



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:46 AM GMT

PDB ID : 2ILP
Title : Clostridium botulinum Serotype A Light Chain inhibited by 4-chlorocinnamic hydroxamate
Authors : Silvaggi, N.R.; Allen, K.N.
Deposited on : 2006-10-03
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

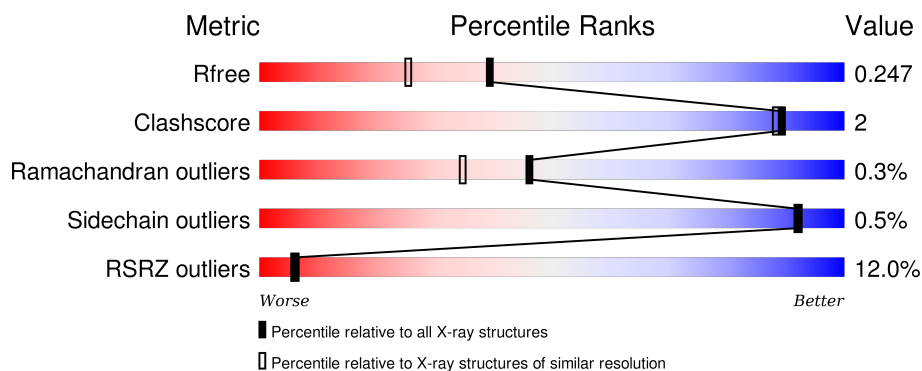
1 Overall quality at a glance

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}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	444	<div> <div>11%</div> <div>86%</div> <div>5% • 8%</div> </div>
1	B	444	<div> <div>11%</div> <div>87%</div> <div>• 8%</div> </div>

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	GB5	A	600	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7294 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 Botulinum neurotoxin A light-chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	1	0
			3308	2133	548	619	8			
1	B	407	Total	C	N	O	S	0	5	0
			3338	2149	553	628	8			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	CLONING ARTIFACT	UNP Q7B8V4
A	-18	GLY	-	CLONING ARTIFACT	UNP Q7B8V4
A	-17	SER	-	CLONING ARTIFACT	UNP Q7B8V4
A	-16	SER	-	CLONING ARTIFACT	UNP Q7B8V4
A	-15	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
A	-14	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
A	-13	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
A	-12	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
A	-11	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
A	-10	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
A	-9	SER	-	CLONING ARTIFACT	UNP Q7B8V4
A	-8	SER	-	CLONING ARTIFACT	UNP Q7B8V4
A	-7	GLY	-	CLONING ARTIFACT	UNP Q7B8V4
A	-6	LEU	-	CLONING ARTIFACT	UNP Q7B8V4
A	-5	VAL	-	CLONING ARTIFACT	UNP Q7B8V4
A	-4	PRO	-	CLONING ARTIFACT	UNP Q7B8V4
A	-3	ARG	-	CLONING ARTIFACT	UNP Q7B8V4
A	-2	GLY	-	CLONING ARTIFACT	UNP Q7B8V4
A	-1	SER	-	CLONING ARTIFACT	UNP Q7B8V4
A	0	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
A	2	GLN	PRO	CONFLICT	UNP Q7B8V4
B	-19	MET	-	CLONING ARTIFACT	UNP Q7B8V4
B	-18	GLY	-	CLONING ARTIFACT	UNP Q7B8V4
B	-17	SER	-	CLONING ARTIFACT	UNP Q7B8V4
B	-16	SER	-	CLONING ARTIFACT	UNP Q7B8V4

