



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:50 PM UTC

PDB ID : 1RUL / pdb_00001rul
Title : Crystal Structure (D) of u.v.-irradiated cationic cyclization antibody 4C6 Fab at pH 5.6 with a data set collected at SSRL beamline 11-1.
Authors : Zhu, X.; Wentworth Jr., P.; Wentworth, A.D.; Eschenmoser, A.; Lerner, R.A.; Wilson, I.A.
Deposited on : 2003-12-11
Resolution : 1.88 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

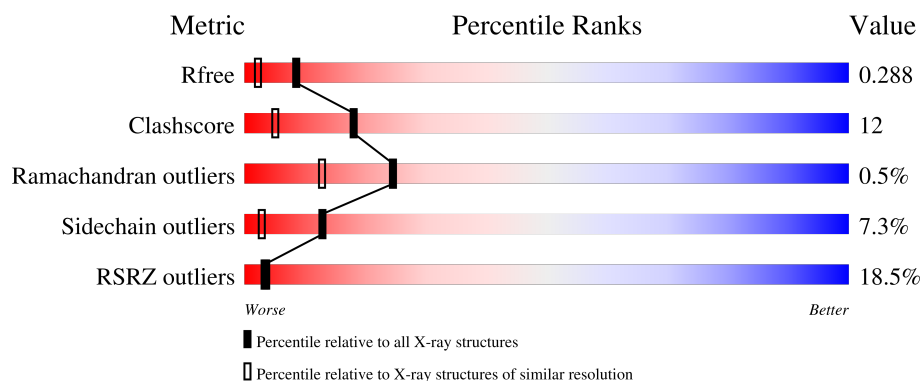
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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	1220 (1.88-1.88)
Clashscore	190562	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)
RSRZ outliers	180081	1220 (1.88-1.88)

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	L	219	24% 68% 25% 6%
2	H	222	13% 77% 20% .

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	GOL	L	621	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3760 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.

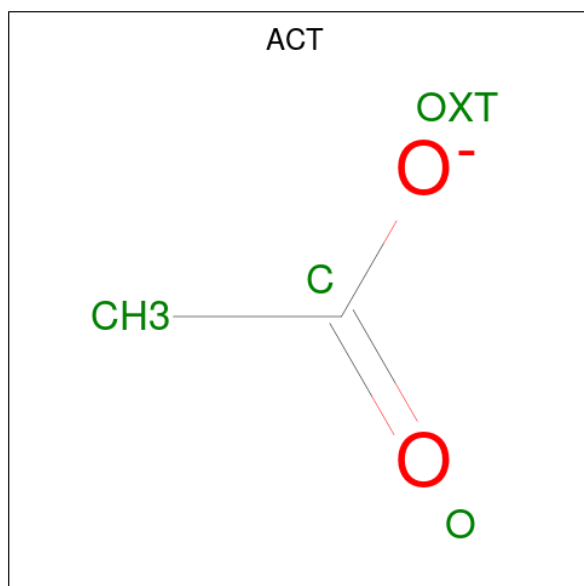
- Molecule 1 is a protein called immunoglobulin igg2a, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	219	Total	C	N	O	S	0	0	0
			1703	1064	291	341	7			

- Molecule 2 is a protein called immunoglobulin igg2a, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	222	Total	C	N	O	S	0	0	0
			1679	1063	277	333	6			

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



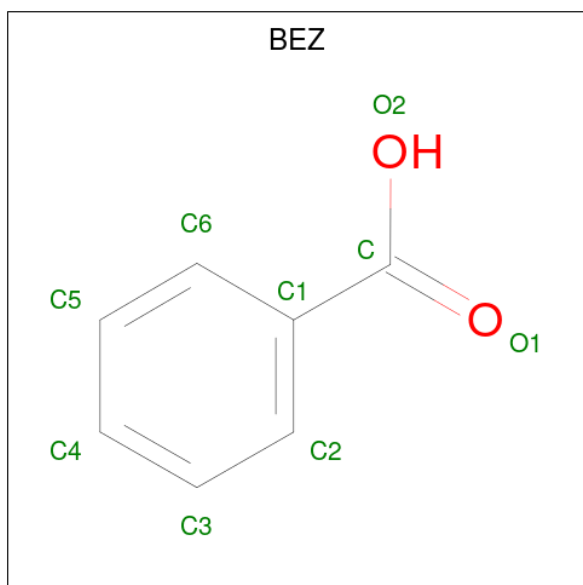
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	L	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is BENZOIC ACID (CCD ID: BEZ) (formula: $C_7H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	H	1	Total	C	O	0	0
			9	7	2		

