



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:58 AM UTC

PDB ID : 3KD4 / pdb_00003kd4
Title : CRYSTAL STRUCTURE OF A PUTATIVE PROTEASE (BDI_1141)
FROM PARABACTEROIDES DISTASONIS ATCC 8503 AT 2.00 Å RES-
OLUTION
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2009-10-22
Resolution : 2.00 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

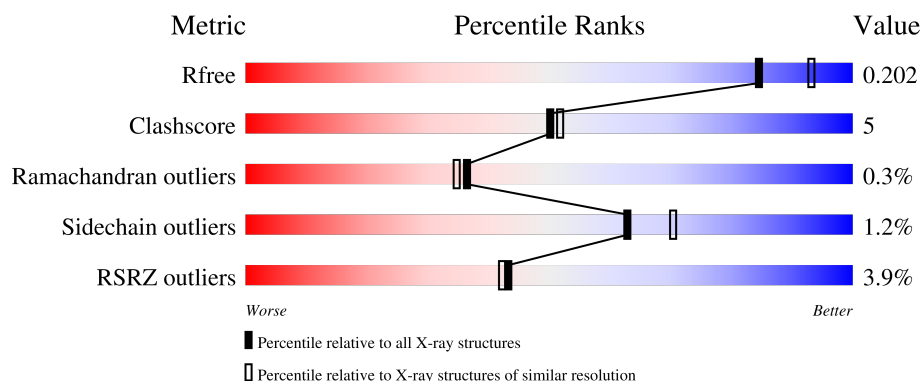
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 $\leq 5\%$. 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	506	4% 90% 9%
1	B	506	4% 91% 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9156 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 Putative protease.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	505	Total	C	N	O	S	Se	0	18	0
			3940	2496	656	772	7	9			
1	B	505	Total	C	N	O	S	Se	0	22	0
			3965	2511	662	775	8	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP A6LB40
B	0	GLY	-	expression tag	UNP A6LB40

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



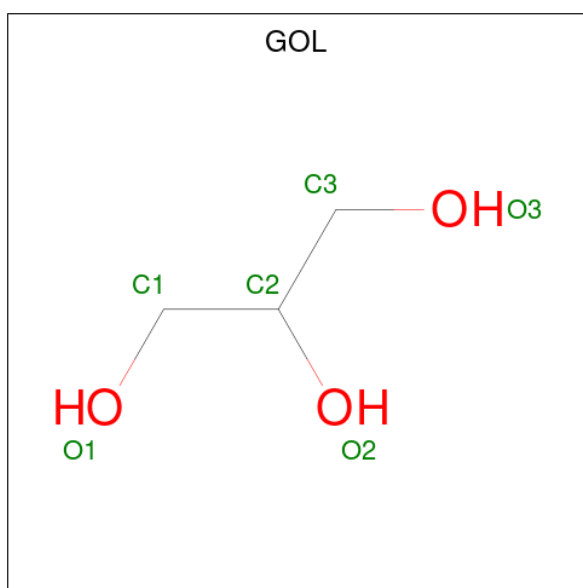
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		

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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

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

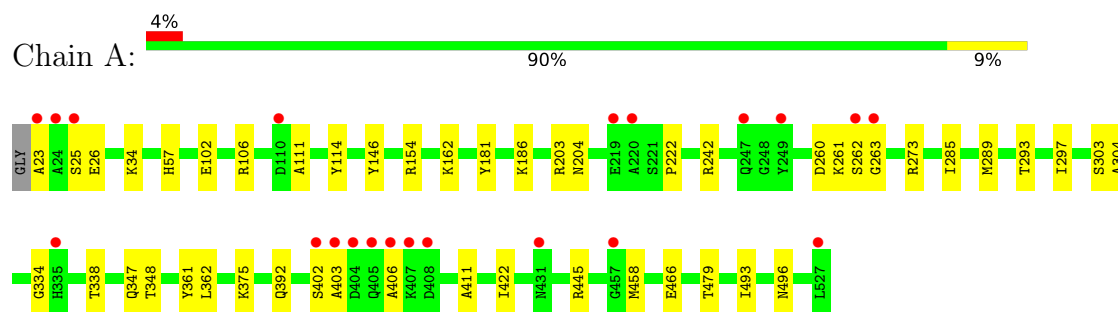
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	549	Total	O	0	0
			549	549		
4	B	546	Total	O	0	0
			546	546		

