



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:16 PM UTC

PDB ID : 8EUD / pdb_00008eud
Title : Co-crystal structure of Chaetomium glucosidase with compound 22
Authors : Karade, S.S.; Mariuzza, R.A.
Deposited on : 2022-10-18
Resolution : 2.37 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

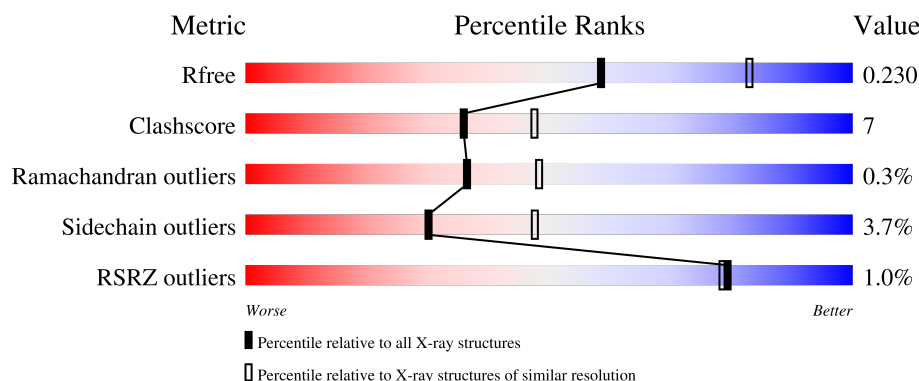
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.37 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	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	819	
1	B	819	

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
4	SO4	B	1009	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12749 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 Chaetomium alpha glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	765	Total	C	N	O	S	0	1	0
			6029	3870	1018	1128	13			
1	B	767	Total	C	N	O	S	0	0	0
			6041	3876	1019	1133	13			

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP G0SFD1
A	0	GLY	-	expression tag	UNP G0SFD1
A	1	ILE	-	expression tag	UNP G0SFD1
A	2	LEU	-	expression tag	UNP G0SFD1
A	3	PRO	-	expression tag	UNP G0SFD1
A	4	SER	-	expression tag	UNP G0SFD1
A	5	PRO	-	expression tag	UNP G0SFD1
A	6	GLY	-	expression tag	UNP G0SFD1
A	7	MET	-	expression tag	UNP G0SFD1
A	8	PRO	-	expression tag	UNP G0SFD1
A	9	ALA	-	expression tag	UNP G0SFD1
A	10	LEU	-	expression tag	UNP G0SFD1
A	11	LEU	-	expression tag	UNP G0SFD1
A	12	SER	-	expression tag	UNP G0SFD1
A	13	LEU	-	expression tag	UNP G0SFD1
A	14	VAL	-	expression tag	UNP G0SFD1
A	15	SER	-	expression tag	UNP G0SFD1
A	16	LEU	-	expression tag	UNP G0SFD1
A	17	LEU	-	expression tag	UNP G0SFD1
A	18	SER	-	expression tag	UNP G0SFD1
A	19	VAL	-	expression tag	UNP G0SFD1
A	20	LEU	-	expression tag	UNP G0SFD1
A	21	LEU	-	expression tag	UNP G0SFD1
A	22	MET	-	expression tag	UNP G0SFD1
A	23	GLY	-	expression tag	UNP G0SFD1

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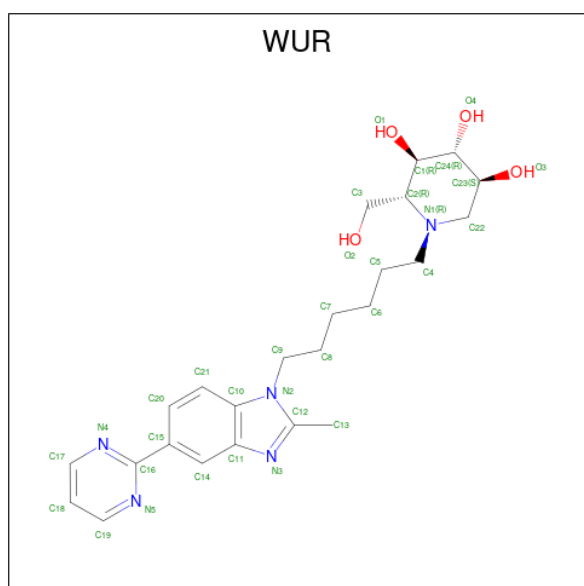
Chain	Residue	Modelled	Actual	Comment	Reference
A	24	CYS	-	expression tag	UNP G0SFD1
A	25	VAL	-	expression tag	UNP G0SFD1
A	26	ALA	-	expression tag	UNP G0SFD1
A	27	GLU	-	expression tag	UNP G0SFD1
A	28	THR	-	expression tag	UNP G0SFD1
A	29	GLY	-	expression tag	UNP G0SFD1
A	810	SER	-	expression tag	UNP G0SFD1
A	811	GLY	-	expression tag	UNP G0SFD1
A	812	HIS	-	expression tag	UNP G0SFD1
A	813	HIS	-	expression tag	UNP G0SFD1
A	814	HIS	-	expression tag	UNP G0SFD1
A	815	HIS	-	expression tag	UNP G0SFD1
A	816	HIS	-	expression tag	UNP G0SFD1
A	817	HIS	-	expression tag	UNP G0SFD1
B	-1	MET	-	initiating methionine	UNP G0SFD1
B	0	GLY	-	expression tag	UNP G0SFD1
B	1	ILE	-	expression tag	UNP G0SFD1
B	2	LEU	-	expression tag	UNP G0SFD1
B	3	PRO	-	expression tag	UNP G0SFD1
B	4	SER	-	expression tag	UNP G0SFD1
B	5	PRO	-	expression tag	UNP G0SFD1
B	6	GLY	-	expression tag	UNP G0SFD1
B	7	MET	-	expression tag	UNP G0SFD1
B	8	PRO	-	expression tag	UNP G0SFD1
B	9	ALA	-	expression tag	UNP G0SFD1
B	10	LEU	-	expression tag	UNP G0SFD1
B	11	LEU	-	expression tag	UNP G0SFD1
B	12	SER	-	expression tag	UNP G0SFD1
B	13	LEU	-	expression tag	UNP G0SFD1
B	14	VAL	-	expression tag	UNP G0SFD1
B	15	SER	-	expression tag	UNP G0SFD1
B	16	LEU	-	expression tag	UNP G0SFD1
B	17	LEU	-	expression tag	UNP G0SFD1
B	18	SER	-	expression tag	UNP G0SFD1
B	19	VAL	-	expression tag	UNP G0SFD1
B	20	LEU	-	expression tag	UNP G0SFD1
B	21	LEU	-	expression tag	UNP G0SFD1
B	22	MET	-	expression tag	UNP G0SFD1
B	23	GLY	-	expression tag	UNP G0SFD1
B	24	CYS	-	expression tag	UNP G0SFD1
B	25	VAL	-	expression tag	UNP G0SFD1
B	26	ALA	-	expression tag	UNP G0SFD1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	27	GLU	-	expression tag	UNP G0SFD1
B	28	THR	-	expression tag	UNP G0SFD1
B	29	GLY	-	expression tag	UNP G0SFD1
B	810	SER	-	expression tag	UNP G0SFD1
B	811	GLY	-	expression tag	UNP G0SFD1
B	812	HIS	-	expression tag	UNP G0SFD1
B	813	HIS	-	expression tag	UNP G0SFD1
B	814	HIS	-	expression tag	UNP G0SFD1
B	815	HIS	-	expression tag	UNP G0SFD1
B	816	HIS	-	expression tag	UNP G0SFD1
B	817	HIS	-	expression tag	UNP G0SFD1

