



# Full wwPDB X-ray Structure Validation Report

Nov 3, 2014 – 04:46 PM EST

PDB ID : 3BC3  
Title : Exploring inhibitor binding at the S subsites of cathepsin L  
Authors : Chowdhury, S.F.; Joseph, L.; Kumar, S.; Tulsidas, S.R.; Bhat, S.; Ziomek, E.;  
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Deposited on : 2007-11-12  
Resolution : 2.20 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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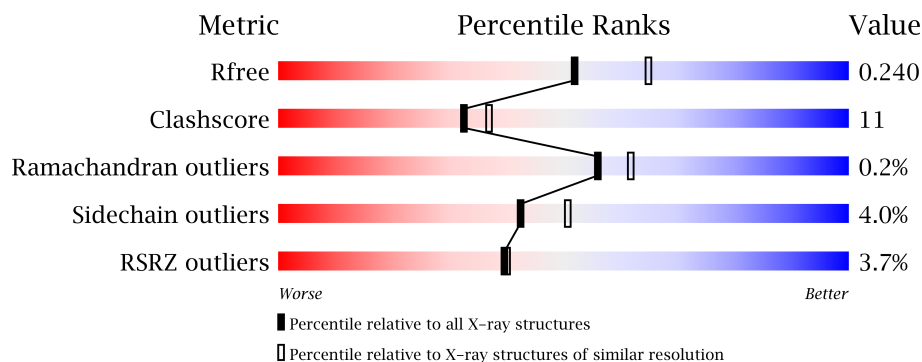
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable24103  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.1.3  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable24103

# 1 Overall quality at a glance

The reported resolution of this entry is 2.20 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))
$R_{free}$	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	220	
1	B	220	

## 2 Entry composition i

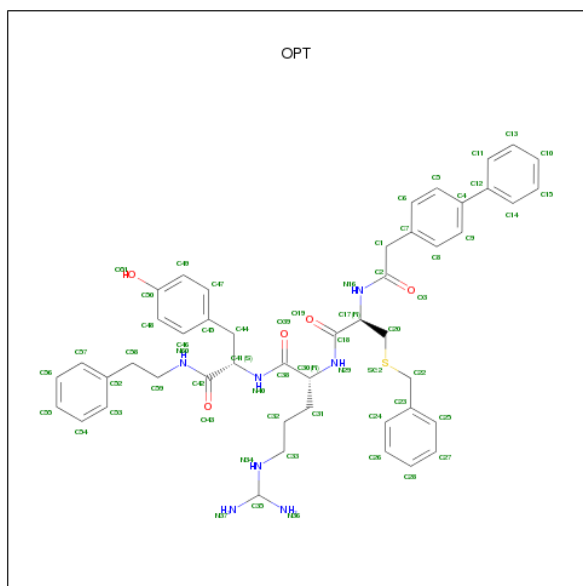
There are 3 unique types of molecules in this entry. The entry contains 3865 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Cathepsin L heavy and light chains.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	0	0
			1661	1041	275	332	13			
1	B	215	Total	C	N	O	S	0	0	0
			1661	1041	275	332	13			

- Molecule 2 is S-BENZYL-N-(BIPHENYL-4-YLACETYL)-L-CYSTEINY-L-N 5 -(DIAMINO METHYL)-D-ORNITHYL-N-(2-PHENYLETHYL)-L-TYROSINAMIDE (three-letter code: OPT) (formula: C<sub>47</sub>H<sub>55</sub>N<sub>7</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			60	47	7	5	1		
2	B	1	Total	C	N	O	S	0	0
			60	47	7	5	1		

- Molecule 3 is water.

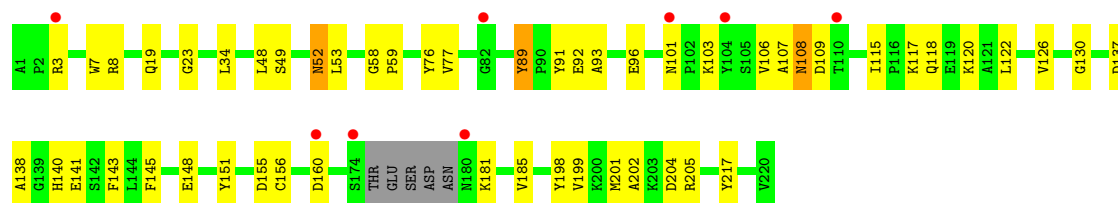
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	206	Total 206	O 206	0	0
3	B	217	Total 217	O 217	0	0

### 3 Residue-property plots

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.