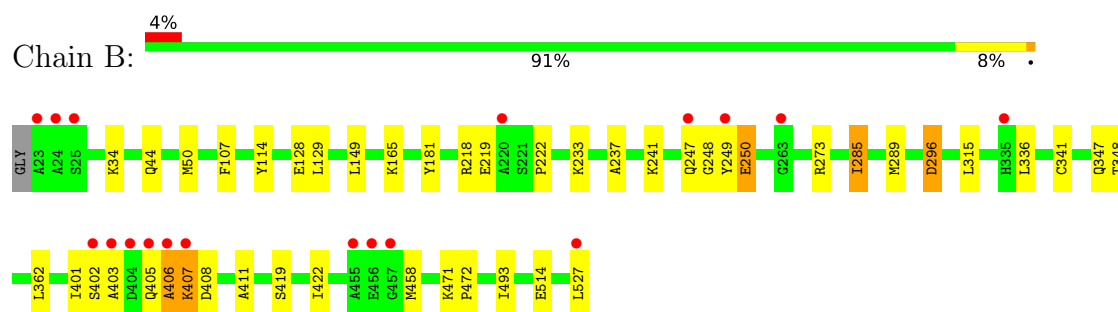
3 Residue-property plots

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: Putative protease



• Molecule 1: Putative protease



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	153.17Å 159.40Å 78.23Å 90.00° 91.64° 90.00°	Depositor
Resolution (Å)	28.93 – 2.00 28.93 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (28.93-2.00) 99.6 (28.93-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0053, PHENIX	Depositor
R, R_{free}	0.170 , 0.200 0.173 , 0.202	Depositor DCC
R_{free} test set	6308 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	24.9	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 49.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.012 for k,h,-l 0.015 for -k,-h,-l 0.145 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9156	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 3.92% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.88	0/4064	0.84	2/5522 (0.0%)
1	B	0.87	0/4088	0.83	0/5552
All	All	0.87	0/8152	0.83	2/11074 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	111	ALA	CA-C-N	5.41	125.49	119.32
1	A	111	ALA	C-N-CA	5.41	125.49	119.32