- Molecule 2 is (2R,3R,4R,5S)-2-(hydroxymethyl)-1-{6-[2-methyl-5-(pyrimidin-2-yl)-1H-benzimidazol-1-yl]hexyl}piperidine-3,4,5-triol (CCD ID: WUR) (formula: C₂₄H₃₃N₅O₄) (labeled as "Ligand of Interest" by depositor).



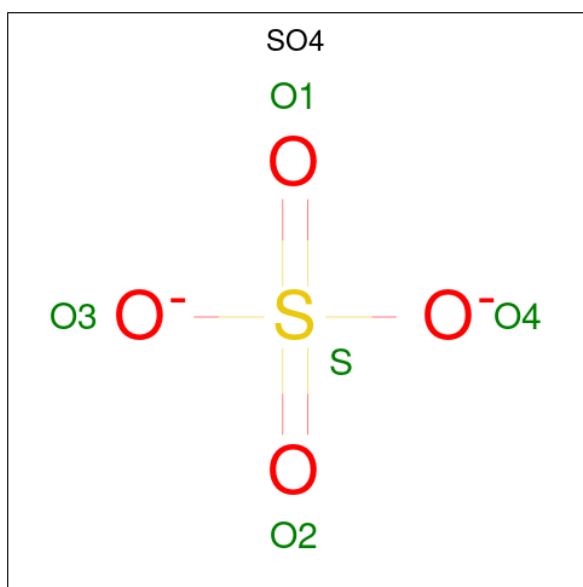
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			33	24	5	4		
2	B	1	Total	C	N	O	0	0
			33	24	5	4		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



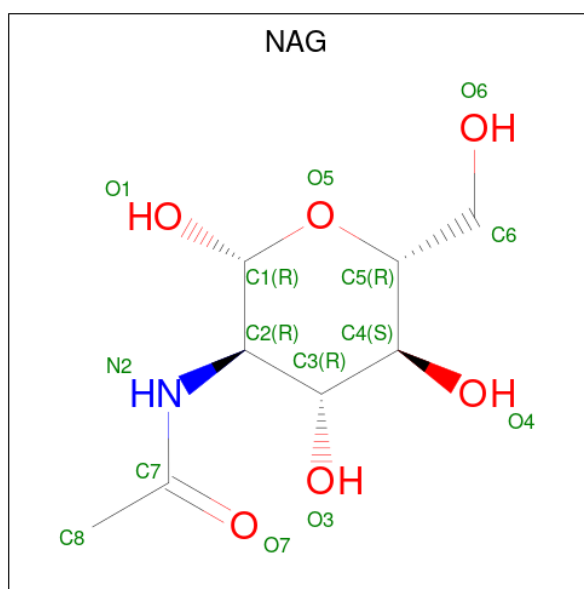
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

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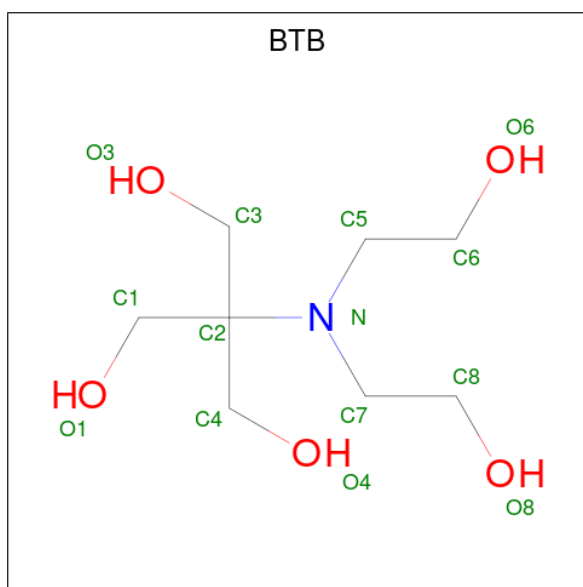
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 6 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (CCD ID: BTB) (formula: $C_8H_{19}NO_5$).



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

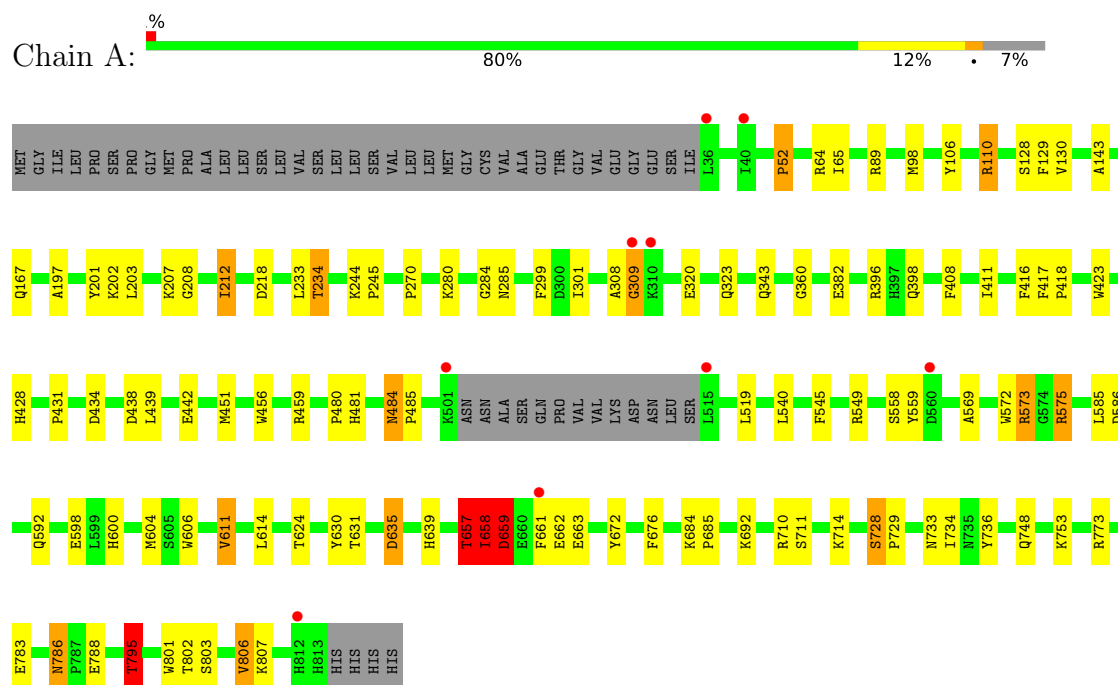
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	252	Total	O	0	0
			252	252		
7	B	270	Total	O	0	0
			270	270		

