Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:35 AM GMT

PDB ID	:	3FA2
Title	:	Crystal Structure of the BRCA1 Associated Ring Domain (BARD1) Tandem BRCT Domains
Authors	:	Fox 3rd, D.; Le Trong, I.; Stenkamp, R.E.; Klevit, R.E.
Deposited on	:	2008-11-14
Resolution	:	2.20 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ①) were used in the production of this report:

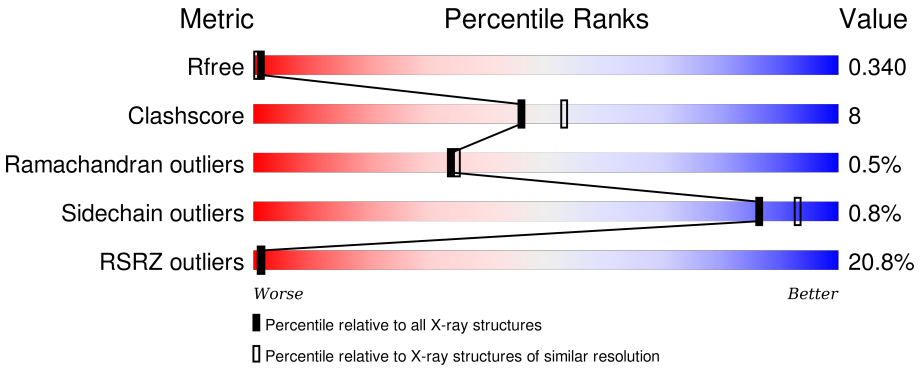
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.20 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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. 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	218	22% 76% 16% • 7%
1	B	218	17% 82% 12% 6%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3439 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.

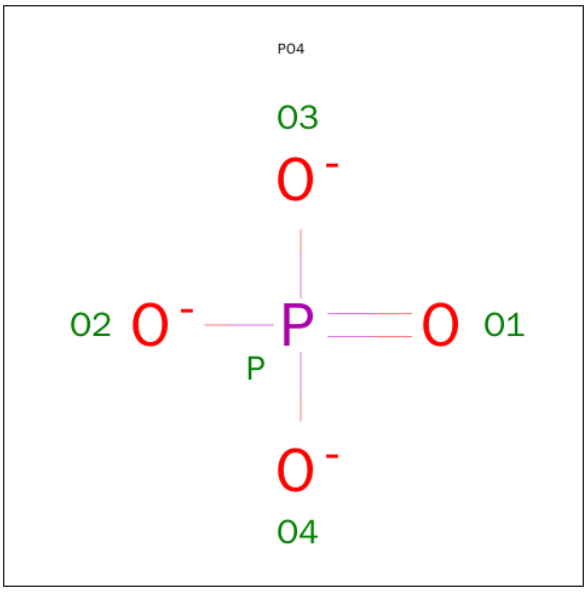
- Molecule 1 is a protein called BRCA1-associated RING domain protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	203	Total	C	N	O	S	0	2	0
			1654	1065	287	291	11			
1	B	205	Total	C	N	O	S	0	2	0
			1667	1074	288	294	11			

There are 12 discrepancies between the modelled and reference sequences:

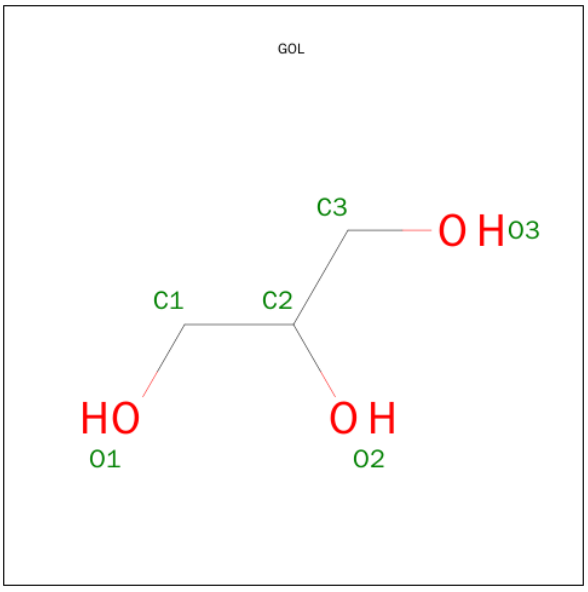
Chain	Residue	Modelled	Actual	Comment	Reference
A	560	GLY	-	EXPRESSION TAG	UNP Q99728
A	561	ILE	-	EXPRESSION TAG	UNP Q99728
A	562	ASP	-	EXPRESSION TAG	UNP Q99728
A	563	PRO	-	EXPRESSION TAG	UNP Q99728
A	564	PHE	-	EXPRESSION TAG	UNP Q99728
A	565	THR	-	EXPRESSION TAG	UNP Q99728
B	560	GLY	-	EXPRESSION TAG	UNP Q99728
B	561	ILE	-	EXPRESSION TAG	UNP Q99728
B	562	ASP	-	EXPRESSION TAG	UNP Q99728
B	563	PRO	-	EXPRESSION TAG	UNP Q99728
B	564	PHE	-	EXPRESSION TAG	UNP Q99728
B	565	THR	-	EXPRESSION TAG	UNP Q99728

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

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

- Molecule 4 is water.

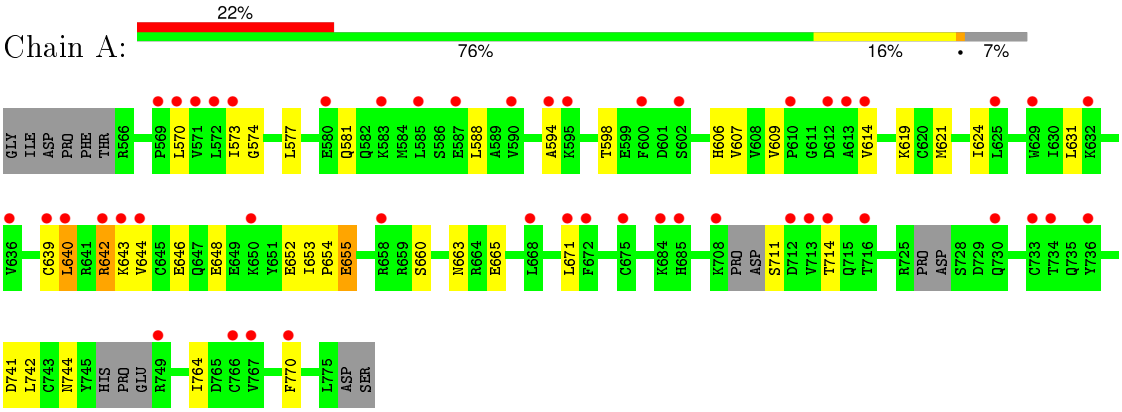
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	43	Total O 44 44	0	1
4	B	45	Total O 47 47	0	2

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 errors 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.

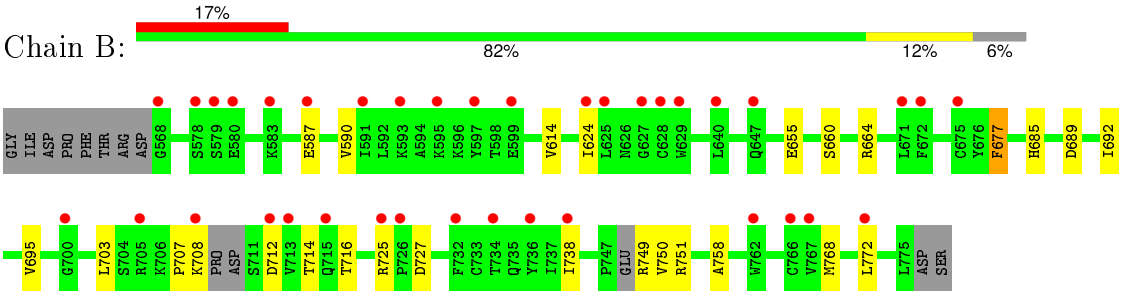
- Molecule 1: BRCA1-associated RING domain protein 1