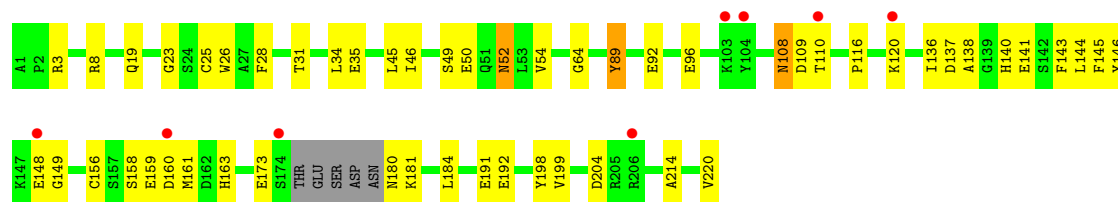
- Molecule 1: Cathepsin L heavy and light chains

Chain A: 



- Molecule 1: Cathepsin L heavy and light chains

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.77Å 90.93Å 126.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.20 45.46 – 2.20	Depositor EDS
% Data completeness (in resolution range)	89.7 (30.00-2.20) 93.0 (45.46-2.20)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.43 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.183 , 0.234 0.191 , 0.240	Depositor DCC
$R_{free}$ test set	1609 reflections (7.79%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.0	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 39.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 20987 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3865	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OPT, CSD

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	0.37	0/1694	0.54	0/2288
1	B	0.36	0/1694	0.53	0/2288
All	All	0.37	0/3388	0.54	0/4576

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1661	0	1541	36	0
1	B	1661	0	1541	39	0
2	A	60	0	53	0	0
2	B	60	0	53	2	0
3	A	206	0	0	10	0
3	B	217	0	0	17	0
All	All	3865	0	3188	75	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 11.