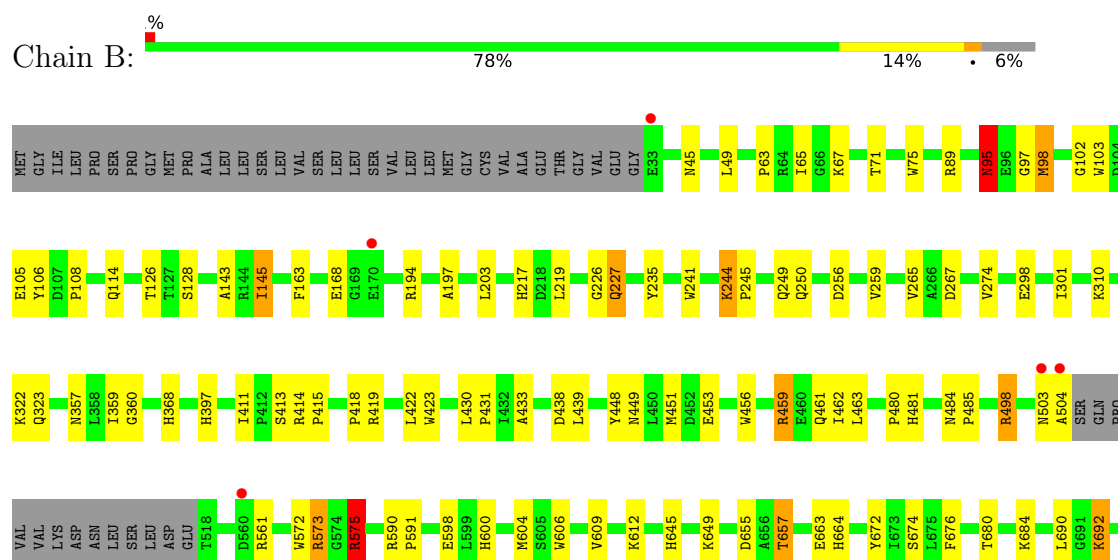
3 Residue-property plots [i](#)

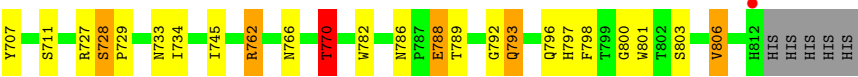
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Chaetomium alpha glucosidase



• Molecule 1: Chaetomium alpha glucosidase





4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	135.03Å 178.12Å 179.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.66 – 2.37 46.66 – 2.38	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.66-2.37) 99.4 (46.66-2.38)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.37Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.178 , 0.230 0.178 , 0.230	Depositor DCC
R_{free} test set	4280 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	28.8	Xtriage
Anisotropy	0.489	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 28.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12749	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% 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: BTB, GOL, SO4, WUR, NAG

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	0.66	1/6208 (0.0%)	1.18	21/8460 (0.2%)
1	B	0.68	1/6217 (0.0%)	1.19	18/8475 (0.2%)
All	All	0.67	2/12425 (0.0%)	1.19	39/16935 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	397	HIS	CE1-NE2	5.89	1.38	1.32
1	A	270	PRO	CA-C	5.54	1.54	1.51

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	575	ARG	CB-CA-C	10.29	126.92	109.53
1	B	575	ARG	CB-CA-C	10.02	126.06	109.53
1	A	657	THR	CB-CA-C	-8.94	93.84	114.41
1	B	575	ARG	CG-CD-NE	-8.58	93.12	112.00
1	B	459	ARG	CG-CD-NE	-8.32	93.69	112.00
1	A	659	ASP	CB-CA-C	-8.04	94.42	110.42
1	A	459	ARG	CG-CD-NE	-8.02	94.36	112.00
1	B	684	LYS	CB-CA-C	7.98	122.11	109.27
1	A	573	ARG	CG-CD-NE	-7.02	96.55	112.00
1	B	45	ASN	CB-CA-C	7.01	121.89	110.88
1	B	194	ARG	CB-CG-CD	6.61	126.50	111.30
1	B	459	ARG	CD-NE-CZ	6.56	133.58	124.40
1	B	657	THR	CB-CA-C	-6.55	95.92	111.65
1	B	770	THR	CB-CA-C	6.31	121.26	110.79
1	A	212	ILE	CB-CA-C	6.04	117.73	110.78
1	A	658	ILE	CA-C-N	6.03	133.05	121.54
1	A	658	ILE	C-N-CA	6.03	133.05	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	202	LYS	CB-CA-C	5.96	120.76	109.37
1	B	573	ARG	CG-CD-NE	-5.94	98.93	112.00
1	A	382	GLU	CB-CG-CD	5.92	122.66	112.60
1	A	684	LYS	CB-CA-C	5.88	118.65	109.42
1	A	416	PHE	CA-C-N	-5.82	117.16	122.28
1	A	416	PHE	C-N-CA	-5.82	117.16	122.28
1	A	802	THR	CA-CB-OG1	-5.81	100.89	109.60
1	A	624	THR	CA-CB-OG1	-5.79	100.92	109.60
1	B	793	GLN	N-CA-CB	-5.62	102.51	111.62
1	A	795	THR	N-CA-CB	-5.62	101.58	110.06
1	A	396	ARG	CG-CD-NE	-5.46	99.98	112.00
1	B	322	LYS	CA-C-N	5.40	127.79	120.44
1	B	322	LYS	C-N-CA	5.40	127.79	120.44
1	A	417	PHE	CB-CA-C	5.35	118.30	110.87
1	A	52	PRO	N-CA-C	-5.30	105.33	112.48
1	B	762	ARG	CG-CD-NE	5.29	123.64	112.00
1	A	484	ASN	CA-CB-CG	5.27	117.87	112.60
1	B	663	GLU	CB-CA-C	5.26	119.01	109.37
1	B	95	ASN	CA-C-N	5.25	128.04	120.38
1	B	95	ASN	C-N-CA	5.25	128.04	120.38
1	A	631	THR	CB-CA-C	5.23	119.47	110.79
1	B	657	THR	CA-CB-OG1	5.00	117.10	109.60

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	6029	0	5639	80	0
1	B	6041	0	5649	91	0
2	A	33	0	0	0	0
2	B	33	0	0	0	0
3	A	6	0	8	3	0
3	B	12	0	16	1	0
4	A	25	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	20	0	0	3	0
5	B	14	0	13	0	0
6	B	14	0	19	3	0
7	A	252	0	0	6	0
7	B	270	0	0	6	0
All	All	12749	0	11344	172	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 7.