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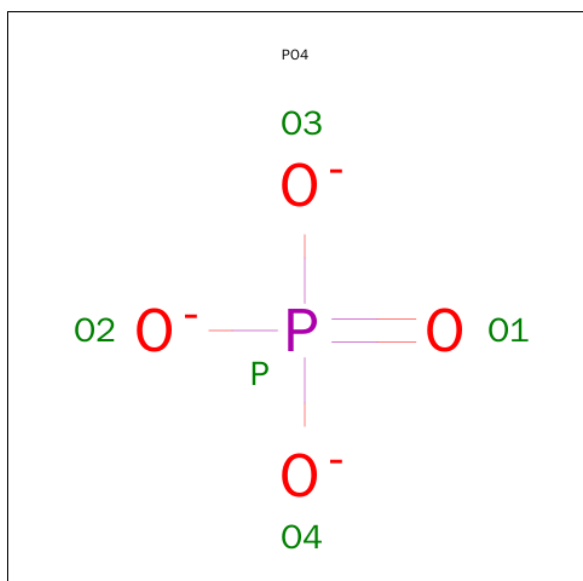
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
B	-14	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
B	-13	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
B	-12	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
B	-11	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
B	-10	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
B	-9	SER	-	CLONING ARTIFACT	UNP Q7B8V4
B	-8	SER	-	CLONING ARTIFACT	UNP Q7B8V4
B	-7	GLY	-	CLONING ARTIFACT	UNP Q7B8V4
B	-6	LEU	-	CLONING ARTIFACT	UNP Q7B8V4
B	-5	VAL	-	CLONING ARTIFACT	UNP Q7B8V4
B	-4	PRO	-	CLONING ARTIFACT	UNP Q7B8V4
B	-3	ARG	-	CLONING ARTIFACT	UNP Q7B8V4
B	-2	GLY	-	CLONING ARTIFACT	UNP Q7B8V4
B	-1	SER	-	CLONING ARTIFACT	UNP Q7B8V4
B	0	HIS	-	CLONING ARTIFACT	UNP Q7B8V4
B	2	GLN	PRO	CONFLICT	UNP Q7B8V4

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

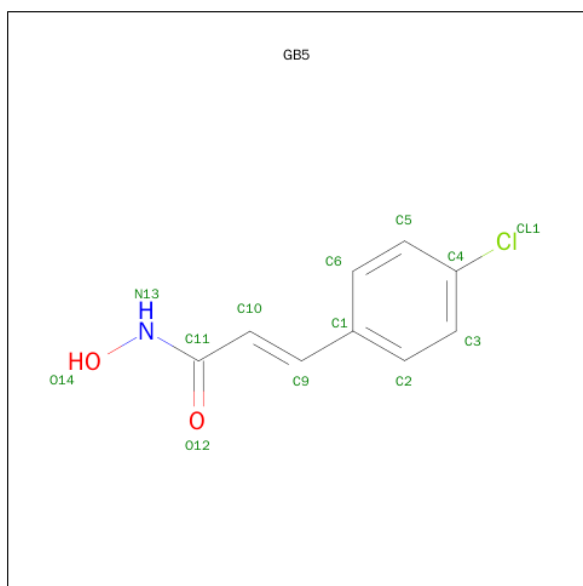
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

- Molecule 4 is (2E)-3-(4-CHLOROPHENYL)-N-HYDROXYACRYLAMIDE (three-letter code: GB5) (formula: C₉H₈ClNO₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	Cl	N	O	0	0
			13	9	1	1	2		
4	A	1	Total	C	Cl	N	O	0	0
			13	9	1	1	2		

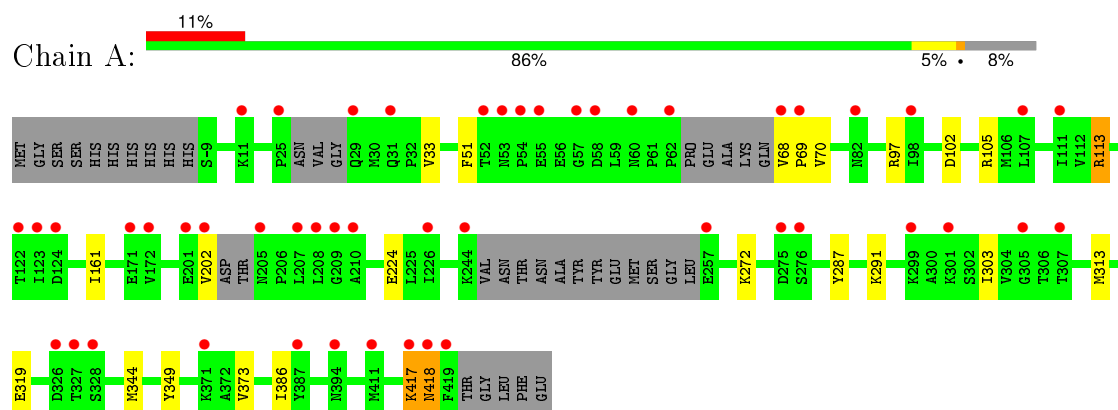
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	313	Total	O	0	0
			313	313		
5	B	302	Total	O	0	0
			302	302		

