



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 01:42 AM BST

PDB ID : 5GNZ
Title : The M3 mutant structure of Bgl6
Authors : Xie, W.; Pang, P.; Cao, L.C.; Liu, Y.H.; Wang, Z.
Deposited on : 2016-07-25
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

<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 : 2.13.1
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) : 2.13.1

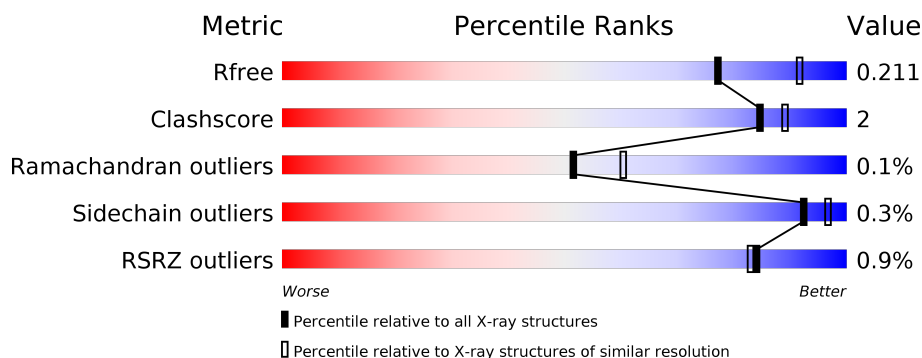
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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 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	467	<div><div></div><div>90%6%.</div></div>
1	B	467	<div><div></div><div>90%6%.</div></div>
1	C	467	<div><div>%</div><div>90%5%.</div></div>
1	D	467	<div><div>%</div><div>90%6%.</div></div>
1	H	467	<div><div>2%</div><div>90%6%.</div></div>
1	I	467	<div><div>%</div><div>91%5%.</div></div>

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Mol	Chain	Length	Quality of chain
1	J	467	<div><div>%</div><div><div></div><div>90%</div><div>6%</div><div></div></div><div></div></div>
1	K	467	<div><div></div><div>90%</div><div>6%</div><div></div></div>

2 Entry composition

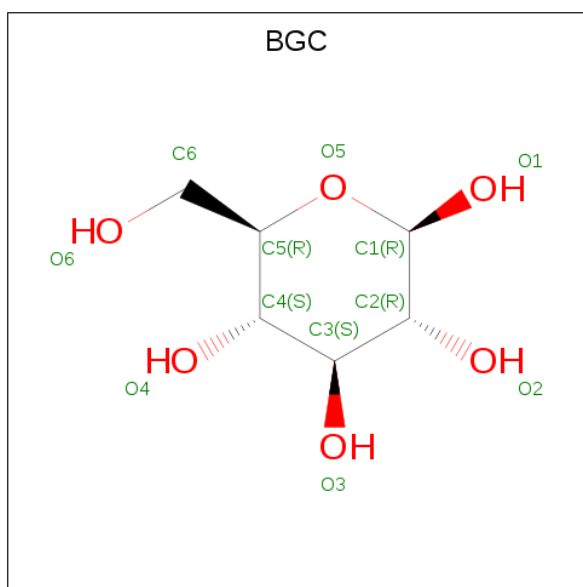
There are 4 unique types of molecules in this entry. The entry contains 30472 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Beta-glucosidase.