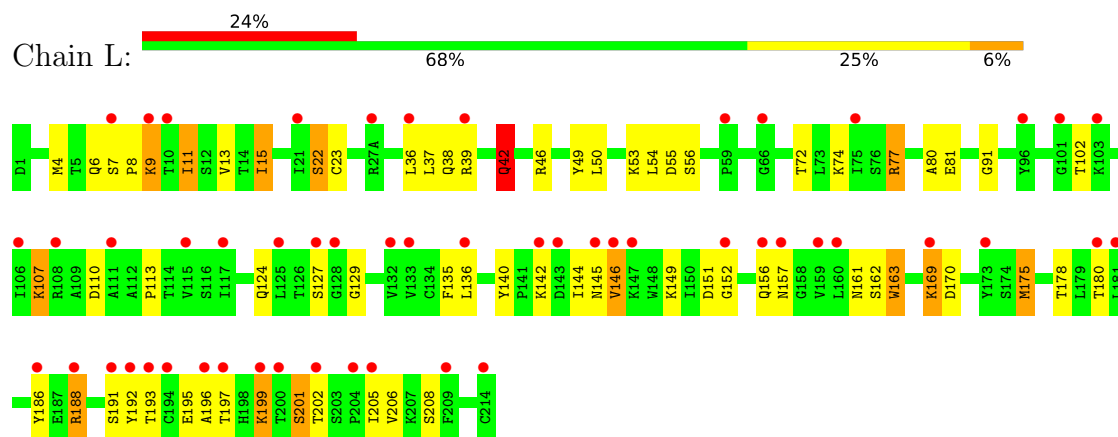
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	L	141	Total	O	0	0
			141	141		
6	H	200	Total	O	0	0
			200	200		

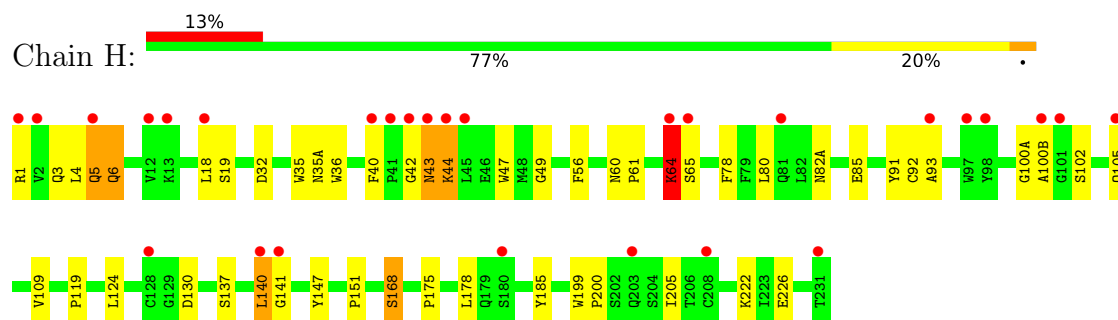
3 Residue-property plots [i](#)

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: immunoglobulin igg2a, light chain



- Molecule 2: immunoglobulin igg2a, heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	63.92Å 63.92Å 265.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.88 50.00 – 1.88	Depositor EDS
% Data completeness (in resolution range)	79.8 (50.00-1.88) 86.9 (50.00-1.88)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.57 (at 1.87Å)	Xtriage
Refinement program	SHELXL-97, CNS	Depositor
R, R_{free}	0.206 , 0.283 (Not available) , 0.288	Depositor DCC
R_{free} test set	2424 reflections (6.01%)	wwPDB-VP
Wilson B-factor (Å ²)	28.7	Xtriage
Anisotropy	0.278	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3760	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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: BEZ, GOL, GHG, ACT, 4HT

