



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 12:25 pm GMT

PDB ID : 1THE
Title : CRYSTAL STRUCTURES OF RECOMBINANT RAT CATHEPSIN B
AND A CATHEPSIN B-INHIBITOR COMPLEX: IMPLICATIONS FOR
STRUCTURE-BASED INHIBITOR DESIGN
Authors : Huber, C.P.; Jia, Z.
Deposited on : 1995-09-15
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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

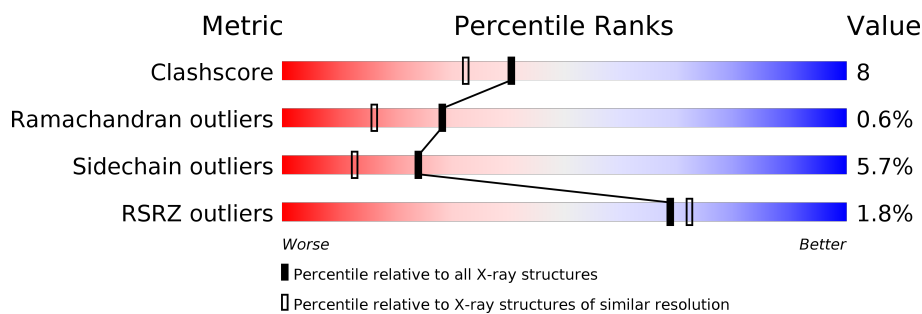
1 Overall quality at a glance

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))
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (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	260	<div> <div>2%</div> <div>78%</div> <div>16%</div> <div>...</div> </div>
1	B	260	<div> <div>%</div> <div>78%</div> <div>16%</div> <div>..</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4170 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.

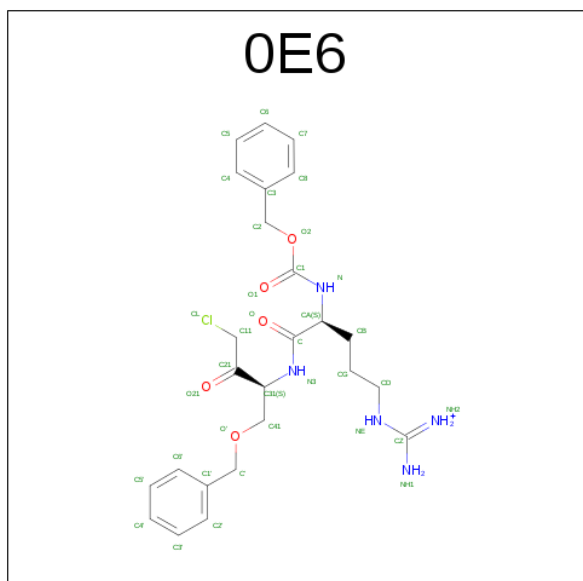
- Molecule 1 is a protein called Cathepsin B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	0	0
			1928	1208	331	371	18			
1	B	253	Total	C	N	O	S	0	0	0
			1934	1210	332	374	18			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	115	ALA	SER	CONFLICT	UNP P00787
A	223	ALA	VAL	SEE REMARK 999	UNP P00787
B	115	ALA	SER	CONFLICT	UNP P00787
B	223	ALA	VAL	SEE REMARK 999	UNP P00787

- Molecule 2 is AMINO{[(4S)-4-{[(BENZYLOXY)CARBONYL]AMINO}-5-{[(2S)-1-(BENZYLOXY)-4-CHLORO-3-OXOBUTAN-2-YL]AMINO}-5-OXOPENTYL]AMINO}METHANIMINIUM (three-letter code: 0E6) (formula: C₂₅H₃₃ClN₅O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			35	25	5	5		
2	B	1	Total	C	N	O	0	0
			35	25	5	5		

