



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 05:19 pm GMT

PDB ID : 3NA5  
Title : Crystal structure of a bacterial phosphoglucomutase, an enzyme important in the virulence of several human pathogens.  
Authors : Mehra-Chaudhary, R.; Beamer, L.J.  
Deposited on : 2010-06-01  
Resolution : 1.70 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](mailto: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.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

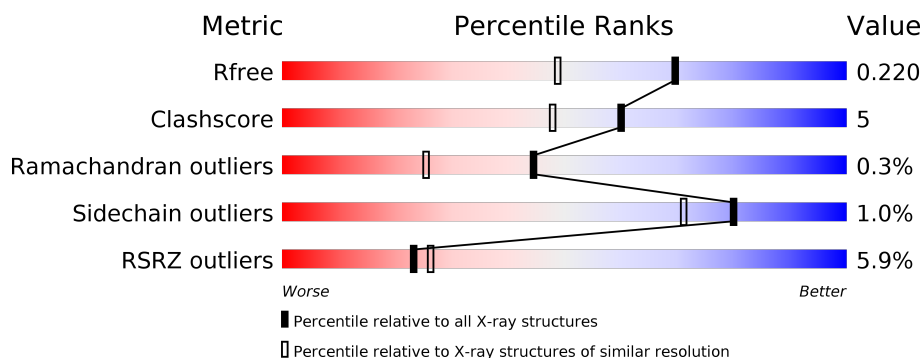
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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))
$R_{free}$	100719	3453 (1.70-1.70)
Clashscore	112137	3876 (1.70-1.70)
Ramachandran outliers	110173	3815 (1.70-1.70)
Sidechain outliers	110143	3815 (1.70-1.70)
RSRZ outliers	101464	3491 (1.70-1.70)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	570	<div> <div>8%</div> <div> <div></div> <div>88%</div> <div>7% . .</div> </div> </div>
1	B	570	<div> <div>3%</div> <div> <div></div> <div>90%</div> <div>5% .</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BTB	A	600	-	-	X	X
2	BTB	B	600	-	-	X	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9161 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 Phosphoglucomutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	545	Total	C	N	O	S	0	7	0
			4058	2561	706	774	17			
1	B	545	Total	C	N	O	S	0	6	0
			4053	2553	708	775	17			

There are 48 discrepancies between the modelled and reference sequences:

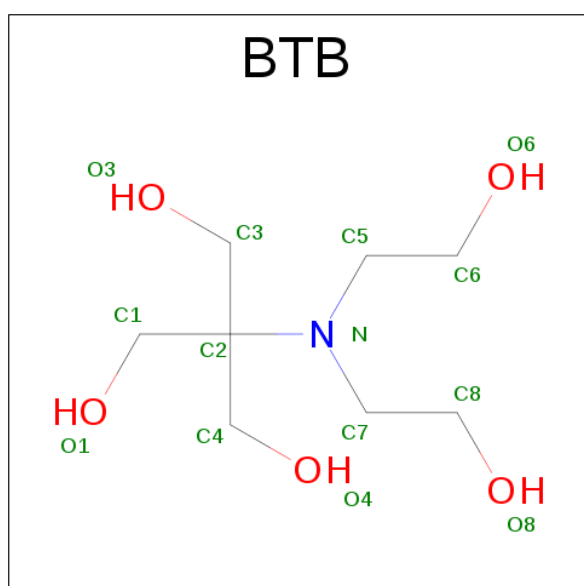
Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	EXPRESSION TAG	UNP Q8ZQW9
A	-22	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
A	-21	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
A	-20	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
A	-19	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
A	-18	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
A	-17	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
A	-16	SER	-	EXPRESSION TAG	UNP Q8ZQW9
A	-15	SER	-	EXPRESSION TAG	UNP Q8ZQW9
A	-14	GLY	-	EXPRESSION TAG	UNP Q8ZQW9
A	-13	VAL	-	EXPRESSION TAG	UNP Q8ZQW9
A	-12	ASP	-	EXPRESSION TAG	UNP Q8ZQW9
A	-11	LEU	-	EXPRESSION TAG	UNP Q8ZQW9
A	-10	GLY	-	EXPRESSION TAG	UNP Q8ZQW9
A	-9	THR	-	EXPRESSION TAG	UNP Q8ZQW9
A	-8	GLU	-	EXPRESSION TAG	UNP Q8ZQW9
A	-7	ASN	-	EXPRESSION TAG	UNP Q8ZQW9
A	-6	LEU	-	EXPRESSION TAG	UNP Q8ZQW9
A	-5	TYR	-	EXPRESSION TAG	UNP Q8ZQW9
A	-4	PHE	-	EXPRESSION TAG	UNP Q8ZQW9
A	-3	GLN	-	EXPRESSION TAG	UNP Q8ZQW9
A	-2	SER	-	EXPRESSION TAG	UNP Q8ZQW9
A	-1	ASN	-	EXPRESSION TAG	UNP Q8ZQW9
A	0	ALA	-	EXPRESSION TAG	UNP Q8ZQW9
B	-23	MET	-	EXPRESSION TAG	UNP Q8ZQW9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-22	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
B	-21	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
B	-20	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
B	-19	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
B	-18	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
B	-17	HIS	-	EXPRESSION TAG	UNP Q8ZQW9
B	-16	SER	-	EXPRESSION TAG	UNP Q8ZQW9
B	-15	SER	-	EXPRESSION TAG	UNP Q8ZQW9
B	-14	GLY	-	EXPRESSION TAG	UNP Q8ZQW9
B	-13	VAL	-	EXPRESSION TAG	UNP Q8ZQW9
B	-12	ASP	-	EXPRESSION TAG	UNP Q8ZQW9
B	-11	LEU	-	EXPRESSION TAG	UNP Q8ZQW9
B	-10	GLY	-	EXPRESSION TAG	UNP Q8ZQW9
B	-9	THR	-	EXPRESSION TAG	UNP Q8ZQW9
B	-8	GLU	-	EXPRESSION TAG	UNP Q8ZQW9
B	-7	ASN	-	EXPRESSION TAG	UNP Q8ZQW9
B	-6	LEU	-	EXPRESSION TAG	UNP Q8ZQW9
B	-5	TYR	-	EXPRESSION TAG	UNP Q8ZQW9
B	-4	PHE	-	EXPRESSION TAG	UNP Q8ZQW9
B	-3	GLN	-	EXPRESSION TAG	UNP Q8ZQW9
B	-2	SER	-	EXPRESSION TAG	UNP Q8ZQW9
B	-1	ASN	-	EXPRESSION TAG	UNP Q8ZQW9
B	0	ALA	-	EXPRESSION TAG	UNP Q8ZQW9

- Molecule 2 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (three-letter code: BTB) (formula: C<sub>8</sub>H<sub>19</sub>NO<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		

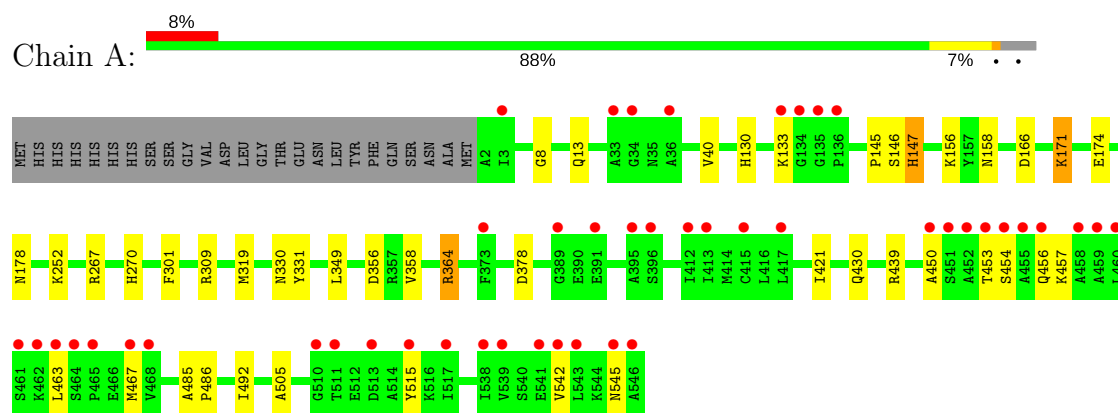
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	502	Total	O	0	0
			502	502		
4	B	518	Total	O	0	0
			518	518		