All (75) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:23:GLY:HA2	3:A:302:HOH:O	1.53	1.08
1:B:23:GLY:HA2	3:B:406:HOH:O	1.67	0.94
1:B:64:GLY:HA2	3:B:599:HOH:O	1.70	0.90
1:B:54:VAL:HA	3:B:599:HOH:O	1.73	0.87
1:A:77:VAL:HG23	3:A:330:HOH:O	1.87	0.74
1:B:160:ASP:HB3	3:B:503:HOH:O	1.88	0.73
1:B:31:THR:O	1:B:35:GLU:HG3	1.90	0.72
1:A:48:LEU:HD21	3:A:503:HOH:O	1.89	0.71
1:A:76:TYR:HD2	3:A:330:HOH:O	1.73	0.70
1:A:108:ASN:HD22	1:A:109:ASP:H	1.42	0.67
1:B:19:GLN:NE2	3:B:406:HOH:O	2.28	0.66
1:B:92:GLU:OE1	1:B:96:GLU:HG3	1.98	0.64
1:A:3:ARG:HH11	1:A:3:ARG:HG3	1.66	0.61
1:A:106:VAL:HG23	3:A:503:HOH:O	2.01	0.60
1:A:107:ALA:HB2	3:A:503:HOH:O	2.01	0.59
1:A:137:ASP:OD2	1:A:140:HIS:HE1	1.86	0.59
1:B:159:GLU:HG3	3:B:503:HOH:O	2.03	0.58
1:B:25:CSD:OD2	1:B:163:HIS:HA	2.04	0.58
1:B:173:GLU:HG2	3:B:522:HOH:O	2.02	0.57
1:A:115:ILE:HD11	1:A:217:TYR:HE1	1.71	0.56
1:A:19:GLN:NE2	3:A:302:HOH:O	2.38	0.55
1:A:8:ARG:HD3	1:A:198:TYR:CZ	2.42	0.54
1:B:141:GLU:HG3	1:B:145:PHE:CD2	2.44	0.53
1:B:3:ARG:HH11	1:B:3:ARG:HG3	1.75	0.52
1:B:137:ASP:OD2	1:B:140:HIS:HE1	1.92	0.52
1:A:202:ALA:HB1	1:A:205:ARG:HG3	1.91	0.51
1:B:144:LEU:HD11	2:B:400:OPT:H9	1.93	0.51
1:A:138:ALA:HB1	1:A:143:PHE:CD2	2.46	0.51
1:A:108:ASN:HD22	1:A:109:ASP:N	2.08	0.50
1:A:205:ARG:NH1	3:A:368:HOH:O	2.46	0.49
1:A:141:GLU:HB2	1:A:145:PHE:CE2	2.48	0.49
1:A:53:LEU:CD2	3:A:330:HOH:O	2.61	0.49
1:B:26:TRP:HZ2	3:B:599:HOH:O	1.96	0.49
1:A:101:ASN:OD1	1:A:103:LYS:HB3	2.13	0.48
1:B:138:ALA:HB1	1:B:143:PHE:CD2	2.49	0.48
1:B:158:SER:HB3	3:B:448:HOH:O	2.14	0.48
1:B:52:ASN:C	1:B:52:ASN:HD22	2.18	0.47
1:B:108:ASN:ND2	1:B:109:ASP:H	2.12	0.47
1:A:185:VAL:HB	1:A:199:VAL:HG13	1.96	0.47
1:B:140:HIS:HD2	3:B:560:HOH:O	1.98	0.47
1:B:110:THR:HG22	1:B:110:THR:O	2.15	0.47
1:B:181:LYS:HD2	1:B:204:ASP:OD2	2.14	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:49:SER:OG	1:B:89:TYR:HB3	2.15	0.46
1:A:160:ASP:O	1:A:160:ASP:OD1	2.33	0.46
1:A:181:LYS:NZ	1:A:204:ASP:HB2	2.31	0.46
1:A:91:TYR:CZ	1:A:93:ALA:HA	2.51	0.46
1:A:49:SER:OG	1:A:89:TYR:HB3	2.17	0.45
1:A:52:ASN:C	1:A:52:ASN:HD22	2.19	0.45
1:A:117:LYS:NZ	3:A:412:HOH:O	2.49	0.45
1:B:180:ASN:N	3:B:441:HOH:O	2.50	0.44
1:B:120:LYS:HG3	3:B:546:HOH:O	2.17	0.44
1:B:214:ALA:HB1	2:B:400:OPT:O51	2.17	0.44
1:A:199:VAL:HG22	1:A:201:MET:HG3	1.98	0.44
1:A:7:TRP:CE2	1:A:130:GLY:HA2	2.52	0.44
1:B:192:GLU:HB2	3:B:443:HOH:O	2.17	0.44
1:A:108:ASN:ND2	1:A:109:ASP:H	2.13	0.44
1:B:116:PRO:HD3	3:B:605:HOH:O	2.16	0.44
1:B:25:CSD:OD1	3:B:406:HOH:O	2.16	0.44
1:B:46:ILE:HD12	1:B:46:ILE:N	2.33	0.43
1:B:8:ARG:HD3	1:B:198:TYR:CZ	2.53	0.43
1:A:58:GLY:N	1:A:59:PRO:CD	2.81	0.43
1:A:120:LYS:HD2	1:A:120:LYS:C	2.39	0.43
1:A:92:GLU:OE2	1:A:96:GLU:HG3	2.19	0.43
1:B:28:PHE:CD2	1:B:50:GLU:HG2	2.53	0.42
1:B:28:PHE:CG	1:B:50:GLU:HG2	2.54	0.42
1:B:136:ILE:CD1	1:B:138:ALA:HB2	2.50	0.42
1:A:122:LEU:O	1:A:126:VAL:HG23	2.20	0.42
1:B:191:GLU:HG3	1:B:192:GLU:OE1	2.20	0.42
1:B:45:LEU:HA	3:B:455:HOH:O	2.20	0.41
1:A:151:TYR:HB3	1:A:201:MET:HG2	2.02	0.41
1:A:34:LEU:HA	1:A:34:LEU:HD23	1.88	0.41
1:B:220:VAL:HG23	1:B:220:VAL:O	2.21	0.40
1:A:3:ARG:NH1	1:A:3:ARG:HG3	2.32	0.40
1:B:146:TYR:CE2	1:B:199:VAL:HG23	2.55	0.40
1:B:149:GLY:HA2	3:B:551:HOH:O	2.21	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	210/220 (96%)	202 (96%)	8 (4%)	0	100	100
1	B	210/220 (96%)	201 (96%)	8 (4%)	1 (0%)	38	38
All	All	420/440 (96%)	403 (96%)	16 (4%)	1 (0%)	56	62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	161	MET

