



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:09 AM UTC

PDB ID : 5UHL / pdb_00005uhl
Title : Crystal structure of the core catalytic domain of human O-GlcNAcase complexed with Thiamet G
Authors : Klein, D.J.; Elsen, N.L.
Deposited on : 2017-01-11
Resolution : 3.14 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

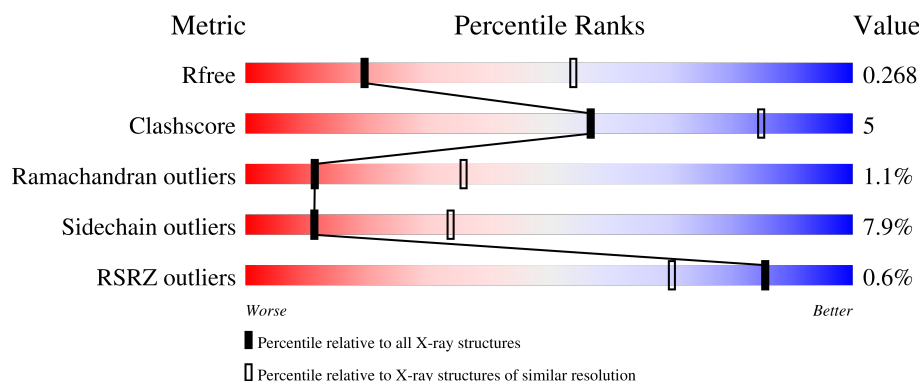
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.14 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	2351 (3.18-3.10)
Clashscore	190562	2452 (3.18-3.10)
Ramachandran outliers	187476	2324 (3.18-3.10)
Sidechain outliers	187428	2324 (3.18-3.10)
RSRZ outliers	180081	2351 (3.18-3.10)

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	345	
1	C	345	
2	B	163	
2	D	163	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6951 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 O-GlcNAcase TIM-barrel domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	0	0
			2498	1616	413	455	14			
1	C	302	Total	C	N	O	S	0	0	0
			2471	1601	405	451	14			

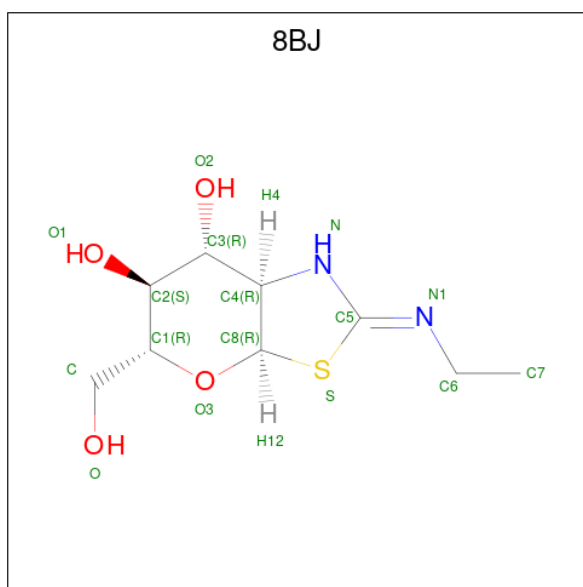
- Molecule 2 is a protein called O-GlcNAcase stalk domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	120	Total	C	N	O	S	0	0	0
			970	627	160	172	11			
2	D	120	Total	C	N	O	S	0	0	0
			973	629	160	173	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	543	MET	-	initiating methionine	UNP O60502
D	543	MET	-	initiating methionine	UNP O60502

- Molecule 3 is (2Z,3aR,5R,6S,7R,7aR)-2-(ethylimino)-5-(hydroxymethyl)hexahydro-3aH-pyrano[3,2-d][1,3]thiazole-6,7-diol (CCD ID: 8BJ) (formula: C₉H₁₆N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			16	9	2	4	1		
3	C	1	Total	C	N	O	S	0	0
			16	9	2	4	1		