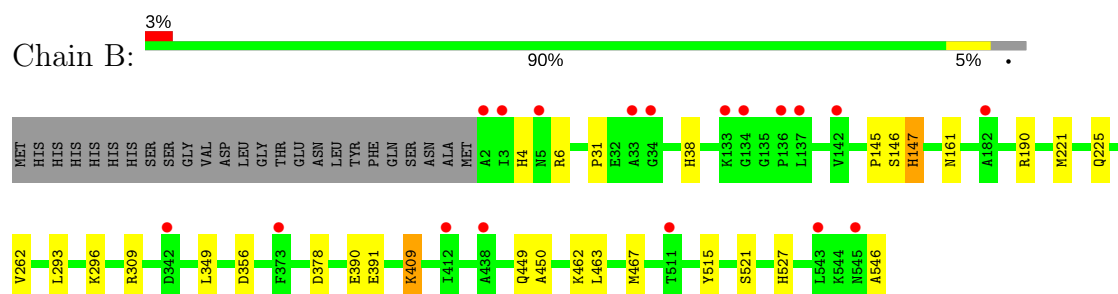
### 3 Residue-property plots

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: Phosphoglucomutase



#### • Molecule 1: Phosphoglucomutase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.47Å 105.79Å 126.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.27 – 1.70 40.62 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.27-1.70) 99.9 (40.62-1.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.72 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.4.0069	Depositor
R, $R_{free}$	0.182 , 0.218 0.186 , 0.220	Depositor DCC
$R_{free}$ test set	6066 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.5	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 45.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9161	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.88 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 5.2117e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical 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: MG, CSS, BTB

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	0.64	0/4158	0.69	5/5657 (0.1%)
1	B	0.62	0/4150	0.65	0/5649
All	All	0.63	0/8308	0.67	5/11306 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	309	ARG	NE-CZ-NH2	-6.97	116.81	120.30
1	A	364	ARG	NE-CZ-NH2	-5.79	117.40	120.30
1	A	319	MET	CG-SD-CE	5.62	109.19	100.20
1	A	309	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	301	PHE	CB-CA-C	-5.44	99.52	110.40

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	4058	0	3953	41	0
1	B	4053	0	3936	25	1
2	A	14	0	19	14	0
2	B	14	0	16	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	502	0	0	11	1
4	B	518	0	0	7	0
All	All	9161	0	7924	85	1

