MSE:HE2	1.91	0.52
1:B:407:LEU:HD23	1:B:453:CYS:HB3	1.91	0.51
1:B:97:ALA:HB2	1:B:166:LEU:HD11	1.92	0.51
1:A:274:ASN:HA	1:A:277:PHE:HD1	1.76	0.51
1:B:40:LEU:HD13	1:B:42:ARG:HH21	1.75	0.51
1:A:242:GLN:HE21	1:A:373:ALA:HA	1.76	0.51
1:B:16:LEU:HG	1:B:81:LYS:HG2	1.93	0.50
1:A:60:ALA:HA	1:A:64:PHE:HB2	1.94	0.50
1:B:423:ARG:HD2	1:B:481:ALA:HA	1.93	0.50
1:A:161:ALA:O	1:A:165[A]:HIS:ND1	2.45	0.49
1:B:140:ILE:O	1:B:144:VAL:HG22	2.13	0.49
1:A:111:MSE:HE3	1:A:122:GLY:HA3	1.93	0.48
1:B:258:THR:HB	1:B:264:VAL:HG13	1.94	0.48
1:B:59:MSE:HE1	1:B:110:THR:HG21	1.96	0.48
1:A:114:ARG:HG3	1:A:116:ASP:OD1	2.14	0.48
1:A:445:PHE:HD1	1:A:450:ILE:HB	1.78	0.47
1:A:510:ARG:HD3	1:A:522:HIS:HB3	1.96	0.47
1:A:66:ASP:HB3	1:A:69:VAL:HG12	1.96	0.47
1:A:326:GLU:HB2	1:A:329:LYS:HB2	1.97	0.47
1:B:89:ASP:N	1:B:89:ASP:OD1	2.47	0.47
1:B:83:ASP:HB3	1:B:86:GLU:HB3	1.96	0.47
1:A:223:TYR:CZ	1:A:614:ARG:HD2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:662:ARG:HG2	1:B:606:ILE:HD13	1.97	0.46
1:A:661:LEU:HG	1:B:606:ILE:HD11	1.98	0.46
1:B:27:GLN:HB2	1:B:80:VAL:HG12	1.98	0.46
1:B:73:MSE:HG3	1:B:141:LEU:HD21	1.98	0.46
1:B:307:GLU:HB3	1:B:399:ARG:HH22	1.81	0.46
1:B:140:ILE:HA	1:B:143:ALA:HB3	1.98	0.46
1:B:338:ILE:HD11	1:B:355:VAL:HG11	1.97	0.46
1:A:390:LEU:HD23	1:A:390:LEU:HA	1.84	0.46
1:B:23:PRO:HG3	1:B:67:ASP:HA	1.98	0.46
1:B:495:LYS:NZ	1:B:499:ASP:OD2	2.39	0.45
1:A:89:ASP:N	1:A:89:ASP:OD1	2.49	0.45
1:B:114:ARG:HG2	1:B:118:LYS:O	2.17	0.45
1:B:598:ASP:OD1	1:B:599:ARG:N	2.43	0.45
1:A:547:LEU:HD22	1:A:591:SER:HB3	1.98	0.45
1:B:478:LEU:HD23	1:B:487:TYR:CZ	2.52	0.45
1:A:70:ALA:HA	1:A:73:MSE:HE3	1.98	0.45
1:A:85:GLU:HB3	1:A:407:LEU:HD11	1.99	0.45
1:B:114:ARG:HG3	1:B:116:ASP:OD1	2.17	0.44
1:A:644:TRP:NE1	1:A:654:PRO:HG3	2.33	0.44
1:B:249:LEU:HD12	1:B:387:ARG:HG2	1.99	0.44