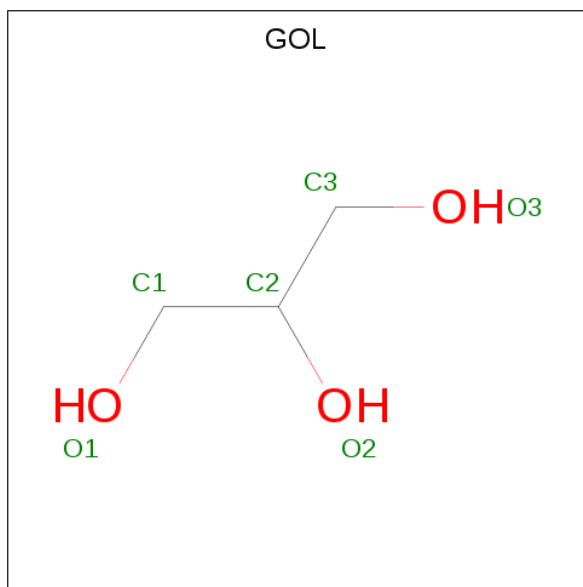
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	448	Total	C	N	O	S	0	0	0
			3586	2287	633	655	11			
1	B	448	Total	C	N	O	S	0	0	0
			3586	2287	633	655	11			
1	C	447	Total	C	N	O	S	0	0	0
			3573	2278	630	654	11			
1	D	448	Total	C	N	O	S	0	0	0
			3582	2284	632	655	11			
1	H	447	Total	C	N	O	S	0	0	0
			3577	2282	632	652	11			
1	I	448	Total	C	N	O	S	0	0	0
			3586	2287	633	655	11			
1	J	448	Total	C	N	O	S	0	0	0
			3579	2283	632	653	11			
1	K	447	Total	C	N	O	S	0	0	0
			3581	2284	632	654	11			

- Molecule 2 is beta-D-glucopyranose (three-letter code: BGC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		
2	C	1	Total	C	O	0	0
			12	6	6		
2	D	1	Total	C	O	0	0
			12	6	6		
2	H	1	Total	C	O	0	0
			12	6	6		
2	I	1	Total	C	O	0	0
			12	6	6		
2	J	1	Total	C	O	0	0
			12	6	6		
2	K	1	Total	C	O	0	0
			12	6	6		

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



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

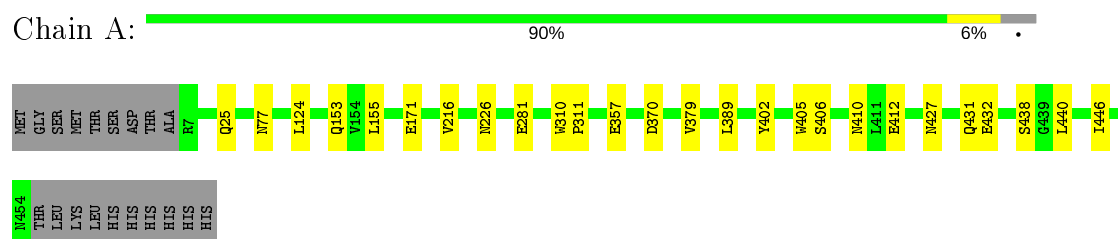
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	260	Total	O	0	0
			260	260		
4	B	214	Total	O	0	0
			214	214		
4	C	199	Total	O	0	0
			199	199		
4	D	216	Total	O	0	0
			216	216		
4	H	176	Total	O	0	0
			176	176		
4	I	231	Total	O	0	0
			231	231		
4	J	182	Total	O	0	0
			182	182		
4	K	242	Total	O	0	0
			242	242		

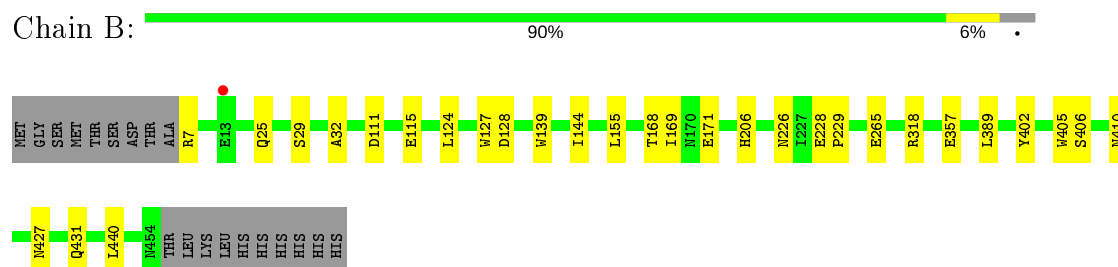
3 Residue-property plots [i](#)

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.