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:B:390:GLU:OE2	1:B:409:LYS:HE2	1.49	1.13
2:A:600:BTB:H32	2:A:600:BTB:H62	1.21	1.07
2:A:600:BTB:C6	2:A:600:BTB:C3	2.38	1.01
2:A:600:BTB:C6	2:A:600:BTB:H32	1.82	1.00
1:A:453:THR:HG23	1:A:456:GLN:OE1	1.60	0.98
2:B:600:BTB:H51	4:B:982:HOH:O	1.63	0.98
1:B:146:SER:OG	1:B:147[A]:HIS:HD2	1.56	0.86
2:A:600:BTB:H41	4:A:984:HOH:O	1.73	0.86
1:A:40:VAL:H	1:A:178:ASN:HD21	1.23	0.85
1:A:349:LEU:HD23	1:A:349:LEU:O	1.82	0.78
1:B:463:LEU:HD22	1:B:467:MET:HE2	1.66	0.78
2:B:600:BTB:H41	4:B:983:HOH:O	1.86	0.75
1:B:521:SER:OG	1:B:527:HIS:HD2	1.69	0.74
1:B:146:SER:OG	1:B:147[A]:HIS:CD2	2.42	0.72
2:A:600:BTB:H31	2:A:600:BTB:C6	2.18	0.72
1:B:147[A]:HIS:CD2	1:B:147[A]:HIS:H	2.08	0.70
1:B:378:ASP:OD1	2:B:600:BTB:C4	2.44	0.65
1:A:147[A]:HIS:H	1:A:147[A]:HIS:CD2	2.14	0.65
1:A:146:SER:OG	1:A:147[A]:HIS:HD2	1.80	0.65
1:A:349:LEU:HD23	1:A:349:LEU:C	2.17	0.65
1:A:349:LEU:HD21	1:A:505:ALA:CB	2.27	0.64
2:B:600:BTB:O6	2:B:600:BTB:C1	2.44	0.62
1:B:378:ASP:OD1	2:B:600:BTB:H41	2.01	0.60
1:A:147[B]:HIS:CD2	4:A:1033:HOH:O	2.55	0.59
1:B:4:HIS:CD2	1:B:6:ARG:H	2.22	0.58
1:A:463:LEU:HD22	1:A:542:VAL:CG1	2.34	0.58
1:B:521:SER:OG	1:B:527:HIS:CD2	2.54	0.58
1:A:453:THR:O	1:A:457:LYS:HG3	2.04	0.57
1:A:349:LEU:HD21	1:A:505:ALA:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:LYS:NZ	1:A:158:ASN:HD21	2.03	0.56
1:A:40:VAL:N	1:A:178:ASN:HD21	1.97	0.56
2:B:600:BTB:O6	2:B:600:BTB:H11	2.05	0.55
2:A:600:BTB:C3	2:A:600:BTB:H62	2.07	0.55
1:B:463:LEU:HD22	1:B:467:MET:CE	2.36	0.53
1:A:378:ASP:OD1	2:A:600:BTB:C4	2.57	0.53
1:B:293:LEU:O	1:B:296:LYS:HG2	2.09	0.53
1:A:166:ASP:HB2	2:A:600:BTB:O1	2.09	0.53
1:B:161:ASN:ND2	2:B:600:BTB:H72	2.24	0.53
1:B:161:ASN:ND2	2:B:600:BTB:H42	2.25	0.51
2:B:600:BTB:H61	4:B:847:HOH:O	2.11	0.51
1:A:349:LEU:HD11	1:A:492:ILE:HD12	1.93	0.50
1:B:190:ARG:NH2	4:B:910:HOH:O	2.38	0.50
1:B:221:MET:O	1:B:225:GLN:HG3	2.12	0.50
1:A:364:ARG:NH2	4:A:948:HOH:O	2.39	0.49
1:A:450:ALA:HB3	1:A:515:TYR:CE2	2.48	0.48
1:B:463:LEU:CD2	1:B:467:MET:CE	2.91	0.48
1:A:130:HIS:HE1	4:A:814:HOH:O	1.98	0.47
1:A:463:LEU:CD2	1:A:542:VAL:CG1	2.93	0.47
1:A:133:LYS:NZ	4:A:807:HOH:O	2.48	0.47
1:A:13[A]:GLN:NE2	1:B:262:VAL:H	2.13	0.47
2:A:600:BTB:H71	2:A:600:BTB:H12	1.30	0.47
1:A:378:ASP:OD1	2:A:600:BTB:H41	2.15	0.46
1:A:463:LEU:HD22	1:A:542:VAL:HG11	1.97	0.46
2:B:600:BTB:C3	4:B:983:HOH:O	2.63	0.46
2:B:600:BTB:C6	4:B:847:HOH:O	2.63	0.46
1:A:40:VAL:H	1:A:178:ASN:ND2	2.02	0.46
2:A:600:BTB:N	4:A:984:HOH:O	2.36	0.45
1:A:171:LYS:NZ	1:A:174:GLU:OE2	2.48	0.45
1:A:13[A]:GLN:HE22	1:A:267:ARG:HH12	1.65	0.45
2:A:600:BTB:H31	2:A:600:BTB:O6	2.17	0.44
1:B:147[A]:HIS:CE1	1:B:309:ARG:NH1	2.86	0.44
1:A:454:SER:HB3	4:A:988:HOH:O	2.17	0.44
1:A:467:MET:HE1	1:A:542:VAL:HG13	2.00	0.43
2:B:600:BTB:H51	2:B:600:BTB:H11	1.50	0.43
1:A:331:TYR:CG	1:A:421:ILE:HG12	2.53	0.43
1:A:146:SER:OG	1:A:147[A]:HIS:CD2	2.67	0.43
1:A:349:LEU:C	1:A:349:LEU:CD2	2.86	0.43
1:A:252:LYS:HE3	4:A:879:HOH:O	2.18	0.42
1:A:330:ASN:HD22	1:A:358:VAL:HG13	1.84	0.42
2:A:600:BTB:H32	4:A:984:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:LEU:HD21	1:A:542:VAL:HG12	2.02	0.42
1:A:430:GLN:NE2	4:A:870:HOH:O	2.53	0.42
1:B:31:PRO:HB3	1:B:38:HIS:HB3	2.01	0.42
2:B:600:BTB:H42	2:B:600:BTB:H72	1.20	0.41
2:A:600:BTB:H11	2:A:600:BTB:H51	1.31	0.41
1:A:156:LYS:HZ1	1:A:158:ASN:HD21	1.67	0.41
1:B:409:LYS:H	1:B:409:LYS:HG3	1.73	0.41
1:B:449:GLN:HG2	1:B:450:ALA:N	2.35	0.41
1:B:449:GLN:HG3	1:B:515:TYR:O	2.21	0.41
1:A:485:ALA:HA	1:A:486:PRO:HD3	1.97	0.41
1:A:439:ARG:NH2	4:A:803:HOH:O	2.54	0.40
1:A:8:GLY:O	1:A:270:HIS:HD2	2.04	0.40
1:B:546:ALA:C	4:B:915:HOH:O	2.59	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:462:LYS:NZ	4:A:891:HOH:O[4_456]	2.14	0.06