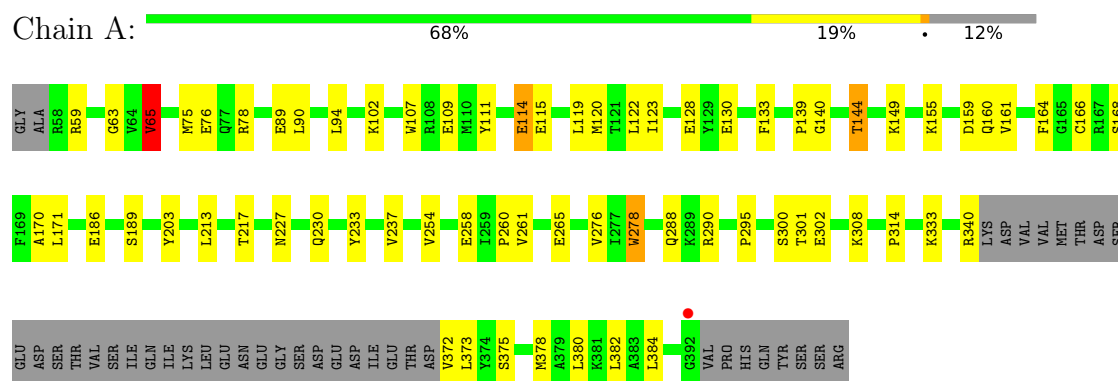
- Molecule 4 is water.

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

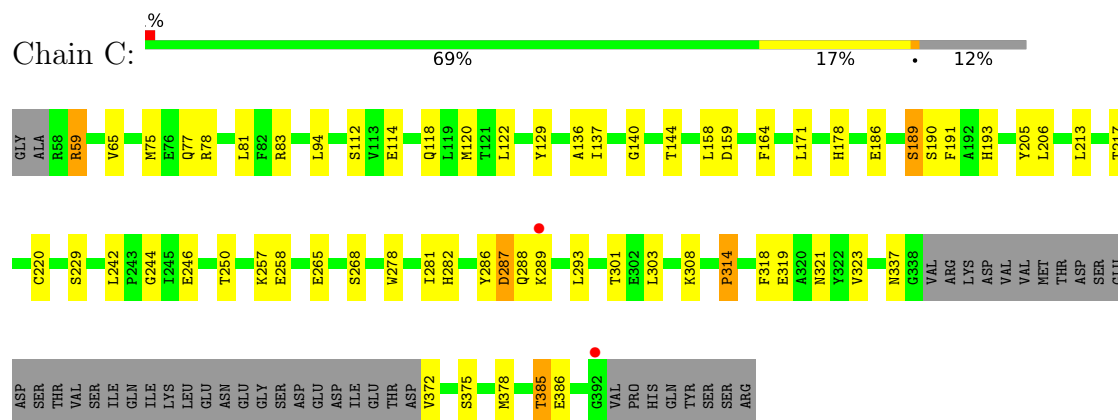
3 Residue-property plots [i](#)

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.

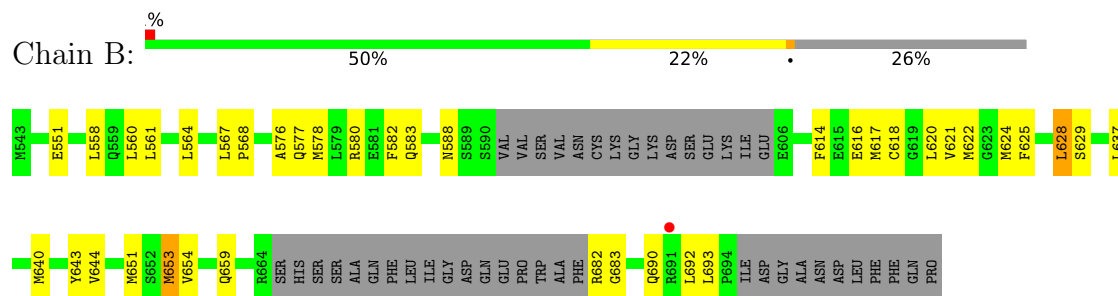
• Molecule 1: O-GlcNAcase TIM-barrel domain