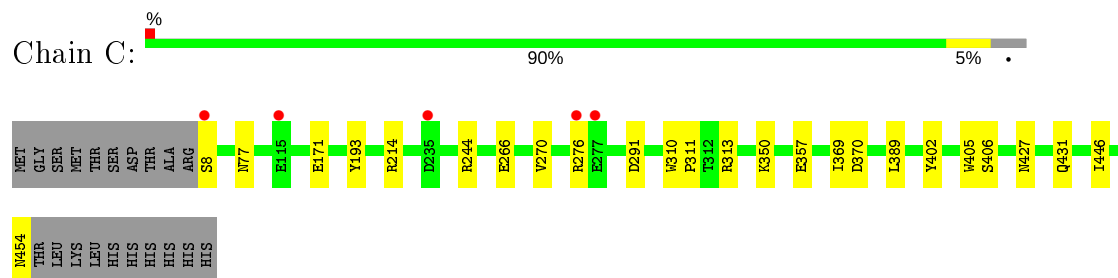
- Molecule 1: Beta-glucosidase



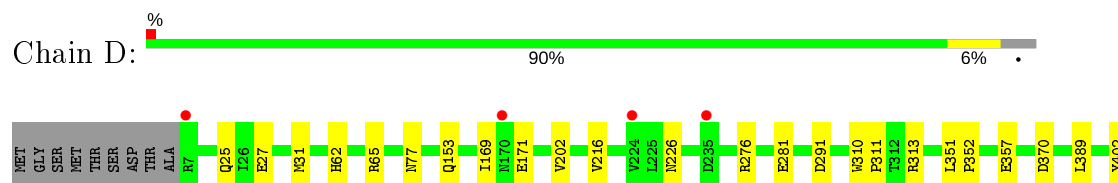
- Molecule 1: Beta-glucosidase



- Molecule 1: Beta-glucosidase

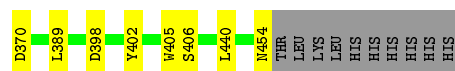
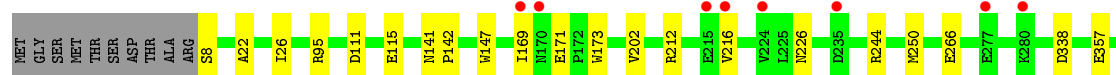
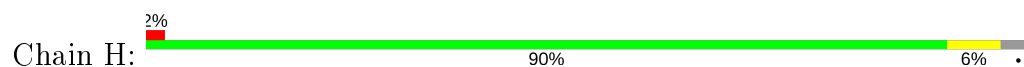


- Molecule 1: Beta-glucosidase

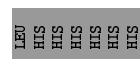
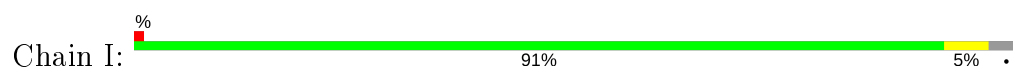




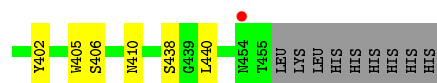
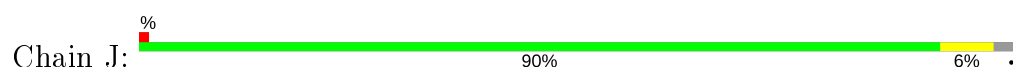
● Molecule 1: Beta-glucosidase



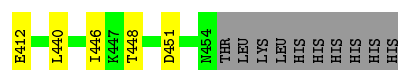
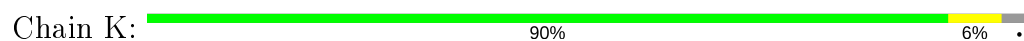
● Molecule 1: Beta-glucosidase