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	L	0.38	0/1723	1.30	3/2332 (0.1%)
2	H	0.43	0/1714	1.37	8/2346 (0.3%)
All	All	0.41	0/3437	1.34	11/4678 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	82(A)	ASN	CA-CB-CG	7.99	120.59	112.60
2	H	93	ALA	CA-C-N	-7.20	115.38	122.36
2	H	93	ALA	C-N-CA	-7.20	115.38	122.36
1	L	188	ARG	CD-NE-CZ	7.06	134.28	124.40
2	H	35(A)	ASN	CA-CB-CG	6.30	118.90	112.60
2	H	42	GLY	CA-C-N	6.15	133.28	121.54
2	H	42	GLY	C-N-CA	6.15	133.28	121.54
2	H	82(A)	ASN	OD1-CG-ND2	-5.47	117.13	122.60
1	L	42	GLN	CA-C-O	5.27	127.97	121.60
1	L	156	GLN	CA-C-O	5.26	124.54	118.55
2	H	56	PHE	CA-CB-CG	5.06	118.86	113.80

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	L	1703	0	1656	51	0
2	H	1679	0	1632	33	0
3	L	4	0	3	0	0
4	H	18	0	24	1	0
4	L	6	0	8	4	0
5	H	9	0	5	1	0
6	H	200	0	0	6	0
6	L	141	0	0	12	0
All	All	3760	0	3328	82	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 12.