### 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	173/178 (97%)	166 (96%)	7 (4%)	42	51
1	B	173/178 (97%)	166 (96%)	7 (4%)	42	51
All	All	346/356 (97%)	332 (96%)	14 (4%)	42	51

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	89	TYR
1	A	108	ASN
1	A	118	GLN
1	A	148	GLU
1	A	155	ASP
1	A	156	CYS
1	B	34	LEU
1	B	52	ASN
1	B	89	TYR
1	B	108	ASN
1	B	148	GLU

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Mol	Chain	Res	Type
1	B	156	CYS
1	B	184	LEU

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	108	ASN
1	A	140	HIS
1	B	108	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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	CSD	A	25	1	7,7,8	6.99	3 (42%)	6,8,10	2.37	3 (50%)
1	CSD	B	25	1	7,7,8	6.75	3 (42%)	6,8,10	2.46	3 (50%)

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	CSD	A	25	1	-	0/3/6/8	0/0/0/0
1	CSD	B	25	1	-	0/3/6/8	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	25	CSD	O-C	18.09	1.23	1.11
1	B	25	CSD	O-C	17.32	1.23	1.11
1	B	25	CSD	OD1-SG	-2.89	1.44	1.47
1	B	25	CSD	CA-C	2.72	1.54	1.49
1	A	25	CSD	CA-C	2.48	1.54	1.49
1	A	25	CSD	OD1-SG	-2.07	1.45	1.47

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	25	CSD	OD2-SG-OD1	4.91	119.04	109.75
1	A	25	CSD	OD2-SG-OD1	4.90	119.02	109.75
1	B	25	CSD	C-CA-N	-2.56	111.28	113.83
1	A	25	CSD	OD1-SG-CB	-2.22	101.44	105.29
1	A	25	CSD	C-CA-N	-2.04	111.79	113.83
1	B	25	CSD	OD1-SG-CB	-2.03	101.77	105.29

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates i

There are no carbohydrates in this entry.

## 5.6 Ligand geometry i

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	OPT	A	300	-	64,64,64	4.11	45 (70%)	83,83,83	2.30	21 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	OPT	B	400	-	64,64,64	4.11	44 (68%)	83,83,83	2.26	20 (24%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OPT	A	300	-	-	0/55/55/55	0/5/5/5
2	OPT	B	400	-	-	0/55/55/55	0/5/5/5