All (172) 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:451:MET:HE1	1:A:540:LEU:HB3	1.18	1.16
1:A:451:MET:CE	1:A:540:LEU:HB3	1.83	1.07
1:A:795:THR:HG23	7:A:1002:HOH:O	1.60	0.99
1:A:657:THR:HG21	7:A:1056:HOH:O	1.63	0.96
1:B:572:TRP:H	1:B:600:HIS:HD2	1.10	0.91
1:B:766:ASN:O	1:B:770:THR:HG23	1.73	0.87
1:B:786:ASN:HD22	1:B:789:THR:H	1.23	0.86
1:A:659:ASP:HB3	1:A:661:PHE:H	1.38	0.86
1:A:451:MET:HE1	1:A:540:LEU:CB	2.03	0.85
1:A:208:GLY:HA2	3:A:902:GOL:H11	1.61	0.82
1:A:559:TYR:CE1	1:A:658:ILE:HD13	2.16	0.81
1:B:217:HIS:HE1	1:B:267:ASP:O	1.64	0.80
1:B:572:TRP:H	1:B:600:HIS:CD2	1.99	0.80
1:B:561:ARG:HE	1:B:664:HIS:HD2	1.31	0.78
1:A:795:THR:CG2	7:A:1002:HOH:O	2.22	0.76
1:A:559:TYR:CD1	1:A:658:ILE:HD13	2.22	0.75
1:A:572:TRP:H	1:A:600:HIS:HD2	1.37	0.71
3:B:1003:GOL:O1	3:B:1003:GOL:O3	2.05	0.70
1:B:561:ARG:HE	1:B:664:HIS:CD2	2.10	0.69
1:A:481:HIS:HE1	7:A:1172:HOH:O	1.74	0.69
1:B:217:HIS:HD2	1:B:219:LEU:H	1.42	0.67
1:A:604:MET:HE3	7:A:1157:HOH:O	1.95	0.66
1:B:575:ARG:HB3	7:B:1121:HOH:O	1.96	0.65
1:B:612:LYS:HE2	7:B:1133:HOH:O	1.97	0.65
1:A:685:PRO:HG3	1:A:748:GLN:HE22	1.62	0.65
1:B:728:SER:N	1:B:729:PRO:HD3	2.12	0.65
1:A:575:ARG:HH22	1:A:592:GLN:HE22	1.44	0.64
1:A:569:ALA:HA	1:A:604:MET:CE	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:658:ILE:HD12	1:A:662:GLU:HA	1.79	0.64
1:B:762:ARG:NH1	4:B:1009:SO4:O1	2.31	0.64
1:B:114:GLN:NE2	1:B:414:ARG:HH12	1.96	0.63
1:B:766:ASN:O	1:B:770:THR:CG2	2.46	0.63
1:B:226:GLY:H	1:B:227:GLN:HE22	1.46	0.63
1:B:128:SER:O	1:B:143:ALA:HA	1.98	0.63
1:A:659:ASP:HB2	1:A:663:GLU:H	1.62	0.63
1:A:598:GLU:OE2	1:A:600:HIS:HE1	1.82	0.62
1:B:368:HIS:HD2	4:B:1007:SO4:O3	1.81	0.62
1:A:208:GLY:HA2	3:A:902:GOL:C1	2.28	0.61
1:B:103:TRP:H	1:B:357:ASN:ND2	1.97	0.61
1:A:658:ILE:CD1	1:A:662:GLU:HA	2.30	0.61
1:A:299:PHE:HA	3:A:902:GOL:H11	1.83	0.61
1:A:451:MET:HE3	1:A:540:LEU:HD22	1.81	0.61
1:A:786:ASN:ND2	1:A:788:GLU:H	1.98	0.61
1:B:728:SER:N	1:B:729:PRO:CD	2.65	0.60
1:A:244:LYS:HB3	1:A:245:PRO:HD3	1.84	0.60
1:B:226:GLY:H	1:B:227:GLN:NE2	2.00	0.60
1:B:707:TYR:HA	1:B:770:THR:HG21	1.84	0.59
1:A:308:ALA:O	1:A:309:GLY:O	2.20	0.59
1:A:545:PHE:CE1	1:A:611:VAL:HG13	2.36	0.59
1:A:545:PHE:CZ	1:A:549:ARG:HD2	2.38	0.58
1:A:234:THR:HG22	1:A:284:GLY:HA2	1.84	0.58
1:A:128:SER:O	1:A:143:ALA:HA	2.04	0.58
1:A:659:ASP:HB3	1:A:661:PHE:N	2.14	0.57
1:A:110:ARG:HH21	1:A:323:GLN:HG3	1.69	0.57
1:A:423:TRP:H	1:A:484:ASN:ND2	2.04	0.56
1:B:728:SER:H	1:B:729:PRO:CD	2.19	0.56
1:B:203:LEU:HD11	1:B:301:ILE:HG23	1.89	0.55
1:B:803:SER:O	1:B:806:VAL:HG23	2.07	0.55
1:A:434:ASP:OD2	1:A:807:LYS:HD3	2.06	0.54
1:B:250:GLN:OE1	6:B:1002:BTB:H61	2.07	0.54
1:B:422:LEU:HB3	1:B:484:ASN:HD22	1.73	0.53
1:B:604:MET:HE2	1:B:645:HIS:CD2	2.43	0.53
6:B:1002:BTB:H62	6:B:1002:BTB:H11	1.89	0.53
1:B:67:LYS:HG2	1:B:168:GLU:CD	2.34	0.53
1:B:786:ASN:HD21	1:B:788:GLU:HB2	1.73	0.53
1:A:672:TYR:CZ	1:A:711:SER:HA	2.44	0.53
1:A:456:TRP:CE2	1:A:480:PRO:HA	2.44	0.53
1:A:728:SER:N	1:A:729:PRO:CD	2.71	0.53
1:B:103:TRP:H	1:B:357:ASN:HD21	1.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:786:ASN:HD22	1:A:788:GLU:H	1.57	0.52
1:A:451:MET:CE	1:A:540:LEU:CB	2.73	0.51
1:B:590:ARG:HB3	1:B:591:PRO:CD	2.40	0.51
1:B:786:ASN:ND2	1:B:789:THR:H	2.01	0.51
1:A:233:LEU:HD22	1:B:265:VAL:HG23	1.92	0.51
1:B:600:HIS:HA	1:B:655:ASP:OD1	2.11	0.51
1:B:561:ARG:NE	1:B:664:HIS:HD2	2.06	0.51
1:A:658:ILE:HD11	1:A:662:GLU:OE1	2.12	0.50
1:B:690:LEU:HD21	1:B:745:ILE:HD13	1.93	0.50
1:B:95:ASN:HD22	1:B:97:GLY:H	1.60	0.50
1:B:598:GLU:OE2	1:B:600:HIS:HE1	1.95	0.50
1:B:733:ASN:HB3	1:B:801:TRP:CG	2.46	0.49
1:B:65:ILE:HD13	1:B:197:ALA:HB1	1.95	0.49
1:B:411:ILE:HD12	1:B:418:PRO:HA	1.95	0.49
1:A:783:GLU:OE1	1:A:795:THR:HB	2.11	0.49
1:B:782:TRP:CG	1:B:792:GLY:HA3	2.48	0.49
1:A:569:ALA:HA	1:A:604:MET:HE2	1.95	0.49
1:A:234:THR:HG22	1:A:284:GLY:CA	2.43	0.48
1:A:423:TRP:H	1:A:484:ASN:HD22	1.60	0.48
1:B:481:HIS:H	1:B:481:HIS:CD2	2.30	0.48