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	3940	0	3956	41	0
1	B	3965	0	3984	41	0
2	A	15	0	0	0	0
2	B	15	0	0	0	0
3	A	72	0	96	9	0
3	B	54	0	72	6	0
4	A	549	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	546	0	0	9	0
All	All	9156	0	8108	85	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 (85) 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:406:ALA:HB2	1:A:411:ALA:HB2	1.52	0.90
3:A:530:GOL:H12	4:A:985:HOH:O	1.77	0.84
3:A:530:GOL:C1	4:A:985:HOH:O	2.28	0.82
1:B:403:ALA:HA	1:B:458:MSE:HE3	1.63	0.80
1:B:406[B]:ALA:O	1:B:408[B]:ASP:N	2.18	0.77
1:B:315:LEU:HD21	1:B:362[A]:LEU:HD12	1.66	0.76
1:A:392:GLN:HE22	1:A:445[A]:ARG:HD3	1.56	0.71
1:B:402:SER:O	1:B:458:MSE:HE1	1.92	0.69
1:A:114:TYR:CD2	1:A:285[A]:ILE:CD1	2.77	0.68
1:B:250:GLU:HB3	4:B:854:HOH:O	1.94	0.67
1:A:23:ALA:HB3	1:A:26:GLU:HG3	1.77	0.67
1:A:114:TYR:CG	1:A:285[A]:ILE:HD13	2.29	0.66
1:B:247:GLN:HB3	4:B:972:HOH:O	1.98	0.64
1:B:247:GLN:OE1	1:B:249:TYR:CE2	2.51	0.64
1:B:406[A]:ALA:HB2	1:B:458:MSE:HE2	1.81	0.63
1:B:165:LYS:NZ	4:B:855:HOH:O	2.32	0.62
1:A:406:ALA:CB	1:A:458:MSE:HE2	2.30	0.62
1:A:57:HIS:NE2	3:A:21:GOL:H31	2.14	0.62
1:A:403:ALA:HA	1:A:458:MSE:HE3	1.82	0.62
1:B:405[B]:GLN:O	1:B:407[B]:LYS:N	2.31	0.61
1:A:402:SER:O	1:A:458:MSE:CE	2.49	0.60
1:A:422:ILE:CD1	1:A:493:ILE:HD13	2.32	0.59
1:B:406[A]:ALA:HB2	1:B:411:ALA:HB2	1.84	0.59
1:A:154:ARG:HG3	4:A:643:HOH:O	2.04	0.57
1:B:347:GLN:O	1:B:348[B]:THR:HG23	2.04	0.57
1:A:392:GLN:NE2	1:A:445[A]:ARG:HD3	2.20	0.56
1:B:128:GLU:HA	3:B:14:GOL:H12	1.88	0.55
1:A:289:MSE:HA	1:A:289:MSE:HE2	1.89	0.55
1:A:114:TYR:CD2	1:A:285[A]:ILE:HD11	2.42	0.55
1:A:402:SER:O	1:A:458:MSE:HE1	2.07	0.55
1:B:402:SER:N	1:B:405[B]:GLN:OE1	2.37	0.54
1:A:406:ALA:HB2	1:A:458:MSE:HE2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:TYR:CG	1:A:285[A]:ILE:CD1	2.91	0.54
1:B:247:GLN:HB2	1:B:296:ASP:OD2	2.08	0.54
1:A:57:HIS:NE2	3:A:21:GOL:C3	2.72	0.53
1:B:406[A]:ALA:CB	1:B:458:MSE:HE2	2.38	0.53
1:A:445[B]:ARG:HH11	1:A:445[B]:ARG:HG2	1.74	0.52
1:B:114:TYR:CG	1:B:285:ILE:HD12	2.45	0.52
1:A:402:SER:O	1:A:458:MSE:HE3	2.11	0.51
1:B:219:GLU:N	4:B:1012:HOH:O	2.43	0.50