Chain A:



- Molecule 1: BRCA1-associated RING domain protein 1

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	44.98Å 67.47Å 86.78Å 90.00° 99.20° 90.00°	Depositor
Resolution (Å)	30.00 – 2.20 28.62 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.0 (30.00-2.20) 95.0 (28.62-2.20)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	2.17 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.222 , 0.298 0.283 , 0.340	Depositor DCC
R_{free} test set	1253 reflections (5.05%)	DCC
Wilson B-factor (Å^2)	51.6	Xtriage
Anisotropy	0.526	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 40.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Outliers	1 of 24883 reflections (0.004%)	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3439	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.29% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, PO4

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	0.82	7/1696 (0.4%)	0.65	2/2286 (0.1%)
1	B	0.70	4/1713 (0.2%)	0.68	1/2315 (0.0%)
All	All	0.76	11/3409 (0.3%)	0.67	3/4601 (0.1%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	648	GLU	CG-CD	13.61	1.72	1.51
1	A	665	GLU	CD-OE2	12.16	1.39	1.25
1	A	665	GLU	CD-OE1	11.99	1.38	1.25
1	B	677	PHE	C-O	9.96	1.42	1.23
1	A	646	GLU	CD-OE2	9.30	1.35	1.25
1	A	646	GLU	CD-OE1	8.69	1.35	1.25
1	B	677	PHE	CB-CG	7.00	1.63	1.51
1	B	677	PHE	CD2-CE2	-6.02	1.27	1.39
1	A	663	ASN	C-O	5.86	1.34	1.23
1	B	677	PHE	CE2-CZ	5.35	1.47	1.37
1	A	648	GLU	CD-OE2	5.26	1.31	1.25

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	648	GLU	OE1-CD-OE2	6.12	130.64	123.30
1	B	677	PHE	CG-CD2-CE2	5.53	126.88	120.80
1	A	665	GLU	OE1-CD-OE2	5.51	129.92	123.30

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	1654	0	1685	32	0
1	B	1667	0	1689	21	0
2	A	5	0	0	0	0
2	B	10	0	0	0	0
3	A	6	0	8	0	0
3	B	6	0	8	2	0
4	A	44	0	0	1	0
4	B	47	0	0	1	0
All	All	3439	0	3390	52	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 8.