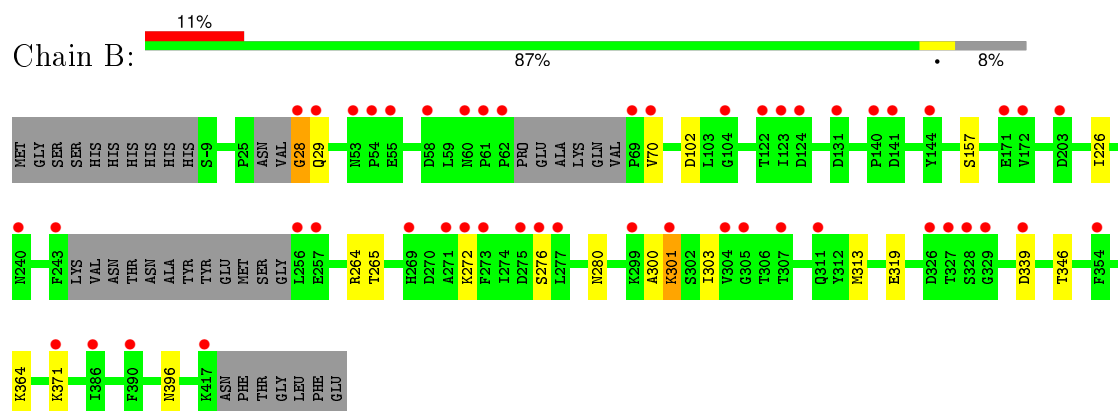
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Botulinum neurotoxin A light-chain



• Molecule 1: Botulinum neurotoxin A light-chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.66Å 67.69Å 98.40Å 90.00° 106.53° 90.00°	Depositor
Resolution (Å)	50.00 – 1.90 16.21 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.9 (50.00-1.90) 98.0 (16.21-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.173 , 0.216 0.215 , 0.247	Depositor DCC
R_{free} test set	3626 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	26.0	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 56.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 71753 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7294	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 4.44% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, GB5, PO4