1:B:727:ARG:O	1:B:728:SER:HB3	2.14	0.47
1:A:52:PRO:HD3	1:A:129:PHE:CE2	2.50	0.47
1:B:485:PRO:HB3	1:B:606:TRP:CE2	2.49	0.47
1:B:786:ASN:ND2	1:B:788:GLU:H	2.13	0.47
1:A:736:TYR:OH	1:A:807:LYS:HE3	2.15	0.47
1:B:244:LYS:HB3	1:B:245:PRO:HD3	1.97	0.47
1:B:762:ARG:HD2	4:B:1009:SO4:O3	2.15	0.47
1:A:575:ARG:HH22	1:A:592:GLN:NE2	2.11	0.46
1:B:108:PRO:HG2	1:B:439:LEU:HD22	1.97	0.46
1:B:707:TYR:CA	1:B:770:THR:HG21	2.45	0.46
1:A:89:ARG:CZ	1:A:98:MET:CE	2.93	0.46
1:A:481:HIS:H	1:A:481:HIS:CD2	2.33	0.46
1:A:803:SER:O	1:A:806[A]:VAL:HG23	2.15	0.46
1:A:203:LEU:HD11	1:A:301:ILE:CG2	2.45	0.46
1:A:545:PHE:HE1	1:A:611:VAL:HG13	1.81	0.46
1:B:106:TYR:HD2	1:B:359:ILE:HG23	1.80	0.46
1:A:106:TYR:CD2	1:A:360:GLY:HA2	2.51	0.45
1:A:728:SER:N	1:A:729:PRO:HD3	2.31	0.45
1:B:481:HIS:CD2	7:B:1352:HOH:O	2.69	0.45
1:B:145:ILE:O	1:B:298:GLU:HA	2.16	0.45
1:A:659:ASP:HB2	1:A:663:GLU:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:433:ALA:O	1:B:498:ARG:NH2	2.50	0.45
1:B:217:HIS:CE1	1:B:267:ASP:O	2.56	0.45
1:A:614:LEU:HB3	1:A:630:TYR:CE2	2.53	0.44
1:B:503:ASN:O	1:B:504:ALA:C	2.61	0.44
1:B:430:LEU:HB2	1:B:431:PRO:HD3	1.99	0.44
1:A:64:ARG:HD3	1:A:408:PHE:CE1	2.53	0.44
1:B:456:TRP:CE2	1:B:480:PRO:HA	2.53	0.44
1:B:786:ASN:HD22	1:B:789:THR:N	2.03	0.44
1:B:71:THR:HB	1:B:163:PHE:CZ	2.53	0.44
1:B:798:PHE:C	1:B:800:GLY:HA3	2.43	0.44
1:B:459:ARG:HG2	7:B:1245:HOH:O	2.18	0.44
1:B:672:TYR:CG	1:B:734:ILE:HG21	2.53	0.43
1:B:590:ARG:HB3	1:B:591:PRO:HD2	2.00	0.43
1:A:89:ARG:NH2	1:A:98:MET:HE2	2.33	0.43
1:A:485:PRO:HB3	1:A:606:TRP:CE2	2.54	0.43
1:B:106:TYR:CE2	1:B:360:GLY:HA2	2.53	0.43
1:B:414:ARG:N	1:B:415:PRO:HD2	2.34	0.43
1:A:411:ILE:HD12	1:A:418:PRO:HA	2.01	0.43
1:A:672:TYR:CE1	1:A:711:SER:HA	2.54	0.43
1:A:167:GLN:NE2	1:A:201:TYR:OH	2.52	0.43
1:A:710:ARG:CZ	1:A:714:LYS:HE2	2.49	0.43
1:B:419:ARG:HD2	1:B:462:ILE:HG12	2.01	0.43
1:B:203:LEU:HD11	1:B:301:ILE:CG2	2.49	0.42
1:B:423:TRP:H	1:B:484:ASN:ND2	2.18	0.42
1:B:89:ARG:CZ	1:B:98:MET:HE1	2.48	0.42
1:B:108:PRO:HG2	1:B:439:LEU:CD2	2.50	0.42
1:B:572:TRP:N	1:B:600:HIS:HD2	1.94	0.42
1:A:64:ARG:HD3	1:A:408:PHE:CD1	2.55	0.42
1:B:235:TYR:HE2	1:B:249:GLN:HE22	1.68	0.42
1:A:658:ILE:HD12	1:A:662:GLU:CA	2.45	0.42
1:B:106:TYR:CD2	1:B:360:GLY:HA2	2.55	0.42
1:A:451:MET:HE1	1:A:540:LEU:CA	2.47	0.42
1:A:234:THR:HA	1:A:285:ASN:OD1	2.20	0.42
1:B:114:GLN:HE22	1:B:414:ARG:HH22	1.68	0.42
1:B:692:LYS:HE3	7:B:1300:HOH:O	2.19	0.42
6:B:1002:BTB:H42	6:B:1002:BTB:H71	1.58	0.41
1:A:456:TRP:CD2	1:A:480:PRO:HA	2.56	0.41
1:B:604:MET:HE2	1:B:645:HIS:HD2	1.84	0.41
1:A:234:THR:HG21	7:A:1231:HOH:O	2.21	0.41
1:A:439:LEU:O	1:A:442:GLU:HB2	2.20	0.41
1:B:796:GLN:O	1:B:797:HIS:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:672:TYR:CE2	1:B:711:SER:HB3	2.55	0.41
1:B:75:TRP:CZ2	1:B:89:ARG:HG3	2.55	0.41
1:B:102:GLY:CA	1:B:357:ASN:HD21	2.34	0.41
1:B:481:HIS:HD2	7:B:1352:HOH:O	2.04	0.41
1:A:519:LEU:HD23	1:A:519:LEU:HA	1.77	0.41
1:B:49:LEU:O	1:B:63:PRO:HA	2.20	0.41
1:B:461:GLN:HE21	1:B:463:LEU:HD21	1.86	0.41
1:B:609:VAL:CG2	1:B:680:THR:HB	2.50	0.41
1:A:428:HIS:O	1:A:431:PRO:HD2	2.21	0.41
1:A:585:LEU:O	1:A:586:ASP:C	2.64	0.41
1:A:635:ASP:O	1:A:639:HIS:HD2	2.04	0.41
1:B:448:TYR:CD2	1:B:451:MET:HE3	2.56	0.41
1:A:672:TYR:CG	1:A:734:ILE:HG21	2.56	0.41
1:B:103:TRP:N	1:B:357:ASN:HD21	2.19	0.41
1:B:256:ASP:O	1:B:259:VAL:HG22	2.21	0.40
1:A:65:ILE:HD13	1:A:197:ALA:HB1	2.02	0.40
1:A:130:VAL:HG21	1:A:320:GLU:CB	2.51	0.40
1:A:733:ASN:HB3	1:A:801:TRP:CG	2.56	0.40
1:B:672:TYR:CE1	1:B:711:SER:HA	2.57	0.40
1:B:786:ASN:HB2	1:B:793:GLN:NE2	2.37	0.40
1:A:398:GLN:HE22	1:B:241:TRP:HZ2	1.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	762/819 (93%)	733 (96%)	26 (3%)	3 (0%)	30	40
1	B	763/819 (93%)	742 (97%)	20 (3%)	1 (0%)	48	62
All	All	1525/1638 (93%)	1475 (97%)	46 (3%)	4 (0%)	36	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	309	GLY
1	A	659	ASP
1	A	728	SER
1	B	728	SER