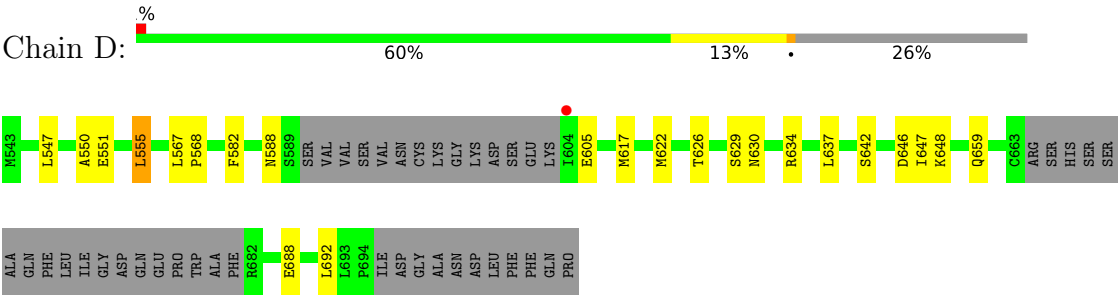
• Molecule 1: O-GlcNAcase TIM-barrel domain



• Molecule 2: O-GlcNAcase stalk domain



• Molecule 2: O-GlcNAcase stalk domain



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	98.20Å 98.20Å 261.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.93 – 3.14 91.93 – 3.14	Depositor EDS
% Data completeness (in resolution range)	99.9 (91.93-3.14) 100.0 (91.93-3.14)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 3.13Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, R_{free}	0.192 , 0.257 0.207 , 0.268	Depositor DCC
R_{free} test set	1167 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	95.6	Xtriage
Anisotropy	0.475	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 104.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6951	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% 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: 8BJ

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	0.91	0/2565	1.48	19/3475 (0.5%)
1	C	0.93	0/2538	1.44	18/3441 (0.5%)
2	B	0.80	0/993	1.49	8/1337 (0.6%)
2	D	0.83	0/996	1.46	4/1341 (0.3%)
All	All	0.89	0/7092	1.46	49/9594 (0.5%)

There are no bond length outliers.

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	286	TYR	CA-C-N	7.05	135.00	121.54
1	C	286	TYR	C-N-CA	7.05	135.00	121.54
1	C	144	THR	CA-C-N	6.37	130.37	120.82
1	C	144	THR	C-N-CA	6.37	130.37	120.82
1	C	301	THR	N-CA-C	-6.26	104.90	112.54
1	A	276	VAL	N-CA-C	-6.00	99.10	107.80
2	B	576	ALA	CA-C-N	5.89	128.43	120.65
2	B	576	ALA	C-N-CA	5.89	128.43	120.65
2	D	642	SER	CA-C-N	5.84	128.03	120.44
2	D	642	SER	C-N-CA	5.84	128.03	120.44
1	C	268	SER	CA-C-N	5.77	128.33	120.54
1	C	268	SER	C-N-CA	5.77	128.33	120.54
1	A	254	VAL	N-CA-C	-5.77	105.00	110.42
1	C	186	GLU	CA-C-N	5.76	128.35	120.46
1	C	186	GLU	C-N-CA	5.76	128.35	120.46
1	A	278	TRP	N-CA-C	-5.67	96.45	107.62
1	A	155	LYS	CA-C-N	5.63	127.83	120.28
1	A	155	LYS	C-N-CA	5.63	127.83	120.28
1	A	260	PRO	CA-C-N	5.60	128.42	120.53
1	A	260	PRO	C-N-CA	5.60	128.42	120.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	144	THR	CA-C-N	5.44	127.88	120.54
1	A	144	THR	C-N-CA	5.44	127.88	120.54
1	C	244	GLY	CA-C-N	5.41	127.82	120.63
1	C	244	GLY	C-N-CA	5.41	127.82	120.63
1	C	257	LYS	N-CA-C	-5.39	105.48	111.36
1	A	217	THR	N-CA-C	-5.35	105.49	112.23
1	C	278	TRP	N-CA-C	-5.35	97.08	107.62
1	A	261	VAL	CA-C-N	5.35	127.39	120.44
1	A	261	VAL	C-N-CA	5.35	127.39	120.44
2	D	659	GLN	CA-C-N	5.33	128.40	120.31
2	D	659	GLN	C-N-CA	5.33	128.40	120.31
1	A	65	VAL	N-CA-CB	5.30	118.13	111.46
1	A	203	TYR	CA-C-N	5.29	127.37	120.28
1	A	203	TYR	C-N-CA	5.29	127.37	120.28
1	C	319	GLU	CA-C-N	5.25	129.50	120.72
1	C	319	GLU	C-N-CA	5.25	129.50	120.72
1	C	191	PHE	CA-CB-CG	5.20	119.00	113.80
1	C	159	ASP	CA-CB-CG	5.16	117.76	112.60
2	B	659	GLN	CA-C-N	5.14	127.17	120.28
2	B	659	GLN	C-N-CA	5.14	127.17	120.28
1	C	303	LEU	N-CA-C	-5.12	107.16	113.41
2	B	616	GLU	CA-C-N	5.12	127.10	120.44
2	B	616	GLU	C-N-CA	5.12	127.10	120.44
1	A	186	GLU	CA-C-N	5.09	127.44	120.77
1	A	186	GLU	C-N-CA	5.09	127.44	120.77
1	A	265	GLU	CA-C-N	5.08	127.39	120.54
1	A	265	GLU	C-N-CA	5.08	127.39	120.54
2	B	643	TYR	CA-C-N	5.02	127.34	120.46
2	B	643	TYR	C-N-CA	5.02	127.34	120.46

