



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:40 PM UTC

PDB ID : 2E40 / pdb_00002e40
Title : Crystal structure of intracellular family 1 beta-glucosidase BGL1A from the basidiomycete *Phanerochaete chrysosporium* in complex with gluconolactone
Authors : Nijikken, Y.; Tsukada, T.; Igarashi, K.; Samejima, M.; Fushinobu, S.
Deposited on : 2006-12-01
Resolution : 1.90 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

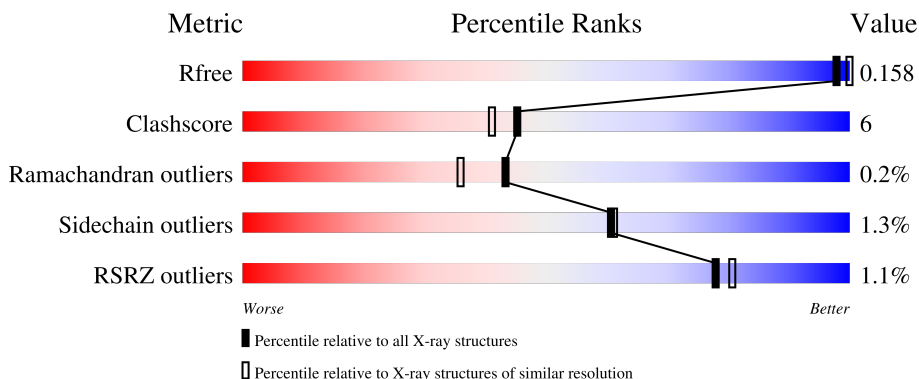
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


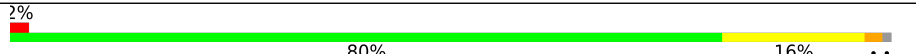
The reported resolution of this entry is 1.90 Å.

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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	465	 83% 15% ..
1	B	465	 2% 80% 16% ..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8369 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.

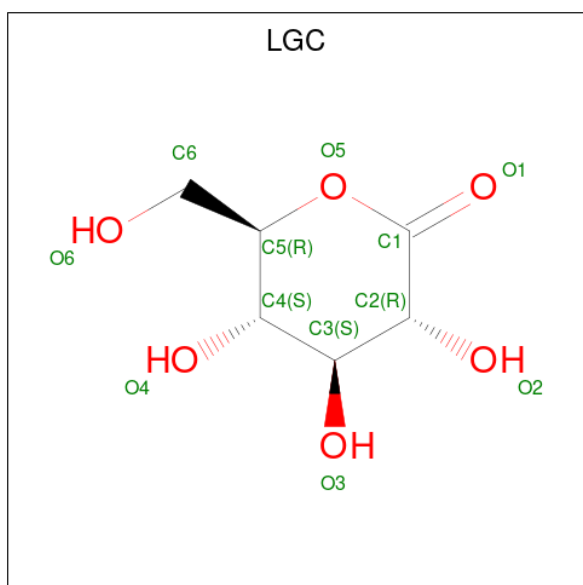
- Molecule 1 is a protein called Beta-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	459	Total 3712	C 2387	N 621	O 699	S 5	0	0	0
1	B	459	Total 3712	C 2387	N 621	O 699	S 5	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	LEU	-	cloning artifact	UNP Q25BW5
A	-1	ALA	-	cloning artifact	UNP Q25BW5
A	0	LEU	-	cloning artifact	UNP Q25BW5
B	-2	LEU	-	cloning artifact	UNP Q25BW5
B	-1	ALA	-	cloning artifact	UNP Q25BW5
B	0	LEU	-	cloning artifact	UNP Q25BW5

- Molecule 2 is D-glucono-1,5-lactone (CCD ID: LGC) (formula: C₆H₁₀O₆).