1:A:562:ILE:HG23	1:A:583:CYS:SG	2.58	0.43
1:B:445:PHE:CE1	1:B:493:LYS:HE2	2.53	0.43
1:B:178:GLN:O	1:B:183:ARG:NH2	2.52	0.43
1:B:241:LEU:HD23	1:B:296:ARG:HG3	2.01	0.43
1:A:48:ILE:HB	1:A:109:LEU:HB3	2.01	0.43
1:B:356:THR:HG22	1:B:358:GLY:H	1.82	0.43
1:A:48:ILE:HG12	1:A:82:VAL:HB	2.00	0.43
1:A:44:ILE:HG12	1:A:78:ILE:HD11	2.01	0.43
1:A:603:LEU:HB2	1:A:644:TRP:CZ2	2.54	0.43
1:A:62:GLU:HB3	1:A:128:ARG:HD2	2.01	0.43
1:B:405:LYS:HB3	1:B:405:LYS:HE2	1.82	0.42
1:A:168:GLY:HA2	1:A:172:ALA:HB2	2.01	0.42
1:B:8:LEU:HD13	1:B:26:TRP:HB3	2.01	0.42
1:B:342:LEU:HB2	1:B:346:ALA:HB2	2.01	0.42
1:B:409[A]:ASP:OD1	1:B:409[A]:ASP:N	2.52	0.42
1:A:637:GLU:HB2	1:A:638:PRO:HD3	2.02	0.42
1:B:602:GLU:O	1:B:606:ILE:HG23	2.20	0.42
1:A:78:ILE:HG13	1:A:78:ILE:O	2.20	0.42
1:B:114:ARG:HB2	1:B:115:PRO:HD2	2.01	0.42
1:A:303:TRP:CE3	1:A:304:LEU:HD12	2.55	0.41
1:B:221:TRP:HB2	1:B:230:ARG:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ILE:H	1:A:126:ILE:HG12	1.73	0.41
1:B:547:LEU:HD22	1:B:591:SER:HB2	2.03	0.41
1:B:56:CYS:HA	1:B:108:PRO:HG3	2.02	0.41
1:B:88:PRO:HD2	1:B:464:LEU:HD11	2.03	0.41
1:B:167:GLU:HG3	1:B:521:LEU:HD11	2.02	0.41
1:A:405:LYS:HB3	1:A:405:LYS:HE2	1.79	0.41
1:B:551:ASP:HB3	1:B:554:LEU:HB3	2.02	0.41
1:A:50:TYR:CZ	1:A:53:CYS:HB2	2.56	0.40
1:A:354:ALA:HB2	1:A:371:HIS:CD2	2.56	0.40
1:A:423:ARG:NH2	1:A:617:ASP:OD2	2.54	0.40
1:B:328:GLY:O	1:B:332:VAL:HG23	2.21	0.40
1:A:55:TRP:HA	1:A:58:VAL:HG22	2.03	0.40
1:A:279:ARG:NH2	1:A:283:TYR:OH	2.54	0.40
1:A:647:LYS:HE3	1:A:647:LYS:HB3	1.97	0.40
1:B:112:PHE:CE1	1:B:144:VAL:HG21	2.56	0.40
1:B:524:TYR:HB2	1:B:526:ASP:OD2	2.22	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	640/668 (96%)	624 (98%)	14 (2%)	2 (0%)	41	72
1	B	609/668 (91%)	593 (97%)	14 (2%)	2 (0%)	41	72
All	All	1249/1336 (94%)	1217 (97%)	28 (2%)	4 (0%)	41	72