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	0.54	0/3383	0.67	2/4569 (0.0%)
1	B	0.53	0/3415	0.62	0/4615
All	All	0.54	0/6798	0.64	2/9184 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	ARG	NE-CZ-NH2	-8.48	116.06	120.30
1	A	113	ARG	NE-CZ-NH1	8.40	124.50	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	417	LYS	Peptide
1	B	28	GLY	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3308	0	3264	19	0
1	B	3338	0	3284	13	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	5	0	0	0	0
4	A	13	0	7	1	0
4	B	13	0	7	0	0
5	A	313	0	0	1	0
5	B	302	0	0	8	0
All	All	7294	0	6562	32	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (32) 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:339:ASP:HB3	5:B:758:HOH:O	1.90	0.70
1:B:102:ASP:OD1	5:B:821:HOH:O	2.10	0.69
1:A:272:LYS:NZ	5:A:639:HOH:O	2.26	0.67
1:B:319:GLU:OE2	5:B:784:HOH:O	2.11	0.67
1:A:102:ASP:OD1	1:A:105:ARG:NH2	2.29	0.66
1:A:417:LYS:HA	1:A:418:ASN:CB	2.27	0.65
1:B:28:GLY:N	1:B:29:GLN:HA	2.19	0.57
1:A:70:VAL:HG22	1:A:161:ILE:HD11	1.87	0.56
1:A:344:MET:HG3	1:A:349:TYR:CZ	2.42	0.53
1:A:417:LYS:HA	1:A:418:ASN:HB2	1.89	0.53
1:A:68:VAL:N	1:A:69:PRO:CD	2.72	0.52
1:A:113:ARG:HD2	5:B:809:HOH:O	2.11	0.51
1:B:70:VAL:HG22	1:B:371:LYS:HG2	1.93	0.50
1:A:303:ILE:HD11	1:A:313:MET:HG3	1.92	0.49
1:B:396:ASN:HB3	5:B:847:HOH:O	2.13	0.48
1:A:417:LYS:HA	1:A:418:ASN:HB3	1.97	0.46
1:B:70:VAL:HG22	1:B:371:LYS:CG	2.45	0.46
1:B:364:LYS:HD2	1:B:364:LYS:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:GLU:HG2	5:B:809:HOH:O	2.17	0.45
1:B:300:ALA:O	1:B:301:LYS:HE3	2.16	0.45
1:B:272:LYS:NZ	5:B:884:HOH:O	2.49	0.45
1:B:226:ILE:CG2	1:B:265:THR:HG23	2.47	0.44
1:A:161:ILE:HD13	1:A:373:VAL:CG2	2.47	0.44
1:A:287:TYR:CE2	1:A:291:LYS:HD2	2.51	0.44
1:A:33:VAL:HG11	1:A:51:PHE:CZ	2.52	0.44
1:A:417:LYS:CA	1:A:418:ASN:CB	2.95	0.43
1:A:319:GLU:CG	5:B:809:HOH:O	2.67	0.42
1:B:303:ILE:HD11	1:B:313:MET:HG3	2.01	0.42
1:B:264[B]:ARG:HD2	1:B:346:THR:HB	2.02	0.42
1:A:161:ILE:HD13	1:A:373:VAL:HG21	2.02	0.41
1:A:224:GLU:OE1	4:A:600:GB5:N13	2.54	0.40
1:A:97:ARG:HA	1:A:386:ILE:HG23	2.03	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	398/444 (90%)	390 (98%)	7 (2%)	1 (0%)	46	35
1	B	404/444 (91%)	397 (98%)	6 (2%)	1 (0%)	52	42
All	All	802/888 (90%)	787 (98%)	13 (2%)	2 (0%)	46	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	418	ASN
1	B	157	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	366/397 (92%)	365 (100%)	1 (0%)	94	95
1	B	370/397 (93%)	367 (99%)	3 (1%)	86	86
All	All	736/794 (93%)	732 (100%)	4 (0%)	92	92

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	202	VAL
1	B	276	SER
1	B	280	ASN
1	B	301	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	205	ASN
1	A	288	ASN
1	B	29	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 for Mogul analysis.

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	PO4	A	501	-	4,4,4	0.52	0	6,6,6	0.28	0
4	GB5	A	600	2	13,13,13	2.86	1 (7%)	16,16,16	1.18	1 (6%)
4	GB5	B	600	2	13,13,13	2.90	1 (7%)	16,16,16	1.38	3 (18%)

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	PO4	A	501	-	-	0/0/0/0	0/0/0/0
4	GB5	A	600	2	-	0/7/7/7	0/1/1/1
4	GB5	B	600	2	-	0/7/7/7	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	600	GB5	C4-CL1	-10.03	1.51	1.74
4	B	600	GB5	C4-CL1	-9.95	1.51	1.74

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	600	GB5	C5-C4-C3	-2.41	117.82	121.26
4	B	600	GB5	C2-C3-C4	2.04	121.49	119.23
4	A	600	GB5	C10-C11-N13	2.39	119.15	113.86
4	B	600	GB5	C10-C11-N13	2.89	120.26	113.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	600	GB5	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	A	407/444 (91%)	0.80	49 (12%) 6 6	22, 32, 44, 56	0
1	B	407/444 (91%)	0.77	49 (12%) 6 6	19, 32, 46, 53	0
All	All	814/888 (91%)	0.78	98 (12%) 6 6	19, 32, 47, 56	0