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	2498	0	2453	24	0
1	C	2471	0	2420	21	0
2	B	970	0	948	19	0
2	D	973	0	949	6	0
3	A	16	0	0	0	0
3	C	16	0	0	0	0
4	A	3	0	0	0	0
4	B	1	0	0	0	0
4	C	3	0	0	0	0
All	All	6951	0	6770	63	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (63) 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:111:TYR:H	1:A:160:GLN:HE22	1.26	0.83
2:B:617:MET:HA	2:B:620:LEU:HD12	1.70	0.71
1:C:375:SER:HB3	1:C:378:MET:HB2	1.77	0.66
1:A:384:LEU:HD22	2:B:558:LEU:HB3	1.78	0.66
2:B:618:CYS:O	2:B:622:MET:HE3	1.97	0.64
2:B:624:MET:HG2	2:B:628:LEU:HD12	1.79	0.64
2:B:682:ARG:CZ	1:C:287:ASP:HB2	2.27	0.64
1:A:78:ARG:HB3	1:A:122:LEU:HD11	1.85	0.59
1:A:227:ASN:ND2	1:A:230:GLN:HB2	2.19	0.58
1:C:220:CYS:HB3	1:C:250:THR:OG1	2.02	0.58
2:B:629:SER:HA	2:B:637:LEU:HD22	1.87	0.56
1:A:290:ARG:NH2	2:B:568:PRO:HA	2.21	0.56
1:A:111:TYR:H	1:A:160:GLN:NE2	1.98	0.55
2:B:621:VAL:HG11	2:B:651:MET:HG3	1.88	0.54
1:A:160:GLN:HG2	1:A:164:PHE:CZ	2.42	0.54
2:B:561:LEU:HD21	2:B:640:MET:HE1	1.90	0.54
1:A:375:SER:HB3	1:A:378:MET:HB2	1.89	0.54
1:C:314:PRO:HB2	1:C:321:ASN:OD1	2.08	0.54
1:A:161:VAL:HA	1:A:164:PHE:CD2	2.44	0.53
2:B:692:LEU:HB3	2:D:582:PHE:HE2	1.73	0.53
2:B:625:PHE:HD1	2:B:644:VAL:HG12	1.75	0.52
1:C:287:ASP:C	1:C:289:LYS:H	2.18	0.52
1:A:295:PRO:HD3	1:A:380:LEU:HD22	1.92	0.51
2:D:629:SER:HA	2:D:637:LEU:HD22	1.92	0.50
1:C:77:GLN:NE2	1:C:318:PHE:HB3	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:94:LEU:HD11	1:C:136:ALA:HB2	1.95	0.48
1:C:385:THR:HG23	2:D:555:LEU:HD13	1.95	0.48
1:A:63:GLY:HA2	1:A:90:LEU:HD13	1.96	0.47
1:A:123:ILE:HD13	1:A:166:CYS:HB2	1.97	0.47
1:A:227:ASN:HD21	1:A:230:GLN:HB2	1.79	0.47