All (89) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	OPT	C2-N16	10.56	1.55	1.34
2	B	400	OPT	C2-N16	10.22	1.54	1.34
2	B	400	OPT	C18-N29	8.69	1.54	1.34
2	A	300	OPT	C18-N29	8.28	1.53	1.34
2	B	400	OPT	C42-N60	7.64	1.49	1.33
2	A	300	OPT	C42-N60	7.62	1.49	1.33
2	B	400	OPT	C6-C7	7.30	1.54	1.38
2	B	400	OPT	C5-C4	7.28	1.54	1.39
2	A	300	OPT	C6-C7	7.12	1.54	1.38
2	A	300	OPT	C14-C12	7.09	1.54	1.39
2	B	400	OPT	C14-C12	7.05	1.54	1.39
2	A	300	OPT	C5-C4	6.87	1.54	1.39
2	B	400	OPT	C11-C12	6.78	1.53	1.39
2	B	400	OPT	C53-C52	6.75	1.53	1.38
2	A	300	OPT	C53-C52	6.71	1.53	1.38
2	A	300	OPT	C11-C12	6.70	1.53	1.39
2	A	300	OPT	C13-C10	6.48	1.54	1.38
2	B	400	OPT	C13-C10	6.43	1.54	1.38
2	B	400	OPT	C15-C14	6.12	1.51	1.38
2	A	300	OPT	C9-C4	6.11	1.52	1.39
2	A	300	OPT	C15-C14	5.94	1.51	1.38
2	B	400	OPT	C9-C4	5.86	1.51	1.39
2	A	300	OPT	C47-C45	5.56	1.51	1.38
2	B	400	OPT	C47-C45	5.53	1.51	1.38
2	B	400	OPT	C10-C15	5.31	1.51	1.38
2	A	300	OPT	C10-C15	5.24	1.51	1.38
2	B	400	OPT	C6-C5	5.24	1.48	1.38
2	A	300	OPT	C6-C5	5.11	1.48	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	400	OPT	C22-SG2	-5.04	1.74	1.82
2	B	400	OPT	C57-C52	4.91	1.49	1.38
2	A	300	OPT	C22-SG2	-4.88	1.74	1.82
2	B	400	OPT	C13-C11	4.83	1.48	1.38
2	A	300	OPT	C13-C11	4.79	1.48	1.38
2	A	300	OPT	C57-C52	4.71	1.49	1.38
2	A	300	OPT	C8-C7	4.51	1.48	1.38
2	A	300	OPT	C59-N60	4.47	1.56	1.46
2	A	300	OPT	C54-C53	4.45	1.48	1.38
2	B	400	OPT	C8-C7	4.41	1.48	1.38
2	B	400	OPT	C59-N60	4.40	1.56	1.46
2	B	400	OPT	C48-C50	4.36	1.48	1.38
2	A	300	OPT	C54-C55	4.34	1.49	1.38
2	A	300	OPT	C48-C50	4.33	1.47	1.38
2	B	400	OPT	C56-C57	4.32	1.47	1.38
2	B	400	OPT	C54-C53	4.30	1.47	1.38
2	B	400	OPT	C55-C56	4.30	1.49	1.38
2	A	300	OPT	C56-C57	4.25	1.47	1.38
2	B	400	OPT	C54-C55	4.24	1.48	1.38
2	A	300	OPT	C46-C45	4.15	1.47	1.38
2	A	300	OPT	C55-C56	4.03	1.48	1.38
2	B	400	OPT	C25-C23	3.90	1.47	1.38
2	A	300	OPT	C33-N34	-3.88	1.38	1.47
2	B	400	OPT	C46-C45	3.86	1.47	1.38
2	B	400	OPT	C33-N34	-3.86	1.38	1.47
2	B	400	OPT	C31-C30	3.85	1.62	1.53
2	A	300	OPT	C31-C30	3.84	1.62	1.53
2	A	300	OPT	C25-C23	3.77	1.47	1.38
2	B	400	OPT	C48-C46	3.74	1.45	1.38
2	A	300	OPT	C48-C46	3.61	1.45	1.38
2	A	300	OPT	C49-C50	3.54	1.46	1.38
2	A	300	OPT	C41-N40	-3.47	1.38	1.45
2	B	400	OPT	C49-C50	3.46	1.46	1.38
2	A	300	OPT	C8-C9	3.45	1.45	1.38
2	B	400	OPT	C41-N40	-3.23	1.38	1.45
2	B	400	OPT	C49-C47	3.06	1.44	1.38
2	B	400	OPT	C8-C9	3.06	1.44	1.38
2	A	300	OPT	C49-C47	2.99	1.44	1.38
2	A	300	OPT	C44-C41	2.78	1.60	1.54
2	B	400	OPT	C44-C41	2.58	1.60	1.54
2	A	300	OPT	C30-C38	-2.54	1.45	1.52
2	B	400	OPT	C26-C24	2.49	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	400	OPT	C22-C23	2.48	1.56	1.51
2	A	300	OPT	C27-C28	2.47	1.44	1.38
2	A	300	OPT	C26-C24	2.43	1.43	1.38
2	A	300	OPT	C1-C2	-2.38	1.45	1.51
2	B	400	OPT	C26-C28	2.36	1.44	1.38
2	A	300	OPT	C22-C23	2.35	1.56	1.51
2	B	400	OPT	C27-C28	2.33	1.44	1.38
2	A	300	OPT	C26-C28	2.29	1.43	1.38
2	A	300	OPT	C30-N29	-2.25	1.40	1.45
2	B	400	OPT	C1-C2	-2.21	1.46	1.51
2	B	400	OPT	O19-C18	2.19	1.27	1.23
2	B	400	OPT	C44-C45	2.18	1.56	1.51
2	B	400	OPT	C27-C25	2.17	1.43	1.38
2	A	300	OPT	C27-C25	2.13	1.43	1.38
2	A	300	OPT	C44-C45	2.12	1.56	1.51
2	B	400	OPT	C30-C38	-2.09	1.47	1.52
2	A	300	OPT	O19-C18	2.07	1.27	1.23
2	B	400	OPT	C20-SG2	-2.03	1.77	1.81
2	A	300	OPT	C20-SG2	-2.02	1.77	1.81