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	418	ASN	8.7
1	B	256	LEU	8.4
1	A	68	VAL	8.4
1	A	202	VAL	8.1
1	B	62	PRO	7.4
1	B	28	GLY	7.0
1	B	277	LEU	6.5
1	A	208	LEU	6.1
1	A	29	GLN	6.0
1	B	124	ASP	5.7
1	B	54	PRO	5.7
1	B	144	TYR	5.7
1	B	69	PRO	5.6
1	B	273	PHE	5.3
1	A	62	PRO	5.2
1	B	327	THR	5.1
1	A	124	ASP	4.9
1	A	305	GLY	4.8
1	A	419	PHE	4.7
1	B	417	LYS	4.5
1	A	417	LYS	4.5
1	A	172	VAL	4.3
1	B	29	GLN	4.2
1	A	69	PRO	4.2

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Mol	Chain	Res	Type	RSRZ
1	B	55	GLU	4.1
1	A	205	ASN	4.0
1	A	327	THR	4.0
1	B	301	LYS	3.9
1	A	201	GLU	3.8
1	A	209	GLY	3.8
1	B	307	THR	3.8
1	A	55	GLU	3.8
1	A	301	LYS	3.7
1	B	203	ASP	3.6
1	B	60	ASN	3.6
1	B	276	SER	3.5
1	B	123	ILE	3.5
1	A	411	MET	3.5
1	B	269[A]	HIS	3.4
1	A	31	GLN	3.4
1	A	387	TYR	3.4
1	A	54	PRO	3.3
1	A	371	LYS	3.3
1	B	140	PRO	3.2
1	A	276	SER	3.2
1	A	299	LYS	3.2
1	B	328	SER	3.2
1	A	60	ASN	3.1
1	A	122	THR	3.1
1	B	299	LYS	3.1
1	B	371	LYS	3.1
1	A	25	PRO	3.1
1	A	307	THR	3.1
1	B	243	PHE	3.1
1	B	172	VAL	3.1
1	B	61	PRO	3.0
1	A	171	GLU	3.0
1	B	354	PHE	3.0
1	A	328	SER	2.9
1	A	57	GLY	2.8
1	B	131	ASP	2.8
1	B	257	GLU	2.8
1	A	107	LEU	2.8
1	B	122	THR	2.7
1	A	11	LYS	2.7
1	B	171	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	207	LEU	2.7
1	B	390	PHE	2.7
1	A	58	ASP	2.7
1	A	123	ILE	2.7
1	A	244	LYS	2.6
1	A	275	ASP	2.5
1	B	275	ASP	2.5
1	A	210	ALA	2.5
1	B	141	ASP	2.4
1	B	386	ILE	2.4
1	B	311	GLN	2.4
1	B	339	ASP	2.3
1	B	70	VAL	2.3
1	B	58	ASP	2.2
1	A	326	ASP	2.2
1	B	326	ASP	2.2
1	B	329	GLY	2.2
1	B	53	ASN	2.1
1	A	98	ILE	2.1
1	B	272	LYS	2.1
1	A	53	ASN	2.1
1	A	52	THR	2.1
1	A	111	ILE	2.1
1	A	226	ILE	2.1
1	B	240	ASN	2.1
1	A	82	ASN	2.0
1	A	394	ASN	2.0
1	B	104	GLY	2.0
1	B	304	VAL	2.0
1	B	271	ALA	2.0
1	B	305	GLY	2.0
1	A	257	GLU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	GB5	A	600	13/13	0.73	0.28	2.75	41,46,47,47	0
4	GB5	B	600	13/13	0.87	0.18	0.93	39,43,45,45	0
2	ZN	A	500	1/1	1.00	0.09	-2.53	32,32,32,32	0
2	ZN	B	500	1/1	0.99	0.05	-3.51	33,33,33,33	0
3	PO4	A	501	5/5	0.77	0.21	-	35,35,36,37	5

6.5 Other polymers [i](#)

There are no such residues in this entry.