All (52) 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:621:MET:HE1	1:A:764:ILE:HG23	1.36	1.06
1:A:621:MET:CE	1:A:764:ILE:HG23	1.91	1.01
1:A:570:LEU:O	1:A:594:ALA:HB1	1.73	0.87
1:A:588:LEU:HB2	1:A:640:LEU:HD11	1.74	0.70
1:A:609:VAL:HG21	1:A:653:ILE:HD11	1.74	0.69
1:A:741:ASP:OD2	1:B:685:HIS:NE2	2.26	0.68
1:B:614:VAL:HG12	4:B:58:HOH:O	1.93	0.68
1:A:631:LEU:HD23	1:A:652:GLU:HA	1.77	0.66
1:A:660:SER:OG	4:A:22:HOH:O	2.15	0.65
1:A:573:ILE:HD11	1:A:619[B]:LYS:NZ	2.12	0.64
1:A:609:VAL:CG2	1:A:653:ILE:HD11	2.26	0.63
1:A:573:ILE:HD11	1:A:619[B]:LYS:HZ2	1.64	0.63
1:B:660:SER:OG	3:B:778:GOL:O1	2.00	0.59
1:B:708:LYS:H	1:B:714:THR:HG21	1.69	0.58
1:A:570:LEU:HD22	1:A:606:HIS:CE1	2.39	0.57
1:B:587:GLU:O	1:B:590:VAL:HG22	2.04	0.57
1:A:588:LEU:HD11	1:A:639:CYS:HB3	1.88	0.55
1:B:749:ARG:CG	1:B:750:VAL:H	2.22	0.53
1:B:738:ILE:HD13	1:B:758:ALA:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:703:LEU:HD13	1:B:707:PRO:HG3	1.90	0.53
1:B:664:ARG:HB2	3:B:778:GOL:H2	1.90	0.52
1:A:621:MET:HE1	1:A:764:ILE:CG2	2.25	0.52
1:A:642:ARG:HB3	1:A:644:VAL:HG22	1.90	0.52
1:B:614:VAL:HG13	1:B:768:MET:CE	2.39	0.52
1:A:574:GLY:HA3	1:A:577:LEU:HD12	1.92	0.51
1:A:614:VAL:HB	1:A:653:ILE:HG21	1.91	0.51
1:B:738:ILE:CD1	1:B:758:ALA:HB3	2.41	0.50
1:A:588:LEU:HD13	1:A:640:LEU:CD1	2.43	0.49
1:A:570:LEU:HD22	1:A:606:HIS:HE1	1.78	0.49
1:A:711:SER:N	1:A:714:THR:HG1	2.11	0.48
1:A:577:LEU:HD22	1:A:581:GLN:HB3	1.94	0.48
1:A:742:LEU:HD11	1:A:744:ASN:ND2	2.30	0.46
1:B:749:ARG:HG2	1:B:750:VAL:H	1.80	0.46
1:B:614:VAL:HG13	1:B:768:MET:HE3	1.98	0.45
1:A:621:MET:HE2	1:A:764:ILE:HG23	1.90	0.45
1:B:749:ARG:HG2	1:B:750:VAL:N	2.32	0.45
1:B:749:ARG:CG	1:B:750:VAL:N	2.80	0.45
1:A:624:ILE:O	1:A:660:SER:OG	2.19	0.44
1:A:654:PRO:O	1:A:655:GLU:HB2	2.17	0.44
1:B:749:ARG:NH1	1:B:751:ARG:HB3	2.32	0.44
1:A:671:LEU:HB2	1:A:770:PHE:CE1	2.52	0.44
1:A:588:LEU:CD1	1:A:639:CYS:HB3	2.48	0.43
1:A:609:VAL:HG21	1:A:653:ILE:CD1	2.45	0.43
1:B:712:ASP:O	1:B:716:THR:OG1	2.20	0.43
1:B:677:PHE:CD2	1:B:695:VAL:HG13	2.53	0.43
1:A:588:LEU:HD13	1:A:640:LEU:HD12	2.01	0.42
1:B:624:ILE:O	1:B:660:SER:OG	2.36	0.42
1:A:573:ILE:CG2	1:A:607:VAL:HG22	2.50	0.42
1:A:598:THR:O	1:A:619[B]:LYS:NZ	2.33	0.41
1:B:689:ASP:HA	1:B:692:ILE:HD12	2.02	0.41
1:A:639:CYS:O	1:A:643:LYS:N	2.53	0.41
1:B:725:ARG:NH1	1:B:727:ASP:OD1	2.53	0.41

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	197/218 (90%)	188 (95%)	8 (4%)	1 (0%)	34 35
1	B	201/218 (92%)	195 (97%)	5 (2%)	1 (0%)	34 35
All	All	398/436 (91%)	383 (96%)	13 (3%)	2 (0%)	34 35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	655	GLU
1	B	655	GLU

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	184/196 (94%)	182 (99%)	2 (1%)	80 89
1	B	186/196 (95%)	185 (100%)	1 (0%)	92 96
All	All	370/392 (94%)	367 (99%)	3 (1%)	86 93

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

Mol	Chain	Res	Type
1	A	640	LEU
1	A	642	ARG
1	B	772	LEU

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

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 carbohydrates in this entry.