● Molecule 1: Beta-glucosidase



● Molecule 1: Beta-glucosidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	97.16Å 214.04Å 99.33Å 90.00° 109.27° 90.00°	Depositor
Resolution (Å)	35.69 – 2.20 35.69 – 2.20	Depositor EDS
% Data completeness (in resolution range)	86.0 (35.69-2.20) 86.0 (35.69-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.84 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.8.2 _1309	Depositor
R, R_{free}	0.177 , 0.211 0.177 , 0.211	Depositor DCC
R_{free} test set	8338 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	26.6	Xtriage
Anisotropy	0.175	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	30472	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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: GOL, BGC

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	0.27	0/3699	0.46	0/5039
1	B	0.27	0/3699	0.45	0/5039
1	C	0.26	0/3686	0.45	0/5024
1	D	0.26	0/3695	0.47	0/5035
1	H	0.26	0/3690	0.46	0/5027
1	I	0.26	0/3699	0.46	0/5039
1	J	0.26	0/3692	0.45	0/5031
1	K	0.27	0/3694	0.48	0/5032
All	All	0.26	0/29554	0.46	0/40266

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	C	0	1
1	J	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	369	ILE	Peptide
1	J	369	ILE	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	3586	0	3405	15	0
1	B	3586	0	3405	19	0
1	C	3573	0	3381	13	0
1	D	3582	0	3394	19	0
1	H	3577	0	3399	16	0
1	I	3586	0	3405	13	0
1	J	3579	0	3392	15	0
1	K	3581	0	3403	16	0
2	A	12	0	12	3	0
2	B	12	0	12	2	0
2	C	12	0	12	2	0
2	D	12	0	12	2	0
2	H	12	0	12	2	0
2	I	12	0	12	2	0
2	J	12	0	12	2	0
2	K	12	0	12	3	0
3	H	6	0	8	0	0
4	A	260	0	0	3	0
4	B	214	0	0	3	0
4	C	199	0	0	2	0
4	D	216	0	0	5	0
4	H	176	0	0	2	0
4	I	231	0	0	2	0
4	J	182	0	0	1	0
4	K	242	0	0	1	0
All	All	30472	0	27288	126	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 2.