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	616/707 (87%)	594 (96%)	22 (4%)	31	49
1	B	619/707 (88%)	594 (96%)	25 (4%)	28	44
All	All	1235/1414 (87%)	1188 (96%)	47 (4%)	30	46

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	110	ARG
1	A	207	LYS
1	A	212	ILE
1	A	218	ASP
1	A	234	THR
1	A	280	LYS
1	A	343	GLN
1	A	438	ASP
1	A	558	SER
1	A	573	ARG
1	A	611	VAL
1	A	635	ASP
1	A	657	THR
1	A	658	ILE
1	A	676	PHE
1	A	692	LYS
1	A	753	LYS
1	A	773	ARG
1	A	786	ASN

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Mol	Chain	Res	Type
1	A	795	THR
1	A	806[A]	VAL
1	A	806[B]	VAL
1	B	95	ASN
1	B	98	MET
1	B	105	GLU
1	B	126	THR
1	B	145	ILE
1	B	227	GLN
1	B	244	LYS
1	B	274	VAL
1	B	310	LYS
1	B	323	GLN
1	B	413	SER
1	B	438	ASP
1	B	449	ASN
1	B	453	GLU
1	B	498	ARG
1	B	573	ARG
1	B	575	ARG
1	B	649	LYS
1	B	657	THR
1	B	674	SER
1	B	676	PHE
1	B	692	LYS
1	B	770	THR
1	B	788	GLU
1	B	806	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	120	GLN
1	A	157	GLN
1	A	167	GLN
1	A	242	GLN
1	A	249	GLN
1	A	323	GLN
1	A	397	HIS
1	A	398	GLN
1	A	461	GLN

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Mol	Chain	Res	Type
1	A	478	GLN
1	A	481	HIS
1	A	484	ASN
1	A	544	GLN
1	A	579	HIS
1	A	592	GLN
1	A	600	HIS
1	A	639	HIS
1	A	748	GLN
1	A	786	ASN
1	A	793	GLN
1	B	95	ASN
1	B	114	GLN
1	B	120	GLN
1	B	137	HIS
1	B	217	HIS
1	B	227	GLN
1	B	249	GLN
1	B	323	GLN
1	B	357	ASN
1	B	368	HIS
1	B	398	GLN
1	B	461	GLN
1	B	481	HIS
1	B	484	ASN
1	B	544	GLN
1	B	600	HIS
1	B	664	HIS
1	B	744	ASN
1	B	748	GLN
1	B	786	ASN
1	B	793	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

16 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	GOL	B	1003	-	5,5,5	0.17	0	5,5,5	0.34	0
2	WUR	B	1005	-	36,36,36	2.53	8 (22%)	48,50,50	2.21	14 (29%)
4	SO4	A	904	-	4,4,4	0.29	0	6,6,6	0.06	0
4	SO4	A	906	-	4,4,4	0.26	0	6,6,6	0.24	0
4	SO4	A	905	-	4,4,4	0.30	0	6,6,6	0.16	0
2	WUR	A	901	-	36,36,36	2.65	10 (27%)	48,50,50	2.19	17 (35%)
4	SO4	A	903	-	4,4,4	0.46	0	6,6,6	0.43	0
4	SO4	A	907	-	4,4,4	0.23	0	6,6,6	0.17	0
4	SO4	B	1006	-	4,4,4	0.21	0	6,6,6	0.22	0
4	SO4	B	1008	-	4,4,4	0.26	0	6,6,6	0.16	0
4	SO4	B	1009	-	4,4,4	0.26	0	6,6,6	0.22	0
5	NAG	B	1001	1	14,14,15	1.41	3 (21%)	17,19,21	2.62	7 (41%)
6	BTB	B	1002	-	13,13,13	1.05	1 (7%)	7,16,16	0.48	0
3	GOL	A	902	-	5,5,5	0.21	0	5,5,5	0.70	0
4	SO4	B	1007	-	4,4,4	0.43	0	6,6,6	0.18	0
3	GOL	B	1004	-	5,5,5	0.20	0	5,5,5	0.75	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	B	1003	-	-	4/4/4/4	-
2	WUR	B	1005	-	-	5/15/35/35	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	WUR	A	901	-	-	2/15/35/35	0/4/4/4
5	NAG	B	1001	1	-	0/6/23/26	0/1/1/1
6	BTB	B	1002	-	-	6/21/21/21	-
3	GOL	A	902	-	-	4/4/4/4	-
3	GOL	B	1004	-	-	2/4/4/4	-

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	WUR	C4-N1	-13.17	1.24	1.47
2	B	1005	WUR	C4-N1	-12.28	1.25	1.47
2	B	1005	WUR	C13-C12	3.91	1.55	1.49
2	B	1005	WUR	C21-C10	3.72	1.45	1.39
2	A	901	WUR	C13-C12	3.36	1.54	1.49
2	A	901	WUR	C21-C10	2.87	1.44	1.39
2	A	901	WUR	C14-C11	2.75	1.44	1.40
2	A	901	WUR	C23-C24	-2.75	1.48	1.52
2	B	1005	WUR	C14-C11	2.59	1.43	1.40
2	A	901	WUR	C22-C23	2.57	1.55	1.52
2	B	1005	WUR	C1-C24	-2.55	1.45	1.52
2	B	1005	WUR	C15-C16	2.52	1.55	1.48
5	B	1001	NAG	C1-C2	2.49	1.55	1.52
2	A	901	WUR	C15-C16	2.48	1.55	1.48
2	A	901	WUR	C12-N3	2.43	1.34	1.31
2	B	1005	WUR	C12-N3	2.32	1.34	1.31
6	B	1002	BTB	C2-N	2.32	1.53	1.48
2	A	901	WUR	O4-C24	2.25	1.48	1.43
2	A	901	WUR	C1-C24	-2.24	1.46	1.52
5	B	1001	NAG	C4-C5	2.17	1.57	1.53
5	B	1001	NAG	O4-C4	2.10	1.48	1.43
2	B	1005	WUR	O4-C24	2.08	1.48	1.43