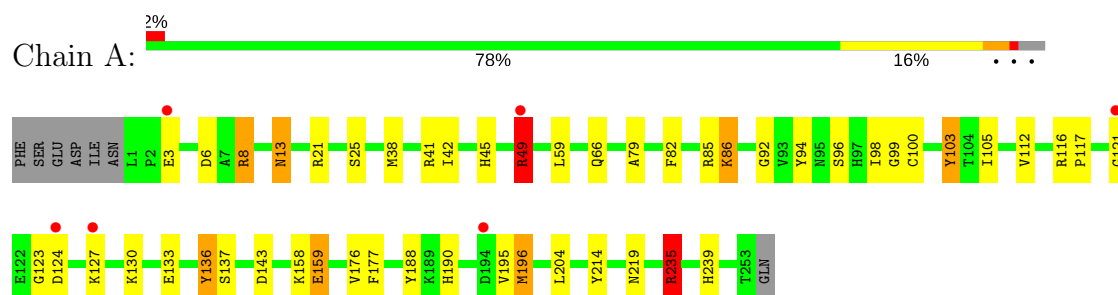
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	133	Total	O	0	0
			133	133		
3	B	105	Total	O	0	0
			105	105		

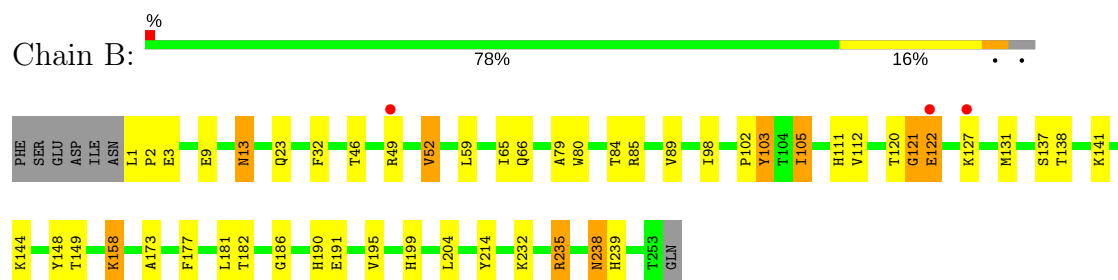
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Cathepsin B



• Molecule 1: Cathepsin B



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	47.11Å 90.15Å 62.31Å 90.00° 97.24° 90.00°	Depositor
Resolution (Å)	8.00 – 1.90 7.99 – 1.90	Depositor EDS
% Data completeness (in resolution range)	96.3 (8.00-1.90) 94.2 (7.99-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	X-PLOR 3.0	Depositor
R, R_{free}	0.170 , (Not available) 0.180 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	11.5	Xtriage
Anisotropy	0.583	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 88.5	EDS
L-test for twinning ¹	$\langle L \rangle = 0.36$, $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4170	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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: 0E6

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	0.90	1/1983 (0.1%)	0.86	6/2693 (0.2%)
1	B	0.91	3/1989 (0.2%)	0.84	2/2701 (0.1%)
All	All	0.90	4/3972 (0.1%)	0.85	8/5394 (0.1%)

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	7
1	B	0	6
All	All	0	13

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	122	GLU	CD-OE2	10.03	1.36	1.25
1	B	85	ARG	CZ-NH1	8.97	1.44	1.33
1	A	159	GLU	CB-CG	-5.39	1.42	1.52
1	B	127	LYS	CB-CG	-5.18	1.38	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	235	ARG	NE-CZ-NH2	-8.94	115.83	120.30
1	B	235	ARG	NE-CZ-NH2	-8.59	116.00	120.30
1	B	235	ARG	NE-CZ-NH1	6.19	123.39	120.30
1	A	159	GLU	OE1-CD-OE2	-5.71	116.45	123.30
1	A	235	ARG	NE-CZ-NH1	5.63	123.11	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3	GLU	OE1-CD-OE2	-5.49	116.72	123.30
1	A	124	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	49	ARG	NE-CZ-NH2	-5.00	117.80	120.30

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	103	TYR	Sidechain
1	A	136	TYR	Sidechain
1	A	21	ARG	Sidechain
1	A	219	ASN	Mainchain
1	A	235	ARG	Sidechain
1	A	41	ARG	Sidechain
1	A	85	ARG	Sidechain
1	B	103	TYR	Sidechain
1	B	105	ILE	Mainchain
1	B	173	ALA	Mainchain
1	B	214	TYR	Sidechain
1	B	235	ARG	Sidechain
1	B	52	VAL	Mainchain

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	1928	0	1776	34	0
1	B	1934	0	1782	27	0
2	A	35	0	31	0	0
2	B	35	0	31	2	0
3	A	133	0	0	3	0
3	B	105	0	0	2	0
All	All	4170	0	3620	62	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 8.