## 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	549/570 (96%)	540 (98%)	7 (1%)	2 (0%)	38	20
1	B	548/570 (96%)	539 (98%)	8 (2%)	1 (0%)	51	31
All	All	1097/1140 (96%)	1079 (98%)	15 (1%)	3 (0%)	44	25

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	545	ASN
1	B	145	PRO
1	A	145	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	412/443 (93%)	408 (99%)	4 (1%)	80	71
1	B	412/443 (93%)	406 (98%)	6 (2%)	70	55
All	All	824/886 (93%)	814 (99%)	10 (1%)	80	64

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	147[A]	HIS
1	A	147[B]	HIS
1	A	171	LYS
1	A	356	ASP
1	B	147[A]	HIS
1	B	147[B]	HIS
1	B	349	LEU
1	B	356	ASP
1	B	391	GLU
1	B	409	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	9	GLN
1	A	54	HIS
1	A	114	ASN
1	A	158	ASN
1	A	178	ASN

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Mol	Chain	Res	Type
1	A	330	ASN
1	A	430	GLN
1	B	4	HIS
1	B	54	HIS
1	B	501	ASN
1	B	527	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	CSS	A	285	1	5,6,7	1.14	1 (20%)	3,6,8	0.80	0
1	CSS	B	285	1	5,6,7	0.95	0	3,6,8	1.15	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
1	CSS	A	285	1	-	0/1/5/7	0/0/0/0
1	CSS	B	285	1	-	0/1/5/7	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	285	CSS	CA-C	2.25	1.53	1.50