1:B:289:MSE:HA	1:B:289:MSE:HE2	1.93	0.50
1:A:338:THR:HG21	1:A:375[B]:LYS:HG2	1.95	0.49
1:B:218[A]:ARG:NH2	4:B:880:HOH:O	2.43	0.49
1:B:471:LYS:HB3	1:B:472:PRO:CD	2.42	0.49
1:B:347:GLN:O	1:B:348[B]:THR:CG2	2.60	0.49
1:A:181:TYR:O	1:A:222:PRO:HA	2.13	0.49
1:A:406:ALA:HB3	1:A:458:MSE:HE2	1.95	0.48
1:B:273:ARG:HG3	1:B:362[B]:LEU:HD23	1.94	0.48
1:B:237:ALA:O	1:B:241:LYS:HG3	2.14	0.48
1:B:181:TYR:O	1:B:222:PRO:HA	2.15	0.47
1:A:445[B]:ARG:NH2	1:A:496:ASN:OD1	2.49	0.46
1:B:248:GLY:N	4:B:767:HOH:O	2.49	0.45
1:B:34:LYS:NZ	4:B:730:HOH:O	2.48	0.45
1:B:422:ILE:CD1	1:B:493:ILE:HD13	2.47	0.45
1:A:303:SER:O	1:A:304:ALA:HB3	2.16	0.45
3:A:528:GOL:H2	4:A:715:HOH:O	2.17	0.45
1:A:260[A]:ASP:OD1	1:A:261:LYS:N	2.50	0.45
1:B:128:GLU:HB3	3:B:14:GOL:H32	1.98	0.44
1:A:34:LYS:NZ	4:A:707:HOH:O	2.39	0.44
1:A:186:LYS:HA	1:A:186:LYS:HE2	1.99	0.43
1:A:347:GLN:O	1:A:348[B]:THR:HG23	2.18	0.43
1:A:422:ILE:HD13	1:A:493:ILE:HD13	1.99	0.43
1:A:466:GLU:HG3	1:A:479:THR:HG22	2.00	0.43
1:A:361:TYR:C	1:A:362[A]:LEU:HD23	2.44	0.43
1:B:402:SER:O	1:B:458:MSE:CE	2.62	0.43
1:A:57:HIS:CE1	3:A:21:GOL:H31	2.54	0.43
1:A:146:TYR:CE2	3:A:7:GOL:H2	2.54	0.42
1:A:242[A]:ARG:NH1	1:A:293[A]:THR:HB	2.35	0.42
1:B:129:LEU:H	3:B:14:GOL:H31	1.84	0.42
1:A:106:ARG:CB	3:A:18:GOL:O3	2.68	0.42
1:B:408[B]:ASP:HB3	4:B:946:HOH:O	2.20	0.42
1:B:233:LYS:NZ	4:B:1074:HOH:O	2.52	0.41
1:A:162[A]:LYS:HD2	1:A:204:ASN:OD1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:GLN:OE1	3:B:11:GOL:C3	2.68	0.41
1:B:336:LEU:HD13	1:B:341[B]:CYS:SG	2.60	0.41
1:B:471:LYS:HB3	1:B:472:PRO:HD2	2.02	0.41
1:A:273:ARG:HG3	1:A:362[B]:LEU:HD23	2.01	0.41
1:A:297:ILE:HD12	1:A:297:ILE:HG23	1.72	0.41
1:B:107:PHE:C	1:B:107:PHE:CD1	2.99	0.41
1:B:405[B]:GLN:C	1:B:407[B]:LYS:N	2.78	0.41
1:A:203:ARG:HH22	3:A:531:GOL:C3	2.34	0.40
1:B:149:LEU:HD12	3:B:11:GOL:O3	2.22	0.40
1:A:334:GLY:O	1:A:375[A]:LYS:HE3	2.21	0.40
1:B:44:GLN:OE1	3:B:11:GOL:H32	2.22	0.40
1:B:406[A]:ALA:HB1	1:B:527:LEU:CB	2.52	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	521/506 (103%)	514 (99%)	6 (1%)	1 (0%)	43	42
1	B	525/506 (104%)	515 (98%)	6 (1%)	4 (1%)	16	11
All	All	1046/1012 (103%)	1029 (98%)	12 (1%)	5 (0%)	36	21