All (62) 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:13:ASN:H	1:B:13:ASN:HD22	1.18	0.88
1:A:49:ARG:CG	1:A:49:ARG:HH11	1.89	0.85
1:B:190:HIS:H	1:B:239:HIS:HE1	1.27	0.82
1:B:158:LYS:HE3	1:B:158:LYS:H	1.44	0.82
1:A:49:ARG:HG2	1:A:49:ARG:HH11	1.45	0.82
1:A:13:ASN:H	1:A:13:ASN:HD22	1.29	0.80
1:A:49:ARG:CB	1:A:49:ARG:HH11	1.94	0.80
1:A:190:HIS:H	1:A:239:HIS:HE1	1.30	0.78
1:B:13:ASN:H	1:B:13:ASN:ND2	1.81	0.77
1:A:49:ARG:CB	1:A:49:ARG:NH1	2.48	0.76
1:A:190:HIS:H	1:A:239:HIS:CE1	2.03	0.76
1:A:158:LYS:HG3	1:A:159:GLU:N	2.01	0.75
1:A:13:ASN:ND2	1:A:13:ASN:H	1.87	0.72
1:A:25:SER:HB3	1:A:121:GLY:O	1.90	0.72
1:A:177:PHE:CE1	1:A:195:VAL:HG22	2.25	0.71
1:B:190:HIS:H	1:B:239:HIS:CE1	2.10	0.69
1:B:98:ILE:O	1:B:102:PRO:HG3	1.98	0.64
1:A:49:ARG:HB3	1:A:49:ARG:HH11	1.68	0.59
1:A:96:SER:OG	1:A:98:ILE:HG22	2.03	0.57
1:A:49:ARG:NH1	1:A:49:ARG:HB2	2.20	0.56
1:A:158:LYS:HG3	1:A:159:GLU:H	1.70	0.56
1:B:148:TYR:CD2	1:B:149:THR:HG23	2.41	0.55
1:B:13:ASN:ND2	1:B:13:ASN:N	2.54	0.55
1:B:59:LEU:HD21	1:B:79:ALA:HB1	1.89	0.53
1:B:141:LYS:HE2	3:B:664:HOH:O	2.09	0.53
1:A:188:TYR:OH	1:A:190:HIS:HB2	2.09	0.52
1:A:38:MET:O	1:A:42:ILE:HG13	2.10	0.52
1:A:42:ILE:HD11	3:A:814:HOH:O	2.11	0.51
1:A:92:GLY:HA3	1:A:98:ILE:CG2	2.42	0.50
1:A:100:CYS:HB2	1:A:143:ASP:OD2	2.11	0.50
1:B:65:ILE:HD12	1:B:66:GLN:H	1.77	0.50
1:B:89:VAL:HG13	1:B:144:LYS:HD3	1.93	0.49
1:B:121:GLY:O	1:B:122:GLU:HG3	2.13	0.49
1:A:177:PHE:HE1	1:A:195:VAL:HG22	1.77	0.49
1:B:199:HIS:HB2	2:B:911:OE6:H3'	1.96	0.48
1:A:49:ARG:CZ	1:A:49:ARG:HB2	2.44	0.47
1:A:6:ASP:OD1	1:A:8:ARG:HB2	2.14	0.47
1:B:177:PHE:CE2	1:B:195:VAL:HG22	2.50	0.47
1:A:59:LEU:HD21	1:A:79:ALA:HB1	1.97	0.47
1:A:133:GLU:OE1	3:A:824:HOH:O	2.21	0.46
2:B:911:OE6:N	2:B:911:OE6:HD2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:GLN:HA	1:B:32:PHE:CZ	2.50	0.46
1:A:92:GLY:HA3	1:A:98:ILE:HG22	1.96	0.46
1:A:99:GLY:HA2	1:A:136:TYR:CE1	2.52	0.45
1:B:186:GLY:O	1:B:232:LYS:HB2	2.17	0.45
1:A:49:ARG:HB3	1:A:49:ARG:NH1	2.27	0.45
1:B:1:LEU:HD23	1:B:2:PRO:HD2	1.99	0.45
1:B:182:THR:HA	3:B:703:HOH:O	2.17	0.44
1:B:65:ILE:HD12	1:B:66:GLN:N	2.31	0.44
1:A:214:TYR:O	1:A:235:ARG:HD3	2.18	0.44
1:B:238:ASN:HA	1:B:238:ASN:HD22	1.55	0.44
1:A:45:HIS:HD2	3:A:813:HOH:O	2.01	0.43
1:B:111:HIS:CD2	1:B:181:LEU:HD22	2.54	0.43
1:B:103:TYR:CE2	1:B:105:ILE:HB	2.54	0.42
1:B:80:TRP:O	1:B:84:THR:HG23	2.19	0.42
1:A:82:PHE:CE1	1:A:86:LYS:HG3	2.54	0.41
1:A:176:VAL:HG12	1:A:196:MET:HG3	2.01	0.41
1:B:89:VAL:CG1	1:B:144:LYS:HD3	2.50	0.41
1:B:46:THR:O	1:B:49:ARG:HG3	2.20	0.41
1:A:103:TYR:CE2	1:A:105:ILE:HB	2.56	0.41
1:B:120:THR:O	1:B:121:GLY:C	2.59	0.40
1:A:116:ARG:HB3	1:A:117:PRO:HD2	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	251/260 (96%)	232 (92%)	17 (7%)	2 (1%)	22	11
1	B	251/260 (96%)	233 (93%)	17 (7%)	1 (0%)	38	26
All	All	502/520 (96%)	465 (93%)	34 (7%)	3 (1%)	28	16