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	WUR	C17-N4-C16	8.09	124.06	116.07
2	B	1005	WUR	C19-N5-C16	6.58	122.57	116.07
5	B	1001	NAG	C2-N2-C7	6.14	131.13	122.90
2	B	1005	WUR	C17-N4-C16	5.85	121.85	116.07
2	A	901	WUR	C19-N5-C16	4.70	120.71	116.07
5	B	1001	NAG	O4-C4-C5	4.69	120.87	109.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1005	WUR	C13-C12-N2	4.42	127.69	123.04
2	A	901	WUR	C18-C17-N4	-4.24	116.70	123.42
5	B	1001	NAG	O3-C3-C2	-3.78	101.55	109.40
2	B	1005	WUR	C15-C16-N4	3.57	121.16	117.34
5	B	1001	NAG	C1-O5-C5	3.50	116.88	112.19
2	B	1005	WUR	C18-C19-N5	-3.47	117.92	123.42
5	B	1001	NAG	C4-C3-C2	3.30	115.86	111.02
2	B	1005	WUR	C5-C4-N1	3.27	122.76	113.88
2	B	1005	WUR	C11-N3-C12	3.22	109.48	105.57
2	A	901	WUR	C11-N3-C12	3.11	109.35	105.57
2	A	901	WUR	C15-C16-N4	3.11	120.67	117.34
2	B	1005	WUR	N2-C12-N3	-3.08	108.42	112.41
2	B	1005	WUR	C18-C17-N4	-3.04	118.61	123.42
2	A	901	WUR	C10-C11-N3	-3.02	106.35	110.19
2	A	901	WUR	O2-C3-C2	-3.02	104.87	111.55
2	B	1005	WUR	O4-C24-C1	-2.90	103.55	110.38
2	A	901	WUR	C13-C12-N2	2.85	126.03	123.04
5	B	1001	NAG	C3-C4-C5	-2.77	105.20	110.23
2	B	1005	WUR	N5-C16-N4	-2.69	119.71	125.54
2	A	901	WUR	N5-C16-N4	-2.66	119.78	125.54
2	A	901	WUR	C3-C2-C1	-2.63	108.97	112.93
2	A	901	WUR	C21-C10-C11	-2.62	119.20	122.23
2	A	901	WUR	O4-C24-C23	-2.61	104.73	110.05
2	A	901	WUR	N2-C12-N3	-2.60	109.04	112.41
5	B	1001	NAG	C6-C5-C4	2.59	119.37	113.02
2	A	901	WUR	C11-C10-N2	2.56	107.58	105.55
2	B	1005	WUR	C10-C11-N3	-2.52	106.98	110.19
2	B	1005	WUR	O2-C3-C2	-2.47	106.08	111.55
2	A	901	WUR	C18-C19-N5	-2.40	119.62	123.42
2	A	901	WUR	C14-C11-N3	2.07	133.77	129.31
2	A	901	WUR	O3-C23-C22	2.04	113.55	109.66
2	B	1005	WUR	C19-C18-C17	2.02	119.25	116.63

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	902	GOL	C1-C2-C3-O3
3	B	1003	GOL	C1-C2-C3-O3
3	B	1003	GOL	O2-C2-C3-O3
3	B	1004	GOL	O1-C1-C2-C3
6	B	1002	BTB	C1-C2-C3-O3

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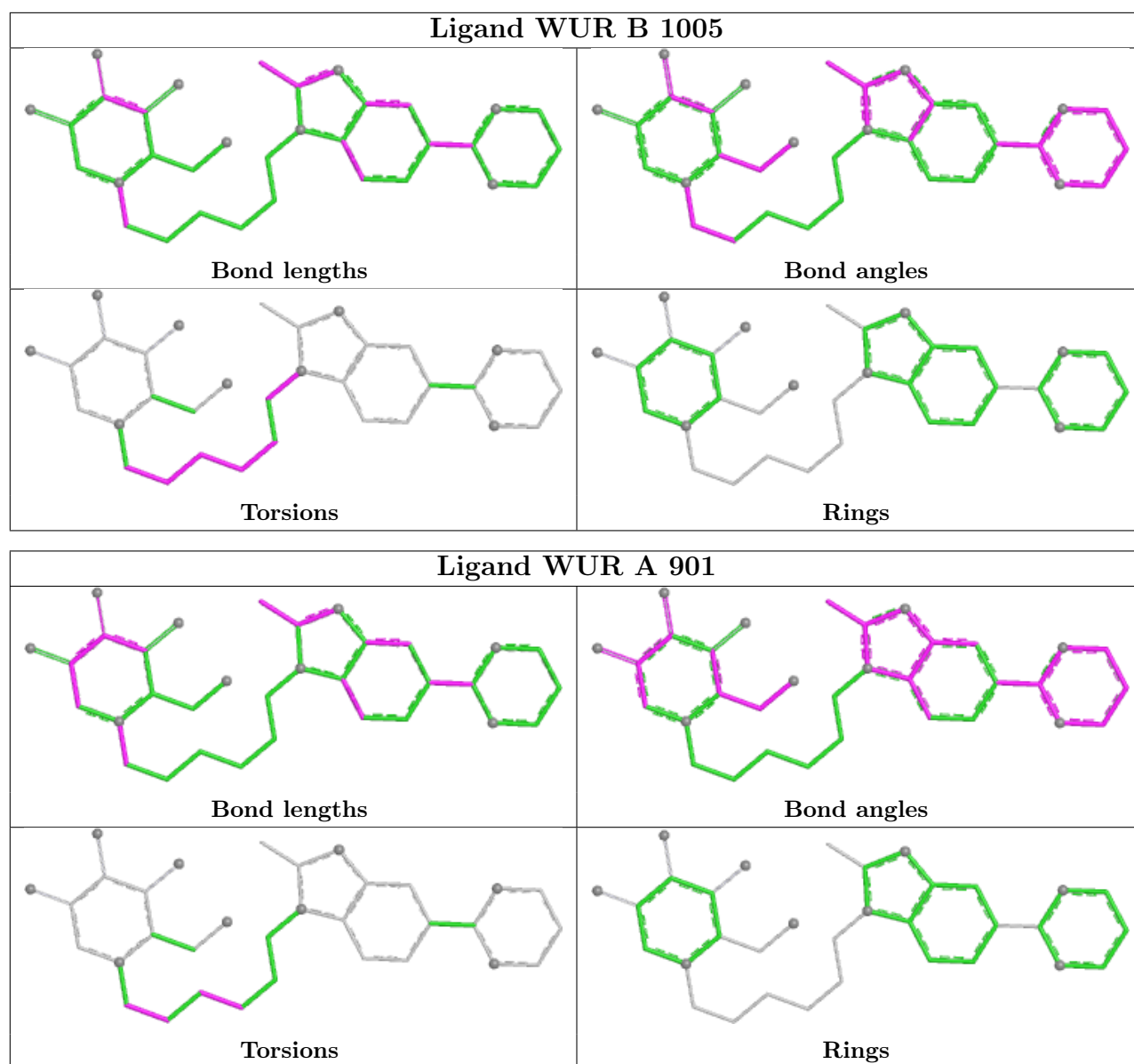
Mol	Chain	Res	Type	Atoms
6	B	1002	BTB	C4-C2-C3-O3
6	B	1002	BTB	N-C2-C3-O3
2	B	1005	WUR	N1-C4-C5-C6
6	B	1002	BTB	N-C7-C8-O8
3	B	1003	GOL	O1-C1-C2-C3
3	A	902	GOL	O2-C2-C3-O3
3	B	1004	GOL	O1-C1-C2-O2
3	A	902	GOL	O1-C1-C2-O2
3	B	1003	GOL	O1-C1-C2-O2
2	B	1005	WUR	C6-C7-C8-C9
2	B	1005	WUR	C4-C5-C6-C7
2	A	901	WUR	N1-C4-C5-C6
2	B	1005	WUR	C5-C6-C7-C8
6	B	1002	BTB	N-C5-C6-O6
3	A	902	GOL	O1-C1-C2-C3
2	A	901	WUR	C5-C6-C7-C8
6	B	1002	BTB	C6-C5-N-C7
2	B	1005	WUR	C8-C9-N2-C10