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	406[A]	ALA
1	B	406[B]	ALA
1	B	407[A]	LYS
1	B	407[B]	LYS
1	A	263	GLY

5.3.2 Protein sidechains ⓘ

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	440/424 (104%)	437 (99%)	3 (1%)	76	82
1	B	441/424 (104%)	433 (98%)	8 (2%)	51	58
All	All	881/848 (104%)	870 (99%)	11 (1%)	63	70

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	SER
1	A	102	GLU
1	A	262	SER
1	B	50[A]	MSE
1	B	50[B]	MSE
1	B	250	GLU
1	B	285	ILE
1	B	296	ASP
1	B	401	ILE
1	B	419	SER
1	B	514	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	156	GLN
1	A	266	GLN
1	A	316	ASN
1	A	360	GLN
1	A	436	ASN
1	B	156	GLN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

27 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	PO4	A	5	-	4,4,4	1.02	0	6,6,6	0.78	0
3	GOL	A	21	-	5,5,5	1.04	1 (20%)	5,5,5	1.18	0
3	GOL	A	530	-	5,5,5	0.49	0	5,5,5	0.74	0
2	PO4	B	4	-	4,4,4	0.80	0	6,6,6	0.45	0
3	GOL	A	529	-	5,5,5	0.26	0	5,5,5	0.70	0
2	PO4	B	1	-	4,4,4	0.75	0	6,6,6	0.58	0
3	GOL	A	15	-	5,5,5	0.34	0	5,5,5	0.61	0
3	GOL	B	20	-	5,5,5	0.53	0	5,5,5	0.51	0
3	GOL	A	528	-	5,5,5	0.48	0	5,5,5	0.65	0
3	GOL	B	528	-	5,5,5	0.55	0	5,5,5	0.83	0
3	GOL	A	7	-	5,5,5	0.46	0	5,5,5	0.93	0
3	GOL	A	10	-	5,5,5	1.06	0	5,5,5	1.73	2 (40%)
2	PO4	A	3	-	4,4,4	0.99	0	6,6,6	0.70	0
3	GOL	B	529	-	5,5,5	0.63	0	5,5,5	0.59	0
3	GOL	B	16	-	5,5,5	0.37	0	5,5,5	0.59	0
3	GOL	B	14	-	5,5,5	0.95	0	5,5,5	1.85	2 (40%)
3	GOL	A	18	-	5,5,5	0.54	0	5,5,5	0.81	0
3	GOL	B	13	-	5,5,5	0.48	0	5,5,5	0.36	0
2	PO4	B	6	-	4,4,4	1.14	0	6,6,6	0.50	0
3	GOL	A	9	-	5,5,5	0.46	0	5,5,5	0.92	0
3	GOL	B	11	-	5,5,5	0.64	0	5,5,5	1.32	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	B	12	-	5,5,5	0.31	0	5,5,5	0.49	0
3	GOL	A	19	-	5,5,5	0.41	0	5,5,5	0.57	0
3	GOL	A	8	-	5,5,5	0.60	0	5,5,5	0.93	0
2	PO4	A	2	-	4,4,4	0.61	0	6,6,6	1.07	0
3	GOL	A	531	-	5,5,5	0.49	0	5,5,5	0.55	0
3	GOL	B	17	-	5,5,5	0.55	0	5,5,5	0.55	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	21	-	-	2/4/4/4	-
3	GOL	A	530	-	-	4/4/4/4	-
3	GOL	A	529	-	-	2/4/4/4	-
3	GOL	A	15	-	-	0/4/4/4	-
3	GOL	B	20	-	-	1/4/4/4	-
3	GOL	A	528	-	-	4/4/4/4	-
3	GOL	B	528	-	-	2/4/4/4	-
3	GOL	A	7	-	-	4/4/4/4	-
3	GOL	A	10	-	-	2/4/4/4	-
3	GOL	B	529	-	-	2/4/4/4	-
3	GOL	B	16	-	-	0/4/4/4	-
3	GOL	B	14	-	-	0/4/4/4	-
3	GOL	A	18	-	-	1/4/4/4	-
3	GOL	B	13	-	-	4/4/4/4	-
3	GOL	A	9	-	-	2/4/4/4	-
3	GOL	B	11	-	-	2/4/4/4	-
3	GOL	B	12	-	-	2/4/4/4	-
3	GOL	A	19	-	-	0/4/4/4	-
3	GOL	A	8	-	-	4/4/4/4	-
3	GOL	A	531	-	-	2/4/4/4	-
3	GOL	B	17	-	-	4/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	21	GOL	O2-C2	-2.16	1.37	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	14	GOL	C3-C2-C1	-2.87	101.25	111.80
3	A	10	GOL	O2-C2-C3	-2.30	99.66	109.18
3	B	11	GOL	C3-C2-C1	-2.24	103.57	111.80
3	A	10	GOL	O3-C3-C2	-2.14	100.75	110.38
3	B	14	GOL	O2-C2-C3	2.08	117.78	109.18

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	8	GOL	C1-C2-C3-O3
3	A	8	GOL	O2-C2-C3-O3
3	A	9	GOL	C1-C2-C3-O3
3	A	10	GOL	O1-C1-C2-C3
3	A	528	GOL	O1-C1-C2-C3
3	A	529	GOL	O1-C1-C2-C3
3	A	530	GOL	C1-C2-C3-O3
3	B	12	GOL	O1-C1-C2-C3
3	B	17	GOL	O1-C1-C2-O2
3	B	17	GOL	O1-C1-C2-C3
3	B	17	GOL	C1-C2-C3-O3
3	B	528	GOL	C1-C2-C3-O3
3	B	529	GOL	O1-C1-C2-O2
3	B	529	GOL	O1-C1-C2-C3
3	A	8	GOL	O1-C1-C2-O2
3	A	9	GOL	O2-C2-C3-O3
3	A	10	GOL	O1-C1-C2-O2
3	B	17	GOL	O2-C2-C3-O3
3	A	7	GOL	O1-C1-C2-C3
3	A	7	GOL	C1-C2-C3-O3
3	A	8	GOL	O1-C1-C2-C3
3	A	18	GOL	C1-C2-C3-O3
3	A	528	GOL	C1-C2-C3-O3
3	A	530	GOL	O1-C1-C2-C3
3	A	531	GOL	O1-C1-C2-C3
3	B	11	GOL	C1-C2-C3-O3
3	B	13	GOL	O1-C1-C2-C3
3	A	528	GOL	O1-C1-C2-O2
3	A	529	GOL	O1-C1-C2-O2
3	A	530	GOL	O2-C2-C3-O3
3	B	12	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
3	B	528	GOL	O2-C2-C3-O3
3	A	531	GOL	O1-C1-C2-O2
3	B	11	GOL	O2-C2-C3-O3
3	B	13	GOL	C1-C2-C3-O3
3	A	7	GOL	O2-C2-C3-O3
3	A	21	GOL	O1-C1-C2-O2
3	A	530	GOL	O1-C1-C2-O2
3	B	13	GOL	O1-C1-C2-O2
3	B	20	GOL	O2-C2-C3-O3
3	A	528	GOL	O2-C2-C3-O3
3	A	7	GOL	O1-C1-C2-O2
3	A	21	GOL	O1-C1-C2-C3
3	B	13	GOL	O2-C2-C3-O3

There are no ring outliers.