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	124	THR
1	A	124	THR

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Mol	Chain	Res	Type
1	B	265	PRO
1	A	265	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	520/523 (99%)	502 (96%)	18 (4%)	36 70
1	B	492/523 (94%)	465 (94%)	27 (6%)	21 52
All	All	1012/1046 (97%)	967 (96%)	45 (4%)	27 61

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ARG
1	A	78	ILE
1	A	95	MSE
1	A	110	THR
1	A	126	ILE
1	A	128	ARG
1	A	266	HIS
1	A	277	PHE
1	A	287	GLU
1	A	304	LEU
1	A	320	ASP
1	A	384	GLU
1	A	390	LEU
1	A	454	ARG
1	A	539	ILE
1	A	620	VAL
1	A	652	LEU
1	A	656	ASP
1	B	4	ASP
1	B	21	ASN
1	B	34	LEU

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Mol	Chain	Res	Type
1	B	39	GLU
1	B	57	HIS
1	B	86	GLU
1	B	109	LEU
1	B	125	TYR
1	B	138	VAL
1	B	139	ASP
1	B	142	HIS
1	B	150	ARG
1	B	205	VAL
1	B	266	HIS
1	B	277	PHE
1	B	291	ASP
1	B	304	LEU
1	B	351	THR
1	B	368	ASN
1	B	369	ARG
1	B	383	VAL
1	B	482	THR
1	B	528	ASP
1	B	600	THR
1	B	606	ILE
1	B	617	ASP
1	B	622	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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	$\#\|Z\| > 2$
2	GOL	A	702	-	5,5,5	0.92	0	5,5,5	0.96	0
3	PO4	B	702	-	4,4,4	0.92	0	6,6,6	0.43	0
3	PO4	B	704	-	4,4,4	0.92	0	6,6,6	0.43	0
3	PO4	A	703	-	4,4,4	0.93	0	6,6,6	0.43	0
3	PO4	B	703	-	4,4,4	0.94	0	6,6,6	0.42	0
3	PO4	B	705	-	4,4,4	0.94	0	6,6,6	0.42	0
2	GOL	A	701	-	5,5,5	0.91	0	5,5,5	1.00	0
2	GOL	B	701	-	5,5,5	0.91	0	5,5,5	0.95	0
3	PO4	A	704	-	4,4,4	0.93	0	6,6,6	0.43	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	702	-	-	2/4/4/4	-
2	GOL	B	701	-	-	2/4/4/4	-
2	GOL	A	701	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	701	GOL	C1-C2-C3-O3
2	B	701	GOL	O2-C2-C3-O3
2	A	702	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
2	A	702	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	631/668 (94%)	0.13	31 (4%)	29	20	36, 58, 101, 136	0
1	B	601/668 (89%)	0.30	41 (6%)	17	10	37, 73, 127, 190	1 (0%)
All	All	1232/1336 (92%)	0.21	72 (5%)	23	15	36, 65, 117, 190	1 (0%)

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	126	ILE	5.4
1	B	21	ASN	4.7
1	A	150	ARG	4.4
1	A	622	VAL	3.8
1	B	144	VAL	3.8
1	B	345	ASP	3.7
1	A	140	ILE	3.6
1	B	349	PHE	3.6
1	B	150	ARG	3.5
1	A	76	PHE	3.5
1	A	142	HIS	3.5
1	A	637	GLU	3.5
1	B	127	PRO	3.4
1	B	74	ASN	3.4
1	B	140	ILE	3.4
1	A	68	ASP	3.4
1	A	77	PHE	3.2
1	B	64	PHE	3.2
1	B	137	PHE	3.1
1	A	640	HIS	3.1
1	B	136	GLY	3.1
1	B	142	HIS	3.0
1	B	125	TYR	3.0
1	B	72	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	71	ALA	3.0
1	A	64	PHE	3.0
1	B	77	PHE	2.9
1	A	621	LEU	2.9
1	B	621	LEU	2.9
1	B	121	TRP	2.8
1	B	61	HIS	2.8
1	A	139	ASP	2.8
1	A	72	VAL	2.8
1	A	597	THR	2.8
1	B	76	PHE	2.7
1	B	363	GLY	2.7
1	A	144	VAL	2.7
1	B	622	VAL	2.7
1	B	63	SER	2.7
1	B	70	ALA	2.7
1	B	141	LEU	2.6
1	B	350	LYS	2.6
1	B	69	VAL	2.6
1	B	65	GLU	2.6
1	A	652	LEU	2.5
1	B	456	GLU	2.5
1	A	70	ALA	2.5
1	A	138	VAL	2.4
1	B	521	LEU	2.4
1	A	75	ALA	2.4
1	A	374	ALA	2.4
1	A	377	PRO	2.4
1	A	349	PHE	2.4
1	B	600	THR	2.3
1	B	102	GLY	2.3
1	B	23	PRO	2.3
1	A	371	HIS	2.3
1	B	68	ASP	2.3
1	A	69	VAL	2.2
1	A	126	ILE	2.2
1	B	40	LEU	2.2
1	B	79	ASN	2.2
1	B	120	PHE	2.2
1	A	348	VAL	2.1
1	A	322	ASP	2.1
1	B	3	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	57	HIS	2.1
1	A	375	GLU	2.1
1	A	664	LEU	2.1
1	B	45	LEU	2.0
1	A	121	TRP	2.0
1	B	148	TRP	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
3	PO4	A	704	5/5	0.84	0.29	45,49,54,58	5
3	PO4	B	702	5/5	0.85	0.29	59,60,68,71	5
3	PO4	A	703	5/5	0.86	0.43	42,44,44,45	5
2	GOL	A	702	6/6	0.87	0.20	55,57,57,59	0
2	GOL	A	701	6/6	0.88	0.27	60,62,63,64	0
3	PO4	B	704	5/5	0.89	0.28	59,59,62,63	5
4	CL	A	705	1/1	0.89	0.19	66,66,66,66	0
3	PO4	B	703	5/5	0.91	0.24	52,54,59,63	5
2	GOL	B	701	6/6	0.93	0.20	47,49,52,53	0
3	PO4	B	705	5/5	0.95	0.33	44,47,51,53	5

6.5 Other polymers (i)

There are no such residues in this entry.