All (126) 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:I:171:GLU:OE2	2:I:501:BGC:O1	2.04	0.75
1:A:171:GLU:OE2	2:A:501:BGC:O1	2.07	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:171:GLU:OE2	2:H:502:BGC:O1	2.08	0.72
1:K:171:GLU:OE2	2:K:501:BGC:O1	2.08	0.70
1:K:244:ARG:NH2	1:K:266:GLU:OE2	2.24	0.69
1:B:171:GLU:OE2	2:B:501:BGC:O1	2.10	0.69
1:C:313:ARG:NH1	4:C:606:HOH:O	2.25	0.68
1:J:171:GLU:OE2	2:J:501:BGC:O1	2.11	0.67
1:D:169:ILE:HD13	1:D:202:VAL:HG13	1.77	0.66
1:K:389:LEU:HD11	1:K:402:TYR:CD1	2.31	0.66
1:K:261:ARG:NH1	4:K:604:HOH:O	2.29	0.65
1:C:357:GLU:OE1	2:C:501:BGC:H1	1.96	0.65
1:H:169:ILE:HD13	1:H:202:VAL:HG13	1.78	0.65
1:B:357:GLU:OE1	2:B:501:BGC:H1	1.97	0.64
1:C:171:GLU:OE2	2:C:501:BGC:O1	2.15	0.64
1:C:193:TYR:HB3	1:C:276:ARG:HH22	1.64	0.62
1:H:357:GLU:OE1	2:H:502:BGC:H1	1.99	0.62
1:J:389:LEU:HD11	1:J:402:TYR:CD1	2.35	0.62
1:C:244:ARG:NH2	1:C:266:GLU:OE2	2.29	0.62
1:H:244:ARG:NH2	1:H:266:GLU:OE2	2.31	0.62
1:J:357:GLU:OE1	2:J:501:BGC:H1	2.00	0.61
1:C:389:LEU:HD11	1:C:402:TYR:CD1	2.35	0.61
1:D:31:MET:SD	4:D:618:HOH:O	2.56	0.60
1:H:389:LEU:HD11	1:H:402:TYR:CD1	2.35	0.60
1:D:389:LEU:HD11	1:D:402:TYR:CD1	2.35	0.60
1:I:65:ARG:NH1	4:I:607:HOH:O	2.35	0.59
1:B:389:LEU:HD11	1:B:402:TYR:CD1	2.38	0.59
1:D:65:ARG:NH1	4:D:612:HOH:O	2.35	0.59
1:K:357:GLU:OE1	2:K:501:BGC:H1	2.03	0.58
1:I:389:LEU:HD11	1:I:402:TYR:CD1	2.39	0.58
1:C:8:SER:HA	1:C:454:ASN:OD1	2.04	0.57
1:I:357:GLU:OE1	2:I:501:BGC:H1	2.04	0.56
1:A:389:LEU:HD11	1:A:402:TYR:CD1	2.40	0.56
1:B:169:ILE:HD13	1:B:206:HIS:HB2	1.88	0.55
1:D:281:GLU:OE1	4:D:601:HOH:O	2.18	0.55
1:I:326:GLU:OE2	4:I:601:HOH:O	2.18	0.54
1:K:27:GLU:HA	1:K:62:HIS:HB3	1.90	0.54
1:C:270:VAL:O	4:C:601:HOH:O	2.19	0.53
1:K:448:THR:HB	1:K:451:ASP:HB2	1.91	0.53
1:B:318:ARG:NH1	4:B:610:HOH:O	2.41	0.53
1:B:7:ARG:N	4:B:612:HOH:O	2.42	0.53
1:A:281:GLU:OE1	4:A:601:HOH:O	2.19	0.52
1:D:276:ARG:NH2	4:D:615:HOH:O	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:357:GLU:OE1	2:A:501:BGC:H1	2.10	0.51
1:I:153:GLN:HG3	1:I:216:VAL:HG21	1.92	0.51
1:H:95:ARG:HD3	1:H:147:TRP:CD1	2.46	0.50
1:A:153:GLN:HG3	1:A:216:VAL:HG21	1.94	0.49
1:H:8:SER:HA	1:H:454:ASN:OD1	2.13	0.49
1:J:25:GLN:O	1:J:410:ASN:HB2	2.12	0.49
1:A:432:GLU:OE1	4:A:602:HOH:O	2.20	0.48
1:J:206:HIS:CE1	1:J:223:ILE:HB	2.48	0.48
1:J:95:ARG:NH1	4:J:609:HOH:O	2.40	0.48
1:B:405:TRP:HA	1:B:406:SER:HA	1.60	0.47
1:A:427:ASN:O	1:A:431:GLN:N	2.48	0.47
1:H:398:ASP:OD2	4:H:602:HOH:O	2.21	0.47
1:J:236:LYS:HB2	1:J:236:LYS:HE3	1.69	0.46
1:D:25:GLN:O	1:D:410:ASN:HB2	2.16	0.46
1:D:27:GLU:HA	1:D:62:HIS:HB3	1.98	0.46
1:H:405:TRP:HA	1:H:406:SER:HA	1.60	0.46
1:J:405:TRP:HA	1:J:406:SER:HA	1.60	0.46
1:A:124:LEU:HD22	1:A:155:LEU:HD12	1.97	0.46
1:A:379:VAL:HG22	1:A:438:SER:HA	1.98	0.46
1:J:153:GLN:HG3	1:J:216:VAL:HG21	1.97	0.46
1:K:405:TRP:HA	1:K:406:SER:HA	1.62	0.46
1:B:171:GLU:HG2	1:B:226:ASN:HB3	1.98	0.46
1:I:405:TRP:HA	1:I:406:SER:HA	1.59	0.45
1:K:362:TRP:H	1:K:378:ARG:NH2	2.15	0.45
1:H:338:ASP:OD2	4:H:601:HOH:O	2.20	0.45
1:K:355:VAL:HG23	1:K:399:LEU:HD11	1.99	0.45