5.6 Ligand geometry

5 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	$\#\|Z\| > 2$
3	GOL	A	1	-	5,5,5	0.29	0	5,5,5	0.39	0
2	PO4	A	3	-	4,4,4	0.46	0	6,6,6	0.27	0
2	PO4	B	1	-	4,4,4	0.47	0	6,6,6	0.26	0
2	PO4	B	2	-	4,4,4	0.36	0	6,6,6	0.28	0
3	GOL	B	778	-	5,5,5	0.39	0	5,5,5	0.40	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	1	-	-	0/4/4/4	0/0/0/0
2	PO4	A	3	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PO4	B	1	-	-	0/0/0/0	0/0/0/0
2	PO4	B	2	-	-	0/0/0/0	0/0/0/0
3	GOL	B	778	-	-	0/4/4/4	0/0/0/0

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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	778	GOL	2	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	203/218 (93%)	1.33	48 (23%)	1	1	20, 28, 36, 40	0
1	B	205/218 (94%)	1.22	37 (18%)	2	2	5, 23, 30, 37	0
All	All	408/436 (93%)	1.27	85 (20%)	1	1	5, 26, 35, 40	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	713	VAL	7.2
1	B	713	VAL	7.0
1	A	712	ASP	5.7
1	B	568	GLY	4.9
1	B	580	GLU	4.5
1	A	613	ALA	4.5
1	A	685	HIS	4.5
1	A	583	LYS	4.1
1	B	712	ASP	4.1
1	A	733	CYS	4.0
1	B	734	THR	3.9
1	A	639	CYS	3.9
1	A	612	ASP	3.8
1	A	590	VAL	3.8
1	B	625	LEU	3.7
1	A	644	VAL	3.7
1	B	736	TYR	3.7
1	A	614	VAL	3.6
1	A	587	GLU	3.6
1	A	594	ALA	3.6
1	B	628	CYS	3.5
1	B	640	LEU	3.4
1	A	671	LEU	3.4
1	B	579	SER	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	767	VAL	3.2
1	B	766	CYS	3.1
1	B	672	PHE	3.1
1	B	772	LEU	3.1
1	B	647	GLN	3.1
1	A	610	PRO	3.1
1	B	671	LEU	3.0
1	A	571	VAL	3.0
1	B	767	VAL	3.0
1	A	675	CYS	3.0
1	B	675	CYS	3.0
1	B	595	LYS	3.0
1	B	591	ILE	2.9
1	A	636	VAL	2.9
1	A	734	THR	2.9
1	B	726	PRO	2.9
1	A	640	LEU	2.9
1	B	578	SER	2.9
1	A	672	PHE	2.8
1	B	705	ARG	2.8
1	A	602	SER	2.8
1	A	642	ARG	2.7
1	B	624	ILE	2.7
1	B	597	TYR	2.7
1	A	595	LYS	2.6
1	B	715	GLN	2.6
1	B	627	GLY	2.5
1	B	587	GLU	2.5
1	B	732	PHE	2.5
1	B	762	TRP	2.5
1	A	716	THR	2.5
1	A	629	TRP	2.5
1	B	629	TRP	2.5
1	A	570	LEU	2.4
1	A	668	LEU	2.4
1	B	599	GLU	2.4
1	A	643	LYS	2.4
1	B	725	ARG	2.4
1	A	573	ILE	2.4
1	B	700	GLY	2.4
1	A	600	PHE	2.3
1	A	766	CYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	585	LEU	2.3
1	A	632	LYS	2.3
1	A	684	LYS	2.3
1	A	580	GLU	2.3
1	A	770	PHE	2.3
1	A	572	LEU	2.3
1	A	708	LYS	2.2
1	B	593	LYS	2.2
1	B	708	LYS	2.2
1	A	625	LEU	2.2
1	A	714	THR	2.2
1	A	650	LYS	2.2
1	B	738	ILE	2.2
1	A	658	ARG	2.1
1	A	749	ARG	2.1
1	A	569	PRO	2.1
1	B	583	LYS	2.0
1	A	730	GLN	2.0
1	A	736	TYR	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
2	PO4	A	3	5/5	0.81	0.19	0.91	127,127,127,127	0
3	GOL	B	778	6/6	0.90	0.20	-0.63	25,28,28,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	GOL	A	1	6/6	0.80	0.16	-2.05	40,41,43,45	0
2	PO4	B	1	5/5	0.93	0.07	-2.17	77,78,78,78	0
2	PO4	B	2	5/5	0.84	0.20	-	97,97,97,98	0

6.5 Other polymers (i)

There are no such residues in this entry.