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		

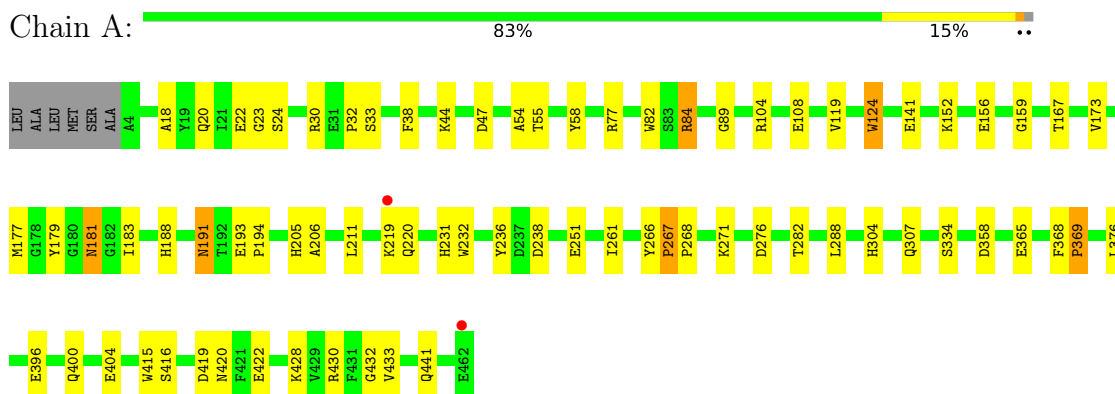
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	521	Total	O	0	0
			521	521		
3	B	400	Total	O	0	0
			400	400		

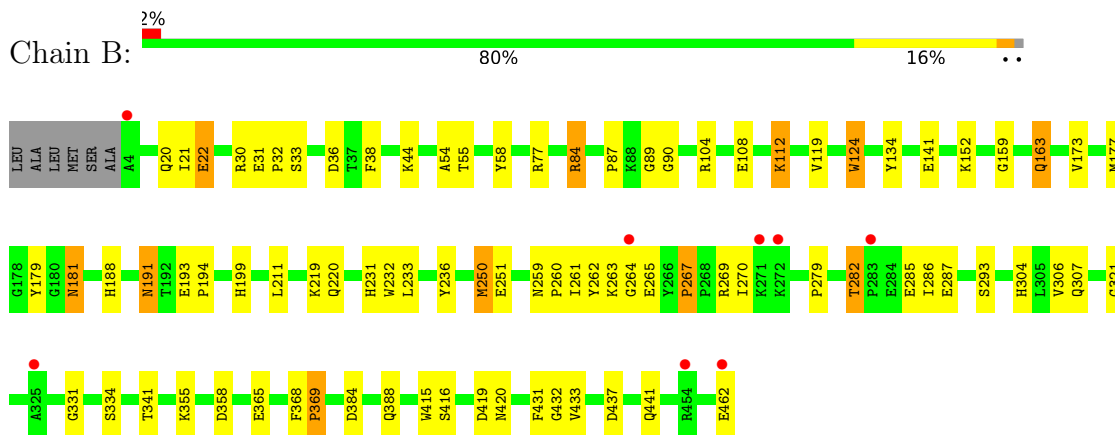
3 Residue-property plots [i](#)

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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.79Å 120.08Å 133.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.57 – 1.90 44.57 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.3 (44.57-1.90) 99.6 (44.57-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 1.89Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.164 , 0.191 0.165 , 0.158	Depositor DCC
R_{free} test set	4158 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtrriage
Anisotropy	0.344	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8369	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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: LGC

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	0.35	0/3825	0.95	24/5196 (0.5%)
1	B	0.34	0/3825	0.92	24/5196 (0.5%)
All	All	0.34	0/7650	0.93	48/10392 (0.5%)

There are no bond length outliers.