All (82) 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:L:195:GLU:HG2	1:L:206:VAL:HG22	1.48	0.92
2:H:6:GHG:HE21	2:H:92:CYS:H	1.17	0.88
1:L:145:ASN:HB2	1:L:197:THR:OG1	1.82	0.79
2:H:18:LEU:HD12	2:H:109:VAL:HG11	1.68	0.73
2:H:140:LEU:HD22	2:H:205:ILE:HD12	1.75	0.68
2:H:5:GLN:HG2	2:H:105:GLN:OE1	1.93	0.68
1:L:163:4HT:NE1	1:L:175:MET:HE3	2.08	0.67
1:L:142:LYS:HG2	6:L:720:HOH:O	1.94	0.67
1:L:124:GLN:HG2	1:L:129:GLY:O	1.95	0.66
1:L:162:SER:OG	2:H:175:PRO:HD2	1.96	0.66
1:L:162:SER:HB3	4:L:621:GOL:H32	1.78	0.65
1:L:110:ASP:OD2	1:L:199:LYS:HE2	1.97	0.65
1:L:54:LEU:HB2	6:L:737:HOH:O	1.96	0.64
1:L:49:TYR:OH	1:L:53:LYS:HE2	1.97	0.64
6:L:752:HOH:O	2:H:1:ARG:HD3	1.98	0.64
2:H:6:GHG:HE21	2:H:92:CYS:N	1.94	0.63
2:H:64:LYS:HG2	6:H:696:HOH:O	1.99	0.62
1:L:54:LEU:HD13	6:L:737:HOH:O	2.00	0.62
1:L:201:SER:HB2	6:L:655:HOH:O	2.01	0.60
2:H:43:ASN:HB2	6:H:644:HOH:O	2.01	0.59
1:L:169:LYS:HG3	1:L:170:ASP:N	2.18	0.58
1:L:180:THR:HB	6:L:735:HOH:O	2.02	0.58
1:L:15:ILE:HD11	1:L:80:ALA:HB2	1.84	0.58
2:H:140:LEU:CD2	2:H:205:ILE:HD12	2.33	0.58
1:L:7:SER:HB3	6:L:740:HOH:O	2.04	0.57
2:H:168:SER:HB3	6:H:810:HOH:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:91:GLY:O	5:H:601:BEZ:H3	2.08	0.54
1:L:149:LYS:HD3	1:L:152:GLY:O	2.08	0.53
2:H:199:TRP:CD1	2:H:200:PRO:HA	2.43	0.53
1:L:74:LYS:HG3	6:L:677:HOH:O	2.09	0.53
1:L:178:THR:CB	4:L:621:GOL:H12	2.39	0.53
1:L:4:MET:HE3	1:L:23:CYS:SG	2.49	0.53
1:L:178:THR:HB	4:L:621:GOL:H12	1.90	0.53
2:H:35:TRP:HB3	2:H:78:PHE:CZ	2.45	0.52
2:H:65:SER:HA	6:H:682:HOH:O	2.11	0.51
1:L:42:GLN:HB3	6:L:711:HOH:O	2.11	0.50
2:H:32:ASP:OD1	4:H:623:GOL:O2	2.29	0.50
2:H:60:ASN:OD1	2:H:61:PRO:HD2	2.11	0.50
1:L:151:ASP:HA	1:L:191:SER:OG	2.11	0.50
1:L:193:THR:HG23	1:L:208:SER:OG	2.12	0.50
1:L:46:ARG:HD2	1:L:55:ASP:CG	2.37	0.49
1:L:113:PRO:HG3	1:L:144:ILE:HD11	1.94	0.49
1:L:107:LYS:HA	1:L:140:TYR:OH	2.13	0.48
2:H:6:GHG:HG	2:H:92:CYS:SG	2.52	0.48
1:L:56:SER:OG	2:H:1:ARG:NH2	2.46	0.48
2:H:222:LYS:HE3	2:H:226:GLU:OE2	2.13	0.48
2:H:199:TRP:CG	2:H:200:PRO:HA	2.49	0.47
2:H:40:PHE:O	2:H:43:ASN:N	2.48	0.46
2:H:124:LEU:HB2	2:H:141:GLY:CA	2.46	0.46
1:L:49:TYR:CE1	1:L:55:ASP:HA	2.51	0.46
2:H:3:GLN:C	2:H:4:LEU:HD12	2.41	0.46
2:H:100(A):GLY:O	2:H:100(B):ALA:HB3	2.16	0.46
1:L:39:ARG:NH2	6:L:755:HOH:O	2.50	0.45
1:L:37:LEU:HD12	1:L:38:GLN:N	2.32	0.45
1:L:163:4HT:CE2	1:L:175:MET:HE3	2.47	0.45
2:H:119:PRO:HB3	2:H:147:TYR:HB3	1.99	0.45
2:H:35:TRP:HB3	2:H:78:PHE:CE1	2.52	0.45
2:H:5:GLN:NE2	6:H:727:HOH:O	2.50	0.44
1:L:149:LYS:HD3	1:L:152:GLY:C	2.42	0.44
2:H:44:LYS:HB3	2:H:44:LYS:HE2	1.63	0.44
1:L:178:THR:OG1	4:L:621:GOL:H12	2.18	0.44
1:L:72:THR:HG21	1:L:74:LYS:NZ	2.33	0.44
1:L:145:ASN:O	1:L:196:ALA:HA	2.17	0.43
1:L:11:ILE:HG12	1:L:13:VAL:HG23	2.01	0.43
2:H:47:TRP:CZ2	2:H:49:GLY:HA2	2.52	0.43
1:L:146:VAL:HA	1:L:195:GLU:O	2.18	0.43
1:L:186:TYR:O	1:L:192:TYR:OH	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:15:ILE:O	1:L:15:ILE:HG22	2.19	0.42
1:L:161:ASN:HB3	1:L:175:MET:HE2	2.01	0.42
1:L:135:PHE:C	1:L:136:LEU:HD12	2.44	0.42
2:H:36:TRP:CE2	2:H:80:LEU:HB2	2.54	0.42
2:H:6:GHG:NE2	2:H:91:TYR:HA	2.35	0.42
1:L:77:ARG:NH1	1:L:77:ARG:HG3	2.35	0.41
1:L:9:LYS:NZ	6:L:698:HOH:O	2.50	0.41
1:L:36:LEU:HD12	1:L:36:LEU:N	2.34	0.41
2:H:185:TYR:OH	6:H:771:HOH:O	2.22	0.41
1:L:8:PRO:O	1:L:102:THR:HG23	2.22	0.40
2:H:178:LEU:HB2	2:H:185:TYR:CE2	2.56	0.40
1:L:6:GLN:HA	1:L:22:SER:O	2.21	0.40
1:L:50:LEU:HD23	1:L:50:LEU:HA	1.90	0.40
1:L:77:ARG:HG3	1:L:77:ARG:HH11	1.86	0.40
1:L:81:GLU:HG3	6:L:662:HOH:O	2.22	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	L	216/219 (99%)	213 (99%)	3 (1%)	0	100	100
2	H	219/222 (99%)	213 (97%)	4 (2%)	2 (1%)	14	4
All	All	435/441 (99%)	426 (98%)	7 (2%)	2 (0%)	24	13