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.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	BTB	A	600	-	13,13,13	0.79	0	9,16,16	1.50	1 (11%)
2	BTB	B	600	-	13,13,13	1.12	2 (15%)	9,16,16	2.22	3 (33%)

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	BTB	A	600	-	-	0/21/21/21	0/0/0/0
2	BTB	B	600	-	-	0/21/21/21	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	600	BTB	C3-C2	-2.24	1.50	1.53
2	B	600	BTB	C1-C2	-2.12	1.50	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	600	BTB	O1-C1-C2	-4.47	98.79	111.37
2	B	600	BTB	O4-C4-C2	-3.81	100.64	111.37
2	A	600	BTB	O4-C4-C2	-2.74	103.67	111.37
2	B	600	BTB	C7-N-C2	-2.26	107.03	113.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	BTB	14	0
2	B	600	BTB	13	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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	544/570 (95%)	0.39	46 (8%)	11 13	16, 25, 44, 87	2 (0%)
1	B	544/570 (95%)	0.16	18 (3%)	47 53	18, 26, 39, 61	0
All	All	1088/1140 (95%)	0.28	64 (5%)	23 26	16, 25, 41, 87	2 (0%)

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	545	ASN	9.9
1	A	391	GLU	6.8
1	B	3	ILE	6.3
1	A	134	GLY	6.2
1	A	542	VAL	6.1
1	A	453	THR	5.8
1	A	543	LEU	5.6
1	A	452	ALA	5.4
1	B	134	GLY	5.1
1	B	2	ALA	4.8
1	A	454	SER	4.5
1	A	546	ALA	4.3
1	A	458	ALA	4.1
1	A	513	ASP	4.0
1	B	5	ASN	4.0
1	A	539	VAL	4.0
1	A	464	SER	3.9
1	B	511	THR	3.7
1	A	456	GLN	3.7
1	A	468	VAL	3.6
1	B	34	GLY	3.5
1	A	450	ALA	3.5
1	A	511	THR	3.5
1	A	459	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	543	LEU	3.3
1	B	545	ASN	3.3
1	A	413	ILE	3.3
1	B	373	PHE	3.2
1	A	133	LYS	3.2
1	A	462	LYS	3.2
1	A	465	PRO	3.2
1	A	515	TYR	3.1
1	A	517	ILE	3.1
1	A	463	LEU	3.1
1	A	451	SER	3.1
1	A	538	ILE	3.0
1	A	541	GLU	3.0
1	A	510	GLY	2.9
1	A	34	GLY	2.9
1	B	33	ALA	2.9
1	A	455	ALA	2.7
1	A	461	SER	2.7
1	B	133	LYS	2.7
1	A	395	ALA	2.7
1	B	136	PRO	2.6
1	A	36	ALA	2.5
1	A	467	MET	2.5
1	A	33	ALA	2.4
1	A	415	CYS	2.4
1	A	373	PHE	2.4
1	A	460	LEU	2.3
1	B	342	ASP	2.3
1	B	438	ALA	2.3
1	A	396	SER	2.3
1	B	137	LEU	2.2
1	A	417	LEU	2.2
1	B	412	ILE	2.2
1	B	142	VAL	2.2
1	A	3	ILE	2.2
1	A	135	GLY	2.1
1	A	389	GLY	2.1
1	B	182	ALA	2.0
1	A	412	ILE	2.0
1	A	136	PRO	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	CSS	A	285	7/8	0.75	0.13	-	24,25,30,32	0
1	CSS	B	285	7/8	0.78	0.15	-	26,27,33,33	0

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	BTB	A	600	14/14	0.75	0.32	10.89	25,32,37,38	14
2	BTB	B	600	14/14	0.81	0.26	4.96	21,27,35,35	14
3	MG	B	547	1/1	0.99	0.11	-2.92	21,21,21,21	0
3	MG	A	547	1/1	0.99	0.09	-4.48	18,18,18,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.