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	121	GLY
1	A	94	TYR
1	A	123	GLY

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	202/211 (96%)	191 (95%)	11 (5%)	26	14
1	B	204/211 (97%)	192 (94%)	12 (6%)	23	12
All	All	406/422 (96%)	383 (94%)	23 (6%)	24	13

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG
1	A	13	ASN
1	A	49	ARG
1	A	66	GLN
1	A	86	LYS
1	A	112	VAL
1	A	127	LYS
1	A	130	LYS
1	A	137	SER
1	A	196	MET
1	A	204	LEU
1	B	3	GLU
1	B	9	GLU
1	B	13	ASN
1	B	52	VAL
1	B	112	VAL
1	B	131	MET
1	B	137	SER
1	B	138	THR
1	B	158	LYS

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Mol	Chain	Res	Type
1	B	191	GLU
1	B	204	LEU
1	B	238	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	19	GLN
1	A	238	ASN
1	A	239	HIS
1	B	13	ASN
1	B	19	GLN
1	B	111	HIS
1	B	238	ASN
1	B	239	HIS

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 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	0E6	A	901	1	35,36,37	1.24	1 (2%)	41,45,46	0.95	2 (4%)
2	0E6	B	911	1	35,36,37	1.32	1 (2%)	41,45,46	0.94	2 (4%)

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	0E6	A	901	1	-	0/34/34/36	0/2/2/2
2	0E6	B	911	1	-	0/34/34/36	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	0E6	O2-C1	6.47	1.47	1.35
2	B	911	0E6	O2-C1	6.87	1.48	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	911	0E6	O'-C'-C1'	-2.53	102.77	110.83
2	A	901	0E6	C'-O'-C41	-2.14	107.78	112.75
2	A	901	0E6	O2-C1-N	2.72	116.39	110.54
2	B	911	0E6	O2-C1-N	3.21	117.44	110.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	911	0E6	2	0

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 [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	253/260 (97%)	-0.54	6 (2%) 59 63	2, 14, 42, 73	0
1	B	253/260 (97%)	-0.58	3 (1%) 79 82	3, 15, 44, 73	0
All	All	506/520 (97%)	-0.56	9 (1%) 69 72	2, 14, 42, 73	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	124	ASP	5.4
1	B	49	ARG	5.1
1	A	49	ARG	4.1
1	B	122	GLU	3.7
1	A	3	GLU	3.6
1	A	127	LYS	3.6
1	A	121	GLY	3.1
1	A	194	ASP	2.9
1	B	127	LYS	2.5

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 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
2	0E6	A	901	35/36	0.95	0.09	1.21	2,12,33,81	0
2	0E6	B	911	35/36	0.96	0.08	0.04	2,15,39,50	0

6.5 Other polymers

There are no such residues in this entry.