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	43	ASN
2	H	64	LYS

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	L	194/194 (100%)	177 (91%)	17 (9%)	9	1
2	H	191/191 (100%)	180 (94%)	11 (6%)	18	5
All	All	385/385 (100%)	357 (93%)	28 (7%)	13	3

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	9	LYS
1	L	11	ILE
1	L	15	ILE
1	L	22	SER
1	L	42	GLN
1	L	77	ARG
1	L	107	LYS
1	L	127	SER
1	L	146	VAL
1	L	157	ASN
1	L	169	LYS
1	L	175	MET
1	L	188	ARG
1	L	199	LYS
1	L	201	SER
1	L	202	THR
1	L	205	ILE
2	H	5	GLN
2	H	19	SER
2	H	44	LYS
2	H	64	LYS
2	H	85	GLU
2	H	102	SER
2	H	130	ASP
2	H	137	SER
2	H	140	LEU
2	H	151	PRO

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Mol	Chain	Res	Type
2	H	168	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	27	GLN
1	L	28	ASN
1	L	157	ASN
1	L	161	ASN
2	H	3	GLN
2	H	77	GLN
2	H	82(A)	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	4HT	L	163	1	15,16,17	1.80	4 (26%)	15,22,24	1.98	3 (20%)
2	GHG	H	6	2	7,9,10	1.15	1 (14%)	7,11,13	4.33	3 (42%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	4HT	L	163	1	-	0/5/6/8	0/2/2/2
2	GHG	H	6	2	-	6/9/10/12	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	163	4HT	OE3-CE3	3.83	1.44	1.36
1	L	163	4HT	CD1-CG	3.51	1.42	1.36
1	L	163	4HT	CD1-NE1	2.44	1.41	1.37
2	H	6	GHG	CG-CD	2.21	1.55	1.52
1	L	163	4HT	CD2-CG	-2.01	1.38	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	6	GHG	OG1-CG-CD	-7.78	94.24	110.80
2	H	6	GHG	OG1-CG-CB	-7.63	89.47	108.31
1	L	163	4HT	CE2-NE1-CD1	-5.98	103.75	109.08
1	L	163	4HT	CD2-CE2-NE1	2.84	111.23	106.88
2	H	6	GHG	OE1-CD-CG	2.76	121.68	119.02
1	L	163	4HT	CB-CG-CD1	-2.11	122.85	126.97

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	6	GHG	OE1-CD-CG-CB
2	H	6	GHG	NE2-CD-CG-CB
2	H	6	GHG	NE2-CD-CG-OG1
2	H	6	GHG	CA-CB-CG-CD
2	H	6	GHG	OE1-CD-CG-OG1
2	H	6	GHG	CA-CB-CG-OG1

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L	163	4HT	2	0
2	H	6	GHG	4	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

6 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	$\# Z > 2$
4	GOL	L	621	-	5,5,5	0.42	0	5,5,5	0.26	0
3	ACT	L	611	-	3,3,3	0.87	0	3,3,3	0.59	0
4	GOL	H	622	-	5,5,5	0.48	0	5,5,5	0.43	0
4	GOL	H	623	-	5,5,5	0.45	0	5,5,5	0.70	0
5	BEZ	H	601	-	9,9,9	3.98	2 (22%)	11,11,11	2.99	6 (54%)
4	GOL	H	624	-	5,5,5	0.51	0	5,5,5	0.38	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
4	GOL	L	621	-	-	4/4/4/4	-
4	GOL	H	622	-	-	3/4/4/4	-
4	GOL	H	623	-	-	2/4/4/4	-
5	BEZ	H	601	-	-	0/4/4/4	0/1/1/1
4	GOL	H	624	-	-	0/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	601	BEZ	C3-C2	11.28	1.58	1.38
5	H	601	BEZ	O2-C	-2.46	1.23	1.30

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	601	BEZ	C4-C3-C2	-5.46	113.51	120.24
5	H	601	BEZ	C5-C4-C3	4.91	126.59	119.87
5	H	601	BEZ	C6-C1-C2	4.37	124.12	118.57
5	H	601	BEZ	C3-C2-C1	-2.91	117.51	120.36
5	H	601	BEZ	C2-C1-C	-2.44	115.54	120.37
5	H	601	BEZ	O2-C-O1	-2.31	118.38	123.35