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	300	OPT	N37-C35-N36	-7.16	113.33	119.91
2	B	400	OPT	N37-C35-N36	-7.13	113.36	119.91
2	A	300	OPT	C33-N34-C35	6.42	137.25	114.70
2	B	400	OPT	C33-N34-C35	5.84	135.20	114.70
2	A	300	OPT	C23-C22-SG2	5.75	127.65	114.07
2	B	400	OPT	C59-C58-C52	5.65	125.26	112.84
2	A	300	OPT	C59-C58-C52	5.43	124.76	112.84
2	B	400	OPT	C23-C22-SG2	5.33	126.66	114.07
2	A	300	OPT	N36-C35-N34	5.31	125.74	120.31
2	A	300	OPT	C31-C30-C38	-4.91	98.66	110.30
2	A	300	OPT	C20-SG2-C22	4.88	111.26	101.62
2	B	400	OPT	C31-C30-C38	-4.81	98.90	110.30
2	B	400	OPT	N36-C35-N34	4.44	124.86	120.31
2	B	400	OPT	C20-SG2-C22	4.40	110.31	101.62
2	B	400	OPT	O43-C42-N60	4.34	131.81	123.07
2	A	300	OPT	O43-C42-N60	4.27	131.67	123.07
2	B	400	OPT	C18-C17-N16	-4.19	99.52	111.26
2	B	400	OPT	C1-C7-C8	-4.06	114.80	120.88
2	B	400	OPT	C58-C59-N60	-3.82	103.03	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	300	OPT	C18-C17-N16	-3.71	100.87	111.26
2	A	300	OPT	C7-C1-C2	3.68	124.83	112.88
2	B	400	OPT	C32-C33-N34	3.68	125.02	112.08
2	A	300	OPT	C58-C59-N60	-3.61	103.52	112.00
2	A	300	OPT	C59-N60-C42	-3.54	115.60	122.58
2	A	300	OPT	C1-C7-C8	-3.50	115.64	120.88
2	A	300	OPT	C32-C33-N34	3.50	124.39	112.08
2	B	400	OPT	C59-N60-C42	-3.36	115.94	122.58
2	B	400	OPT	C41-C42-N60	-3.27	110.26	116.75
2	B	400	OPT	C20-C17-C18	3.22	116.90	109.64
2	B	400	OPT	C7-C1-C2	3.21	123.30	112.88
2	A	300	OPT	C20-C17-C18	3.12	116.67	109.64
2	A	300	OPT	C41-C42-N60	-3.09	110.62	116.75
2	B	400	OPT	C20-C17-N16	-2.91	103.15	110.94
2	A	300	OPT	O19-C18-C17	2.85	126.57	120.31
2	A	300	OPT	C20-C17-N16	-2.55	104.12	110.94
2	A	300	OPT	C17-C18-N29	-2.48	111.07	116.81
2	B	400	OPT	O19-C18-C17	2.37	125.51	120.31
2	A	300	OPT	O39-C38-C30	-2.27	115.32	120.31
2	B	400	OPT	C9-C4-C12	-2.19	117.55	121.40
2	B	400	OPT	C8-C7-C6	2.17	121.67	118.13
2	A	300	OPT	C32-C31-C30	2.02	120.59	113.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	215/220 (97%)	-0.01	8 (3%)	39 40	18, 27, 40, 57	0
1	B	215/220 (97%)	-0.10	8 (3%)	39 40	18, 28, 42, 56	0
All	All	430/440 (97%)	-0.06	16 (3%)	39 40	18, 28, 41, 57	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	ARG	5.2
1	B	104	TYR	4.8
1	A	101	ASN	4.0
1	A	104	TYR	4.0
1	B	148	GLU	3.3
1	B	103	LYS	3.3
1	A	180	ASN	3.2
1	B	110	THR	3.1
1	A	160	ASP	3.0
1	B	174	SER	3.0
1	A	110	THR	3.0
1	A	174	SER	2.7
1	B	120	LYS	2.5
1	B	206	ARG	2.5
1	B	160	ASP	2.5
1	A	82	GLY	2.1

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

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	CSD	B	25	8/9	0.11	0.15	23,25,28,29	0
1	CSD	A	25	8/9	0.08	-1.42	17,21,24,24	0

### 6.3 Carbohydrates

There are no carbohydrates 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. 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, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	OPT	A	300	60/60	0.19	1.34	19,26,32,35	0
2	OPT	B	400	60/60	0.18	1.12	20,29,40,42	0

### 6.5 Other polymers

There are no such residues in this entry.