1:K:25:GLN:O	1:K:410:ASN:HB2	2.17	0.45
1:I:383:GLN:HG3	1:I:384:THR:N	2.32	0.44
1:B:427:ASN:O	1:B:431:GLN:N	2.49	0.44
1:K:77:ASN:O	1:K:446:ILE:HG21	2.17	0.44
1:J:310:TRP:HA	1:J:311:PRO:HA	1.75	0.44
1:K:291:ASP:O	1:K:352:PRO:HG2	2.18	0.44
1:D:310:TRP:HA	1:D:311:PRO:HA	1.80	0.44
1:C:214:ARG:HH22	1:C:291:ASP:CG	2.21	0.44
1:H:171:GLU:HG2	1:H:226:ASN:HB3	2.00	0.44
1:D:405:TRP:HA	1:D:406:SER:HA	1.62	0.43
1:B:168:THR:HB	1:B:169:ILE:HD12	2.00	0.43
1:C:405:TRP:HA	1:C:406:SER:HA	1.62	0.43
1:J:231:TYR:O	1:J:303:PRO:HD2	2.18	0.43
1:H:22:ALA:O	1:H:26:ILE:HG12	2.19	0.43
1:B:124:LEU:HD22	1:B:155:LEU:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:25:GLN:O	1:I:410:ASN:HB2	2.19	0.43
1:I:379:VAL:HG22	1:I:438:SER:HA	2.00	0.43
1:D:153:GLN:HG3	1:D:216:VAL:HG11	2.01	0.43
1:A:310:TRP:HA	1:A:311:PRO:HA	1.81	0.42
1:A:171:GLU:HG2	1:A:226:ASN:HB3	2.02	0.42
1:B:139:TRP:CE3	1:B:144:ILE:HD13	2.54	0.42
1:J:379:VAL:HG22	1:J:438:SER:HA	2.00	0.42
1:C:427:ASN:O	1:C:431:GLN:N	2.51	0.42
1:D:313:ARG:NH1	4:D:625:HOH:O	2.51	0.42
1:K:153:GLN:HG3	1:K:216:VAL:HG21	2.01	0.42
1:C:310:TRP:HA	1:C:311:PRO:HA	1.79	0.42
1:C:77:ASN:O	1:C:446:ILE:HG21	2.19	0.42
1:D:291:ASP:O	1:D:352:PRO:HG2	2.20	0.42
1:B:128:ASP:N	1:B:128:ASP:OD2	2.53	0.42
1:B:228:GLU:HA	1:B:229:PRO:HD2	1.89	0.42
1:D:357:GLU:OE2	2:D:501:BGC:O2	2.37	0.42
1:J:69:ASP:O	1:J:73:MET:HG3	2.20	0.42
1:A:77:ASN:O	1:A:446:ILE:HG21	2.19	0.42
1:A:412:GLU:OE2	2:A:501:BGC:H6C1	2.20	0.42
1:B:127:TRP:N	1:B:127:TRP:CD1	2.88	0.42
1:B:29:SER:HB3	1:B:32:ALA:HB3	2.01	0.42
1:H:111:ASP:O	1:H:115:GLU:HG3	2.19	0.42
1:K:412:GLU:OE1	2:K:501:BGC:H6C1	2.20	0.42
1:D:412:GLU:OE1	2:D:501:BGC:O4	2.32	0.42
1:K:171:GLU:HG2	1:K:226:ASN:HB3	2.02	0.42
1:H:212:ARG:O	1:H:216:VAL:HG22	2.19	0.41
1:I:243:ARG:HA	1:I:303:PRO:HG2	2.02	0.41
4:A:758:HOH:O	1:D:276:ARG:HD2	2.20	0.41
1:I:107:ASP:HA	1:I:159:PHE:HE1	1.85	0.41
1:D:351:LEU:HA	1:D:352:PRO:HD2	1.90	0.41
1:H:141:ASN:HA	1:H:142:PRO:HD2	1.92	0.41
1:A:405:TRP:HA	1:A:406:SER:HA	1.60	0.41
1:J:121:LEU:HD22	1:J:165:THR:HB	2.02	0.41
1:A:25:GLN:O	1:A:410:ASN:HB2	2.20	0.41
1:B:25:GLN:O	1:B:410:ASN:HB2	2.19	0.41
1:H:173:TRP:CD1	1:H:250:MET:HA	2.55	0.41
1:D:171:GLU:HG2	1:D:226:ASN:HB3	2.02	0.41
1:J:375:ASP:OD1	1:J:375:ASP:N	2.53	0.41
1:D:77:ASN:O	1:D:446:ILE:HG21	2.21	0.41
1:B:265:GLU:OE1	4:B:601:HOH:O	2.21	0.40
1:B:111:ASP:O	1:B:115:GLU:HG3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:171:GLU:HG2	1:I:226:ASN:HB3	2.02	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	446/467 (96%)	436 (98%)	9 (2%)	1 (0%)	47	55
1	B	446/467 (96%)	436 (98%)	10 (2%)	0	100	100
1	C	445/467 (95%)	435 (98%)	9 (2%)	1 (0%)	47	55
1	D	446/467 (96%)	436 (98%)	9 (2%)	1 (0%)	47	55
1	H	445/467 (95%)	435 (98%)	9 (2%)	1 (0%)	47	55
1	I	446/467 (96%)	436 (98%)	10 (2%)	0	100	100
1	J	446/467 (96%)	435 (98%)	10 (2%)	1 (0%)	47	55
1	K	445/467 (95%)	435 (98%)	10 (2%)	0	100	100
All	All	3565/3736 (95%)	3484 (98%)	76 (2%)	5 (0%)	51	60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	370	ASP
1	J	370	ASP
1	D	370	ASP
1	H	370	ASP
1	A	370	ASP