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	433	VAL	N-CA-C	-11.57	101.37	112.83
1	A	22	GLU	N-CA-C	11.18	123.03	111.07
1	B	22	GLU	N-CA-C	10.59	122.40	111.07
1	B	433	VAL	N-CA-C	-9.22	102.20	112.80
1	A	419	ASP	N-CA-C	-7.96	98.69	110.23
1	B	419	ASP	N-CA-C	-7.67	99.91	110.35
1	A	119	VAL	N-CA-C	6.56	117.31	107.80
1	B	306	VAL	N-CA-C	6.42	117.15	108.17
1	A	231	HIS	N-CA-C	-6.41	100.98	110.46
1	B	89	GLY	N-CA-C	6.29	123.54	114.67
1	B	231	HIS	N-CA-C	-6.12	101.40	110.46
1	A	267	PRO	CA-C-N	5.97	125.18	118.97
1	A	267	PRO	C-N-CA	5.97	125.18	118.97
1	B	119	VAL	N-CA-C	5.88	116.58	107.99
1	B	282	THR	N-CA-C	-5.82	102.56	110.36
1	A	232	TRP	N-CA-C	-5.81	100.20	109.96
1	A	89	GLY	N-CA-C	5.77	122.75	115.42
1	B	267	PRO	CA-C-N	5.72	124.92	118.97
1	B	267	PRO	C-N-CA	5.72	124.92	118.97
1	A	33	SER	N-CA-C	-5.70	101.77	110.14
1	B	432	GLY	N-CA-C	5.69	119.82	112.54
1	A	159	GLY	N-CA-C	5.63	120.76	113.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	32	PRO	N-CA-C	5.61	120.01	111.15
1	A	282	THR	N-CA-C	-5.56	103.74	110.13
1	A	432	GLY	N-CA-C	5.54	119.63	112.54
1	B	90	GLY	N-CA-C	5.53	120.46	112.82
1	A	84	ARG	N-CA-C	-5.49	106.71	113.41
1	B	33	SER	N-CA-C	-5.47	102.09	110.14
1	A	141	GLU	N-CA-C	5.39	117.23	111.36
1	A	58	TYR	N-CA-C	-5.38	105.49	111.36
1	B	232	TRP	N-CA-C	-5.36	100.96	109.96
1	A	18	ALA	N-CA-C	5.34	117.53	111.02
1	A	268	PRO	N-CA-C	5.34	121.10	113.47
1	A	124	TRP	N-CA-C	5.31	121.61	113.28
1	B	54	ALA	CB-CA-C	-5.31	110.44	116.54
1	B	58	TYR	N-CA-C	-5.29	105.42	111.14
1	A	358	ASP	N-CA-C	5.28	118.72	111.54
1	B	269	ARG	N-CA-C	5.25	116.69	111.07
1	A	32	PRO	N-CA-C	5.22	119.42	111.11
1	B	36	ASP	N-CA-C	-5.18	105.63	111.28
1	B	261	ILE	N-CA-C	5.13	115.90	110.72
1	A	54	ALA	CB-CA-C	-5.12	110.65	116.54
1	B	124	TRP	N-CA-C	5.12	121.31	113.28
1	B	358	ASP	N-CA-C	5.09	118.47	111.54
1	A	376	LEU	N-CA-C	5.07	116.45	110.07
1	B	141	GLU	N-CA-C	5.03	116.45	111.07
1	A	261	ILE	N-CA-C	5.03	115.75	110.62
1	B	84	ARG	N-CA-C	-5.02	107.32	113.50

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	3712	0	3534	37	0
1	B	3712	0	3534	49	0
2	A	12	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	12	0	10	0	0
3	A	521	0	0	2	0
3	B	400	0	0	4	0
All	All	8369	0	7088	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 6.