There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1003	GOL	1	0
4	B	1009	SO4	2	0
6	B	1002	BTB	3	0
3	A	902	GOL	3	0
4	B	1007	SO4	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	765/819 (93%)	-0.40	9 (1%) 76 76	15, 28, 50, 78	1 (0%)
1	B	767/819 (93%)	-0.49	6 (0%) 82 82	15, 27, 46, 102	0
All	All	1532/1638 (93%)	-0.44	15 (0%) 79 78	15, 27, 49, 102	1 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	504	ALA	6.3
1	B	812	HIS	4.6
1	A	560	ASP	3.4
1	A	812	HIS	3.4
1	A	36	LEU	3.0
1	B	170	GLU	3.0
1	B	560	ASP	2.8
1	A	310	LYS	2.6
1	A	661	PHE	2.5
1	A	501	LYS	2.4
1	A	515	LEU	2.3
1	B	33	GLU	2.3
1	A	40	ILE	2.2
1	B	503	ASN	2.2
1	A	309	GLY	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

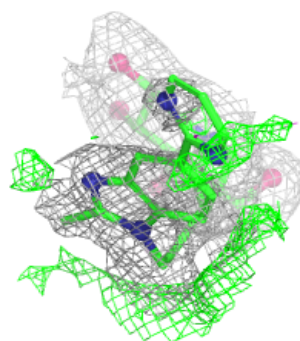
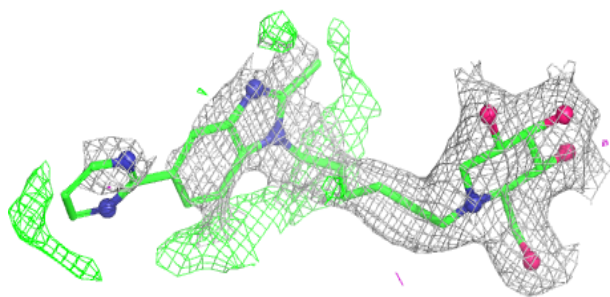
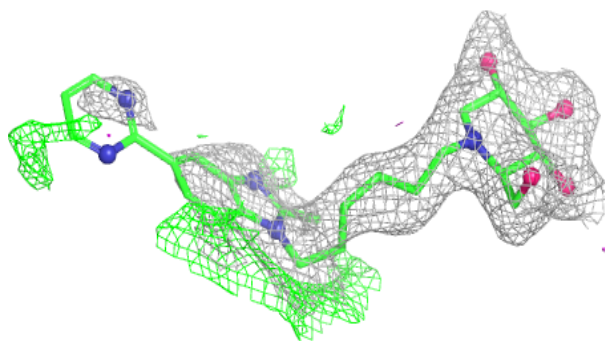
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SO4	A	907	5/5	0.83	0.15	65,66,78,79	0
5	NAG	B	1001	14/15	0.86	0.11	30,43,50,52	0
3	GOL	A	902	6/6	0.88	0.17	39,52,59,63	0
2	WUR	B	1005	33/33	0.91	0.20	17,76,131,147	0
3	GOL	B	1003	6/6	0.91	0.10	38,42,46,52	0
6	BTB	B	1002	14/14	0.92	0.09	40,46,48,50	0
4	SO4	A	905	5/5	0.94	0.10	54,55,64,68	0
3	GOL	B	1004	6/6	0.94	0.09	21,28,33,37	0
4	SO4	A	906	5/5	0.95	0.18	50,53,64,69	0
4	SO4	B	1006	5/5	0.96	0.09	41,46,50,58	0
4	SO4	B	1008	5/5	0.96	0.09	39,45,51,53	0
4	SO4	A	904	5/5	0.96	0.13	54,55,63,67	0
2	WUR	A	901	33/33	0.96	0.11	17,48,88,93	0
4	SO4	B	1009	5/5	0.97	0.09	41,42,52,59	0
4	SO4	B	1007	5/5	0.98	0.06	27,27,33,34	0
4	SO4	A	903	5/5	0.99	0.04	23,26,31,33	0

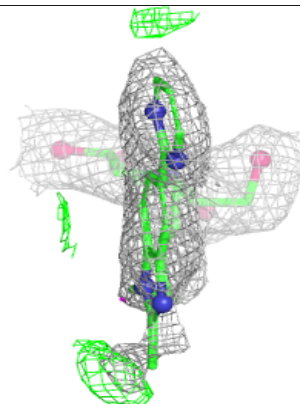
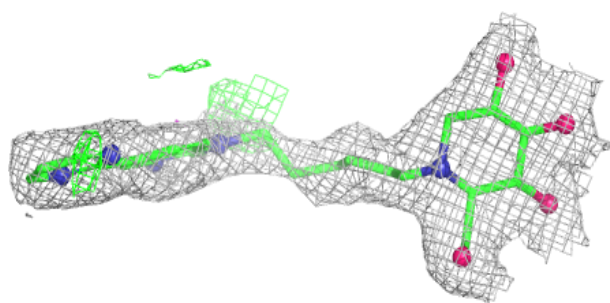
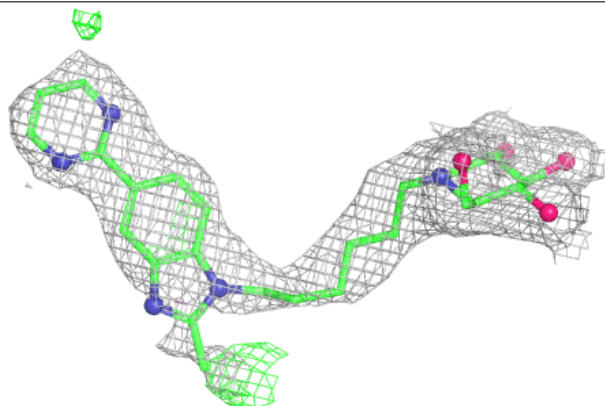
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around WUR B 1005:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around WUR A 901:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.