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	361/379 (95%)	360 (100%)	1 (0%)	92	97
1	B	361/379 (95%)	360 (100%)	1 (0%)	92	97
1	C	359/379 (95%)	358 (100%)	1 (0%)	92	97
1	D	360/379 (95%)	359 (100%)	1 (0%)	92	97
1	H	360/379 (95%)	359 (100%)	1 (0%)	92	97
1	I	361/379 (95%)	360 (100%)	1 (0%)	92	97
1	J	359/379 (95%)	358 (100%)	1 (0%)	92	97
1	K	361/379 (95%)	360 (100%)	1 (0%)	92	97
All	All	2882/3032 (95%)	2874 (100%)	8 (0%)	92	97

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	440	LEU
1	B	440	LEU
1	C	350	LYS
1	D	440	LEU
1	H	440	LEU
1	I	440	LEU
1	J	440	LEU
1	K	440	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	J	77	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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	BGC	D	501	-	12,12,12	0.59	0	17,17,17	1.64	4 (23%)
3	GOL	H	501	-	5,5,5	0.37	0	5,5,5	0.31	0
2	BGC	I	501	-	12,12,12	0.78	0	17,17,17	1.07	1 (5%)
2	BGC	J	501	-	12,12,12	0.75	0	17,17,17	0.77	0
2	BGC	K	501	-	12,12,12	0.78	0	17,17,17	0.81	0
2	BGC	H	502	-	12,12,12	0.72	0	17,17,17	1.02	1 (5%)
2	BGC	A	501	-	12,12,12	0.76	0	17,17,17	1.23	2 (11%)
2	BGC	B	501	-	12,12,12	0.76	0	17,17,17	0.92	1 (5%)
2	BGC	C	501	-	12,12,12	0.77	0	17,17,17	0.73	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	BGC	D	501	-	-	0/2/22/22	0/1/1/1
3	GOL	H	501	-	-	0/4/4/4	-
2	BGC	I	501	-	-	0/2/22/22	0/1/1/1
2	BGC	J	501	-	-	2/2/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BGC	K	501	-	-	2/2/22/22	0/1/1/1
2	BGC	H	502	-	-	0/2/22/22	0/1/1/1
2	BGC	A	501	-	-	2/2/22/22	0/1/1/1
2	BGC	B	501	-	-	2/2/22/22	0/1/1/1
2	BGC	C	501	-	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	BGC	C1-O5-C5	4.70	122.53	113.66
2	A	501	BGC	C1-O5-C5	-3.51	107.04	113.66
2	I	501	BGC	C1-O5-C5	-3.09	107.82	113.66
2	D	501	BGC	O5-C1-C2	2.68	115.07	110.28
2	H	502	BGC	C1-O5-C5	-2.57	108.81	113.66
2	A	501	BGC	C1-C2-C3	-2.43	105.27	110.31
2	D	501	BGC	C4-C3-C2	-2.38	106.67	110.82
2	D	501	BGC	C3-C4-C5	-2.11	106.47	110.24
2	B	501	BGC	C1-O5-C5	-2.06	109.78	113.66