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:250:MET:HA	1:B:250:MET:HE2	1.71	0.73
1:A:219:LYS:HG3	1:A:220:GLN:HG3	1.73	0.71
1:A:428:LYS:N	1:A:428:LYS:HD2	2.05	0.70
1:B:282:THR:OG1	1:B:285:GLU:HG3	1.94	0.68
1:B:104:ARG:O	1:B:108:GLU:HG3	1.95	0.66
1:A:152:LYS:HB2	1:A:211:LEU:HD21	1.78	0.66
1:B:112:LYS:HB2	1:B:112:LYS:NZ	2.09	0.66
1:B:233:LEU:CD1	1:B:250:MET:HE3	2.31	0.60
1:A:167:THR:OG1	1:A:205:HIS:HD2	1.83	0.60
1:B:233:LEU:HD12	1:B:250:MET:HG2	1.83	0.60
1:A:219:LYS:HG3	1:A:220:GLN:N	2.16	0.60
1:B:263:LYS:HE2	1:B:263:LYS:HA	1.82	0.59
1:B:251:GLU:CD	1:B:267:PRO:HB2	2.30	0.57
1:B:181:ASN:C	1:B:181:ASN:HD22	2.12	0.57
1:A:104:ARG:O	1:A:108:GLU:HG3	2.04	0.57
1:B:219:LYS:HG3	1:B:220:GLN:HG3	1.87	0.57
1:A:181:ASN:C	1:A:181:ASN:HD22	2.13	0.56
1:A:251:GLU:CD	1:A:267:PRO:HB2	2.31	0.55
1:A:191:ASN:HD22	1:A:191:ASN:H	1.55	0.55
1:A:177:MET:HA	1:A:181:ASN:HD21	1.73	0.54
1:B:191:ASN:H	1:B:191:ASN:HD22	1.56	0.54
1:A:236:TYR:CG	1:A:307:GLN:HG2	2.43	0.53
1:B:304:HIS:HE1	3:B:2126:HOH:O	1.92	0.53
1:A:267:PRO:O	1:A:271:LYS:HG3	2.09	0.52
1:B:369:PRO:HD3	1:B:431:PHE:CE1	2.45	0.52
1:B:124:TRP:CD1	1:B:124:TRP:N	2.77	0.51
1:B:30:ARG:HB2	1:B:84:ARG:HG2	1.92	0.50
1:B:38:PHE:CZ	1:B:44:LYS:HD2	2.46	0.50
1:A:193:GLU:N	1:A:194:PRO:HD2	2.26	0.50
1:A:206:ALA:HB1	1:A:288:LEU:HG	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:250:MET:HA	1:B:250:MET:CE	2.41	0.49
1:A:124:TRP:CH2	1:A:173:VAL:HG11	2.48	0.49
1:B:177:MET:HA	1:B:181:ASN:HD21	1.78	0.48
1:A:20:GLN:O	1:A:420:ASN:HB2	2.12	0.48
1:A:191:ASN:HD22	1:A:191:ASN:N	2.09	0.48
1:B:437:ASP:O	1:B:441:GLN:N	2.43	0.48
1:A:124:TRP:CD1	1:A:124:TRP:N	2.80	0.48
1:B:159:GLY:HA3	1:B:220:GLN:NE2	2.28	0.48
1:B:236:TYR:CB	1:B:307:GLN:HG2	2.43	0.48
1:A:266:TYR:HB2	1:A:271:LYS:HD3	1.96	0.48
1:B:191:ASN:HD22	1:B:191:ASN:N	2.11	0.47
1:B:264:GLY:O	1:B:286:ILE:HG23	2.15	0.47
1:A:304:HIS:HE1	3:A:1451:HOH:O	1.97	0.47
1:B:179:TYR:HA	1:B:188:HIS:HB2	1.97	0.46
1:A:38:PHE:CZ	1:A:44:LYS:HD2	2.50	0.46
1:B:259:ASN:HB3	1:B:260:PRO:HD3	1.97	0.46
1:A:415:TRP:HA	1:A:416:SER:HA	1.71	0.46
1:B:20:GLN:O	1:B:420:ASN:HB2	2.16	0.46
1:A:55:THR:HA	1:A:441:GLN:HE22	1.81	0.45
1:B:55:THR:HA	1:B:441:GLN:HE22	1.81	0.45
1:A:179:TYR:HA	1:A:188:HIS:HB2	1.97	0.45
1:A:369:PRO:HA	1:A:430:ARG:O	2.17	0.45
1:B:77:ARG:NH1	1:B:365:GLU:HG3	2.32	0.45
1:B:124:TRP:CH2	1:B:173:VAL:HG11	2.51	0.45
1:B:152:LYS:HB2	1:B:211:LEU:HD21	1.98	0.45
1:B:193:GLU:N	1:B:194:PRO:HD2	2.32	0.45
1:B:331:GLY:HA3	1:B:341:THR:O	2.17	0.44
1:B:30:ARG:HD2	1:B:84:ARG:HG3	1.99	0.44
1:A:422:GLU:O	1:A:422:GLU:HG3	2.17	0.44
1:A:152:LYS:O	1:A:156:GLU:HG3	2.18	0.44
1:B:219:LYS:HG3	1:B:220:GLN:N	2.32	0.43
1:B:199:HIS:CG	1:B:279:PRO:HB2	2.53	0.43
1:A:23:GLY:O	1:A:24:SER:C	2.61	0.43
1:B:163:GLN:HE21	1:B:163:GLN:HB2	1.64	0.43
1:A:181:ASN:HD22	1:A:183:ILE:H	1.66	0.43
1:B:265:GLU:HB3	3:B:2186:HOH:O	2.19	0.43
1:B:321:GLY:C	3:B:2400:HOH:O	2.60	0.43
1:A:77:ARG:NH1	1:A:365:GLU:HG3	2.35	0.42
1:B:267:PRO:HG2	1:B:270:ILE:HG22	2.01	0.42
1:B:21:ILE:HG13	1:B:22:GLU:N	2.35	0.42
1:B:355:LYS:HD2	3:B:2364:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:415:TRP:HA	1:B:416:SER:HA	1.72	0.42
1:B:31:GLU:HG3	1:B:87:PRO:HB3	2.01	0.41
1:B:233:LEU:HD12	1:B:250:MET:HE3	2.02	0.41
1:A:47:ASP:HB3	1:A:428:LYS:HD3	2.03	0.41
1:B:112:LYS:HB2	1:B:112:LYS:HZ3	1.83	0.41
1:A:82:TRP:HB2	3:A:1028:HOH:O	2.21	0.41
1:A:276:ASP:HB2	1:B:134:TYR:HB3	2.03	0.41
1:A:334:SER:HB3	1:A:368:PHE:CE1	2.56	0.41
1:A:396:GLU:O	1:A:400:GLN:HG3	2.20	0.41
1:A:30:ARG:HB2	1:A:84:ARG:HG2	2.02	0.41
1:A:400:GLN:O	1:A:404:GLU:HB3	2.21	0.41
1:B:334:SER:HB3	1:B:368:PHE:CE1	2.56	0.40
1:B:262:TYR:CE1	1:B:293:SER:HB3	2.57	0.40
1:B:384:ASP:O	1:B:388:GLN:HG3	2.21	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	457/465 (98%)	436 (95%)	20 (4%)	1 (0%)	43	36
1	B	457/465 (98%)	438 (96%)	18 (4%)	1 (0%)	43	36
All	All	914/930 (98%)	874 (96%)	38 (4%)	2 (0%)	43	36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	369	PRO
1	B	369	PRO