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	623	GOL	O1-C1-C2-O2
4	H	623	GOL	O1-C1-C2-C3
4	L	621	GOL	O1-C1-C2-C3
4	L	621	GOL	C1-C2-C3-O3
4	L	621	GOL	O2-C2-C3-O3
4	H	622	GOL	O2-C2-C3-O3
4	L	621	GOL	O1-C1-C2-O2
4	H	622	GOL	O1-C1-C2-O2
4	H	622	GOL	O1-C1-C2-C3

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	621	GOL	4	0
4	H	623	GOL	1	0
5	H	601	BEZ	1	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	L	218/219 (99%)	1.53	53 (24%) 2 1	22, 34, 57, 79	0
2	H	221/222 (99%)	1.25	28 (12%) 8 9	20, 28, 43, 76	0
All	All	439/441 (99%)	1.39	81 (18%) 3 3	20, 30, 54, 79	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	202	THR	5.1
2	H	42	GLY	4.8
2	H	41	PRO	4.7
2	H	64	LYS	4.3
2	H	1	ARG	4.3
1	L	205	ILE	4.1
2	H	65	SER	3.6
2	H	44	LYS	3.6
1	L	146	VAL	3.6
1	L	157	ASN	3.4
2	H	208	CYS	3.3
1	L	209	PHE	3.1
1	L	106	ILE	3.0
1	L	125	LEU	2.9
2	H	5	GLN	2.9
1	L	200	THR	2.9
2	H	231	THR	2.9
1	L	196	ALA	2.9
1	L	66	GLY	2.9
1	L	142	LYS	2.9
1	L	188	ARG	2.9
2	H	97	TRP	2.9
1	L	181	LEU	2.9
2	H	18	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
2	H	45	LEU	2.8
1	L	169	LYS	2.8
1	L	136	LEU	2.8
1	L	197	THR	2.8
1	L	192	TYR	2.8
1	L	173	TYR	2.7
2	H	105	GLN	2.7
2	H	43	ASN	2.7
1	L	115	VAL	2.7
2	H	12	VAL	2.7
2	H	40	PHE	2.6
1	L	9	LYS	2.6
2	H	140	LEU	2.6
1	L	101	GLY	2.6
1	L	127	SER	2.6
1	L	194	CYS	2.6
1	L	103	LYS	2.6
1	L	180	THR	2.5
1	L	36	LEU	2.5
1	L	21	ILE	2.5
2	H	2	VAL	2.5
2	H	98	TYR	2.4
2	H	13	LYS	2.4
1	L	145	ASN	2.4
1	L	186	TYR	2.4
2	H	93	ALA	2.4
1	L	132	VAL	2.4
2	H	101	GLY	2.4
1	L	117	ILE	2.4
2	H	81	GLN	2.4
1	L	128	GLY	2.4
1	L	214	CYS	2.4
1	L	152	GLY	2.3
1	L	159	VAL	2.3
1	L	39	ARG	2.3
1	L	199	LYS	2.3
1	L	59	PRO	2.2
2	H	100(B)	ALA	2.2
1	L	108	ARG	2.2
1	L	156	GLN	2.2
1	L	111	ALA	2.2
1	L	147	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	L	27(A)	ARG	2.2
1	L	133	VAL	2.2
2	H	141	GLY	2.2
1	L	204	PRO	2.2
1	L	10	THR	2.2
1	L	193	THR	2.2
1	L	191	SER	2.2
2	H	180	SER	2.2
1	L	96	TYR	2.1
1	L	7	SER	2.1
1	L	160	LEU	2.1
1	L	143	ASP	2.1
2	H	203	GLN	2.0
2	H	128	CYS	2.0
1	L	75	ILE	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
1	4HT	L	163	15/16	0.88	0.15	30,68,79,79	0
2	GHG	H	6	10/11	0.91	0.10	27,31,44,46	1

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
4	GOL	L	621	6/6	0.72	0.33	47,72,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	H	622	6/6	0.84	0.16	29,44,49,62	0
3	ACT	L	611	4/4	0.85	0.24	42,48,49,51	0
4	GOL	H	624	6/6	0.87	0.14	37,39,40,41	0
4	GOL	H	623	6/6	0.88	0.14	33,36,44,78	0
5	BEZ	H	601	9/9	0.88	0.13	27,31,36,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.