8 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	21	GOL	3	0
3	A	530	GOL	2	0
3	A	528	GOL	1	0
3	A	7	GOL	1	0
3	B	14	GOL	3	0
3	A	18	GOL	1	0
3	B	11	GOL	3	0
3	A	531	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, 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	497/506 (98%)	-0.19	21 (4%)	40	39	11, 22, 35, 54	17 (3%)
1	B	497/506 (98%)	-0.28	18 (3%)	46	45	11, 21, 34, 48	21 (4%)
All	All	994/1012 (98%)	-0.24	39 (3%)	43	42	11, 22, 35, 54	38 (3%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	407[A]	LYS	7.6
1	A	23	ALA	7.3
1	B	23	ALA	7.1
1	A	403	ALA	5.6
1	B	457	GLY	4.9
1	A	24	ALA	4.5
1	B	403	ALA	4.5
1	B	247	GLN	4.4
1	B	263	GLY	4.2
1	A	406	ALA	4.1
1	B	406[A]	ALA	4.1
1	A	407	LYS	3.9
1	B	24	ALA	3.9
1	B	249	TYR	3.6
1	B	404	ASP	3.3
1	A	404	ASP	3.2
1	A	402	SER	3.1
1	A	219	GLU	3.1
1	A	408	ASP	3.1
1	B	455	ALA	3.0
1	A	25	SER	2.9
1	A	262	SER	2.9
1	B	25	SER	2.8
1	B	527	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	249	TYR	2.7
1	A	335[A]	HIS	2.6
1	A	527	LEU	2.6
1	A	247	GLN	2.6
1	B	335	HIS	2.6
1	B	456	GLU	2.5
1	B	402	SER	2.4
1	A	405	GLN	2.4
1	B	220	ALA	2.3
1	A	110	ASP	2.3
1	A	457	GLY	2.3
1	B	405[A]	GLN	2.2
1	A	220	ALA	2.2
1	A	263	GLY	2.2
1	A	431	ASN	2.1

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 oligosaccharides 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
3	GOL	B	14	6/6	0.78	0.21	34,41,45,47	0
3	GOL	A	528	6/6	0.80	0.21	54,55,56,56	0
3	GOL	A	531	6/6	0.81	0.18	73,74,75,75	0
3	GOL	A	8	6/6	0.81	0.18	41,48,50,51	0
3	GOL	A	530	6/6	0.83	0.18	57,57,58,58	0
3	GOL	B	12	6/6	0.84	0.16	48,53,55,58	0
3	GOL	B	529	6/6	0.84	0.18	52,53,53,55	0
3	GOL	A	18	6/6	0.86	0.16	45,48,50,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PO4	A	3	5/5	0.86	0.23	42,43,44,45	5
3	GOL	A	529	6/6	0.86	0.17	59,59,59,60	0
3	GOL	A	10	6/6	0.86	0.17	33,39,47,53	0
3	GOL	B	20	6/6	0.87	0.16	50,51,51,52	0
3	GOL	A	21	6/6	0.88	0.15	32,40,41,43	0
3	GOL	A	15	6/6	0.89	0.15	33,35,37,38	0
2	PO4	B	6	5/5	0.89	0.19	59,60,60,61	5
3	GOL	B	528	6/6	0.89	0.16	35,39,40,41	0
3	GOL	A	19	6/6	0.89	0.19	71,71,72,72	0
3	GOL	B	16	6/6	0.90	0.14	36,36,38,38	0
3	GOL	B	11	6/6	0.90	0.14	37,39,42,43	0
3	GOL	A	9	6/6	0.91	0.13	35,38,39,42	0
3	GOL	B	13	6/6	0.91	0.13	41,45,47,48	0
3	GOL	B	17	6/6	0.91	0.14	36,41,42,42	0
3	GOL	A	7	6/6	0.92	0.12	24,36,37,39	0
2	PO4	A	2	5/5	0.93	0.20	39,44,44,46	0
2	PO4	A	5	5/5	0.97	0.15	32,37,38,39	0
2	PO4	B	1	5/5	0.97	0.06	36,36,37,37	5
2	PO4	B	4	5/5	0.98	0.09	18,20,22,22	5

6.5 Other polymers [i](#)

There are no such residues in this entry.