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	386/390 (99%)	383 (99%)	3 (1%)	73	75
1	B	386/390 (99%)	379 (98%)	7 (2%)	51	50
All	All	772/780 (99%)	762 (99%)	10 (1%)	61	61

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

Mol	Chain	Res	Type
1	A	181	ASN
1	A	191	ASN
1	A	238	ASP
1	B	112	LYS
1	B	163	GLN
1	B	181	ASN
1	B	191	ASN
1	B	250	MET
1	B	287	GLU
1	B	462	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	128	GLN
1	A	181	ASN
1	A	191	ASN
1	A	205	HIS
1	A	304	HIS
1	A	441	GLN
1	A	459	HIS
1	B	66	GLN
1	B	128	GLN
1	B	145	GLN
1	B	163	GLN

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Mol	Chain	Res	Type
1	B	181	ASN
1	B	191	ASN
1	B	259	ASN
1	B	304	HIS
1	B	307	GLN
1	B	441	GLN
1	B	459	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	LGC	B	2001	-	12,12,12	0.93	0	15,17,17	0.99	1 (6%)
2	LGC	A	1001	-	12,12,12	1.04	1 (8%)	15,17,17	0.92	1 (6%)

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	LGC	B	2001	-	-	1/2/22/22	0/1/1/1
2	LGC	A	1001	-	-	0/2/22/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	LGC	C3-C2	2.64	1.56	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2001	LGC	O5-C5-C6	3.10	109.17	106.05
2	A	1001	LGC	O5-C5-C6	2.76	108.83	106.05

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2001	LGC	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	459/465 (98%)	-0.43	2 (0%) 88 90	11, 17, 30, 46	0
1	B	459/465 (98%)	-0.25	8 (1%) 69 72	13, 20, 35, 49	0
All	All	918/930 (98%)	-0.34	10 (1%) 78 80	11, 18, 32, 49	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	4	ALA	4.4
1	B	264	GLY	3.4
1	A	462	GLU	3.2
1	B	325	ALA	3.0
1	B	462	GLU	2.8
1	B	283	PRO	2.7
1	A	219	LYS	2.6
1	B	271	LYS	2.3
1	B	454	ARG	2.2
1	B	272	LYS	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 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(\AA^2)	Q<0.9
2	LGC	B	2001	12/12	0.96	0.06	12,16,18,18	0
2	LGC	A	1001	12/12	0.97	0.05	12,14,16,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.