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	J	501	BGC	O5-C5-C6-O6
2	J	501	BGC	C4-C5-C6-O6
2	A	501	BGC	C4-C5-C6-O6
2	A	501	BGC	O5-C5-C6-O6
2	B	501	BGC	O5-C5-C6-O6
2	K	501	BGC	O5-C5-C6-O6
2	K	501	BGC	C4-C5-C6-O6
2	B	501	BGC	C4-C5-C6-O6

There are no ring outliers.

8 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	501	BGC	2	0
2	I	501	BGC	2	0
2	J	501	BGC	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	501	BGC	3	0
2	H	502	BGC	2	0
2	A	501	BGC	3	0
2	B	501	BGC	2	0
2	C	501	BGC	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, 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	448/467 (95%)	-0.43	0 100 100	10, 17, 30, 45	0
1	B	448/467 (95%)	-0.32	1 (0%) 95 94	13, 20, 33, 49	0
1	C	447/467 (95%)	-0.12	5 (1%) 80 79	14, 24, 39, 53	0
1	D	448/467 (95%)	-0.18	4 (0%) 84 83	12, 22, 37, 50	0
1	H	447/467 (95%)	-0.11	8 (1%) 68 66	16, 27, 42, 56	0
1	I	448/467 (95%)	-0.17	4 (0%) 84 83	12, 22, 37, 51	0
1	J	448/467 (95%)	-0.08	7 (1%) 72 70	13, 25, 43, 58	0
1	K	447/467 (95%)	-0.35	2 (0%) 92 91	11, 19, 34, 47	0
All	All	3581/3736 (95%)	-0.22	31 (0%) 84 83	10, 22, 38, 58	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	215	GLU	3.6
1	I	7	ARG	3.2
1	C	8	SER	3.1
1	H	169	ILE	2.7
1	J	370	ASP	2.6
1	D	224	VAL	2.6
1	J	396	GLY	2.5
1	H	280	LYS	2.5
1	C	115	GLU	2.4
1	C	277	GLU	2.4
1	I	350	LYS	2.4
1	B	13	GLU	2.3
1	C	276	ARG	2.3
1	J	281	GLU	2.3
1	J	454	ASN	2.3
1	D	235	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	H	216	VAL	2.2
1	D	7	ARG	2.2
1	H	170	ASN	2.2
1	J	9	TYR	2.2
1	H	235	ASP	2.2
1	K	369	ILE	2.2
1	I	405	TRP	2.2
1	J	13	GLU	2.2
1	J	8	SER	2.2
1	C	235	ASP	2.1
1	H	277	GLU	2.1
1	H	224	VAL	2.1
1	D	170	ASN	2.0
1	K	370	ASP	2.0
1	I	8	SER	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, 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	BGC	B	501	12/12	0.85	0.33	25,31,41,48	9
2	BGC	C	501	12/12	0.85	0.42	33,37,43,44	7
2	BGC	A	501	12/12	0.87	0.25	25,29,39,45	6
2	BGC	K	501	12/12	0.88	0.30	23,29,41,47	8
2	BGC	H	502	12/12	0.89	0.30	32,35,47,49	9
2	BGC	I	501	12/12	0.90	0.33	27,32,41,44	7
2	BGC	J	501	12/12	0.91	0.30	27,35,41,46	9
2	BGC	D	501	12/12	0.91	0.34	29,34,42,48	8

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GOL	H	501	6/6	0.95	0.12	22,31,33,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.