1:C:213:LEU:HD23	1:C:246:GLU:HB2	1.96	0.47
2:B:653:MET:H	2:B:653:MET:HG2	1.62	0.46
2:B:567:LEU:HB3	2:B:568:PRO:HD2	1.97	0.46
2:B:582:PHE:HE2	2:D:692:LEU:HB2	1.81	0.46
1:A:111:TYR:HB3	1:A:115:GLU:HB3	1.97	0.46
2:D:567:LEU:HB3	2:D:568:PRO:HD2	1.97	0.45
1:A:89:GLU:HB2	1:A:333:LYS:HD3	1.97	0.45
1:A:65:VAL:CG2	1:A:94:LEU:HD23	2.48	0.44
1:A:373:LEU:H	1:A:373:LEU:HD12	1.83	0.44
2:D:550:ALA:HB1	2:D:630:ASN:HB3	1.98	0.44
1:A:114:GLU:CD	1:A:114:GLU:H	2.26	0.43
1:C:75:MET:HE3	1:C:118:GLN:HB3	2.00	0.43
1:A:119:LEU:O	1:A:123:ILE:HG13	2.18	0.43
2:B:580:ARG:HA	2:B:583:GLN:HE21	1.82	0.43
2:B:582:PHE:HB2	2:B:614:PHE:CZ	2.54	0.43
1:A:233:TYR:O	1:A:237:VAL:HG23	2.19	0.43
2:B:682:ARG:NH1	1:C:287:ASP:HB2	2.33	0.43
1:A:133:PHE:O	1:A:168:SER:HB2	2.19	0.43
1:C:293:LEU:O	1:C:323:VAL:HG11	2.19	0.43
2:B:560:LEU:O	2:B:564:LEU:HG	2.18	0.43
1:A:107:TRP:CD1	1:A:139:PRO:HA	2.54	0.42
1:C:78:ARG:O	1:C:81:LEU:HB3	2.20	0.41
1:C:158:LEU:HD22	1:C:206:LEU:HD11	2.02	0.41
1:C:281:ILE:HG23	1:C:282:HIS:ND1	2.35	0.41
1:C:83:ARG:HG2	1:C:129:TYR:CE1	2.56	0.41
1:C:205:TYR:CD1	1:C:205:TYR:C	2.99	0.41
1:C:75:MET:SD	1:C:122:LEU:HD22	2.61	0.41
1:C:190:SER:H	1:C:193:HIS:CD2	2.39	0.41
1:A:170:ALA:HA	1:A:213:LEU:O	2.20	0.41
1:A:300:SER:OG	1:A:302:GLU:HB2	2.21	0.41
2:B:690:GLN:HA	2:B:693:LEU:HD12	2.02	0.41
1:C:59:ARG:HB3	1:C:308:LYS:HE3	2.03	0.41
1:C:120:MET:HG2	1:C:164:PHE:HA	2.04	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	300/345 (87%)	275 (92%)	22 (7%)	3 (1%)	12	38
1	C	298/345 (86%)	273 (92%)	20 (7%)	5 (2%)	7	27
2	B	114/163 (70%)	106 (93%)	7 (6%)	1 (1%)	14	41
2	D	114/163 (70%)	108 (95%)	6 (5%)	0	100	100
All	All	826/1016 (81%)	762 (92%)	55 (7%)	9 (1%)	11	36

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	140	GLY
1	C	287	ASP
1	C	140	GLY
1	C	189	SER
1	C	288	GLN
1	C	314	PRO
1	A	288	GLN
2	B	683	GLY
1	A	314	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	272/310 (88%)	250 (92%)	22 (8%)	11	33
1	C	268/310 (86%)	251 (94%)	17 (6%)	16	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	102/141 (72%)	95 (93%)	7 (7%)	14	38
2	D	102/141 (72%)	89 (87%)	13 (13%)	4	17
All	All	744/902 (82%)	685 (92%)	59 (8%)	11	34

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	ARG
1	A	65	VAL
1	A	75	MET
1	A	76	GLU
1	A	102	LYS
1	A	109	GLU
1	A	114	GLU
1	A	120	MET
1	A	128	GLU
1	A	130	GLU
1	A	144	THR
1	A	149	LYS
1	A	159	ASP
1	A	171	LEU
1	A	189	SER
1	A	258	GLU
1	A	278	TRP
1	A	301	THR
1	A	308	LYS
1	A	340	ARG
1	A	372	VAL
1	A	382	LEU
2	B	551	GLU
2	B	577	GLN
2	B	578	MET
2	B	588	ASN
2	B	628	LEU
2	B	653	MET
2	B	654	VAL
1	C	59	ARG
1	C	65	VAL
1	C	112	SER
1	C	114	GLU
1	C	137	ILE

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Mol	Chain	Res	Type
1	C	171	LEU
1	C	178	HIS
1	C	189	SER
1	C	217	THR
1	C	229	SER
1	C	242	LEU
1	C	258	GLU
1	C	265	GLU
1	C	337	ASN
1	C	372	VAL
1	C	385	THR
1	C	386	GLU
2	D	547	LEU
2	D	551	GLU
2	D	555	LEU
2	D	588	ASN
2	D	605	GLU
2	D	617	MET
2	D	622	MET
2	D	626	THR
2	D	634	ARG
2	D	646	ASP
2	D	647	ILE
2	D	648	LYS
2	D	688	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	GLN
1	A	160	GLN
1	A	288	GLN
1	A	313	ASN
2	B	583	GLN
1	C	86	GLN
1	C	193	HIS
1	C	227	ASN
2	D	577	GLN
2	D	583	GLN

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
3	8BJ	A	501	-	14,17,17	1.25	1 (7%)	16,24,24	1.72	2 (12%)
3	8BJ	C	501	-	14,17,17	0.81	1 (7%)	16,24,24	1.77	2 (12%)

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	8BJ	A	501	-	-	0/4/33/33	0/2/2/2
3	8BJ	C	501	-	-	0/4/33/33	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	8BJ	C5-N	-4.35	1.28	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	501	8BJ	C5-N	-2.57	1.30	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	501	8BJ	S-C5-N	5.92	117.95	111.25
3	A	501	8BJ	S-C5-N	5.02	116.93	111.25
3	A	501	8BJ	C8-O3-C1	3.87	119.50	112.56
3	C	501	8BJ	C8-O3-C1	2.83	117.64	112.56

There are no chirality outliers.

There are no torsion outliers.

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	304/345 (88%)	-0.29	1 (0%) 90 80	67, 96, 125, 181	0
1	C	302/345 (87%)	-0.34	2 (0%) 84 68	71, 101, 131, 144	0
2	B	120/163 (73%)	0.02	1 (0%) 82 65	73, 111, 163, 189	0
2	D	120/163 (73%)	-0.10	1 (0%) 82 65	74, 105, 146, 162	0
All	All	846/1016 (83%)	-0.24	5 (0%) 85 70	67, 101, 139, 189	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	691	ARG	3.4
1	A	392	GLY	3.3
1	C	392	GLY	2.7
1	C	289	LYS	2.6
2	D	604	ILE	2.2

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	8BJ	A	501	16/16	0.96	0.08	80,80,80,80	0
3	8BJ	C	501	16/16	0.97	0.07	87,87,87,87	0

6.5 Other polymers [i](#)

There are no such residues in this entry.