



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2018 – 03:15 am GMT

PDB ID : 5CXC  
Title : Structure of Ytm1 bound to the C-terminal domain of Erb1 in P 65 2 2 space group  
Authors : Wegrecki, M.; Bravo, J.  
Deposited on : 2015-07-28  
Resolution : 3.10 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](mailto: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.

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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  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

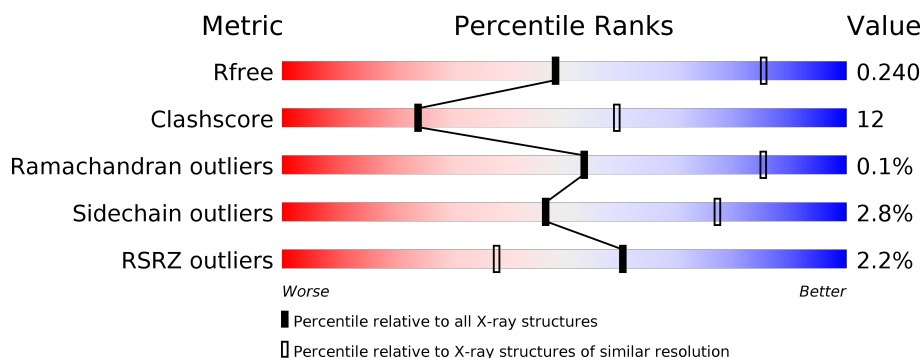
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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))
$R_{free}$	111664	1115 (3.12-3.08)
Clashscore	122126	1042 (3.10-3.10)
Ramachandran outliers	120053	1010 (3.10-3.10)
Sidechain outliers	120020	1010 (3.10-3.10)
RSRZ outliers	108989	1089 (3.12-3.08)

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. 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	510	<div> <div>2%</div> <div> <div></div> <div>67%</div> <div>20%</div> <div>• 11%</div> </div> </div>
2	B	369	<div> <div>2%</div> <div> <div></div> <div>69%</div> <div>23%</div> <div>• • 6%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6170 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 Ribosome biogenesis protein YTM1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	0	0
			3418	2139	598	675	6			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	initiating methionine	UNP G0SFB5
A	-13	ALA	-	expression tag	UNP G0SFB5
A	-12	HIS	-	expression tag	UNP G0SFB5
A	-11	HIS	-	expression tag	UNP G0SFB5
A	-10	HIS	-	expression tag	UNP G0SFB5
A	-9	HIS	-	expression tag	UNP G0SFB5
A	-8	HIS	-	expression tag	UNP G0SFB5
A	-7	HIS	-	expression tag	UNP G0SFB5
A	-6	SER	-	expression tag	UNP G0SFB5
A	-5	SER	-	expression tag	UNP G0SFB5
A	-4	GLY	-	expression tag	UNP G0SFB5
A	-3	LEU	-	expression tag	UNP G0SFB5
A	-2	GLU	-	expression tag	UNP G0SFB5
A	-1	VAL	-	expression tag	UNP G0SFB5
A	0	LEU	-	expression tag	UNP G0SFB5

- Molecule 2 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	348	Total	C	N	O	S	0	1	0
			2750	1754	505	485	6			

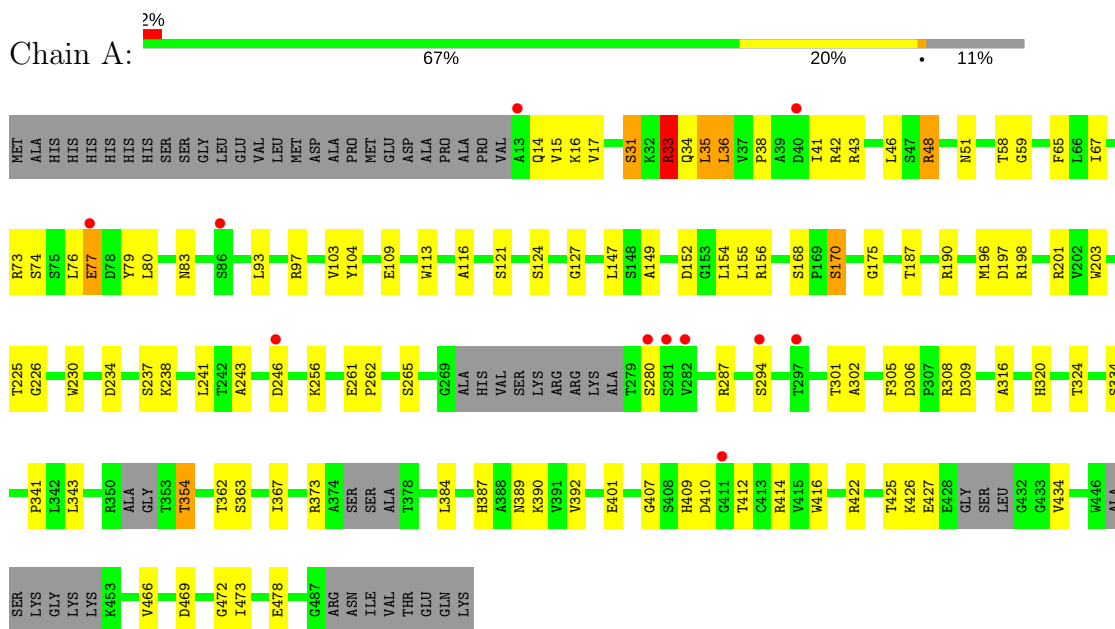
- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Cl 1	0	0
3	A	1	Total 1	Cl 1	0	0

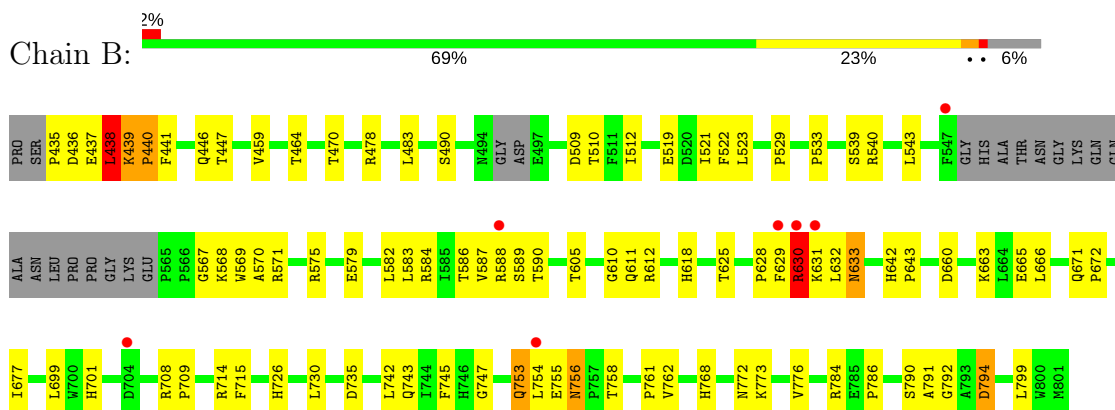
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Ribosome biogenesis protein YTM1



#### • Molecule 2: Ribosome biogenesis protein ERB1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	169.11Å 169.11Å 154.04Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.82 – 3.10 48.82 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.82-3.10) 100.0 (48.82-3.10)	Depositor EDS
$R_{merge}$	0.28	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.10 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.194 , 0.239 0.197 , 0.240	Depositor DCC
$R_{free}$ test set	1237 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	97.2	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 85.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6170	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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:  
CL

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	0.29	0/3490	0.59	2/4753 (0.0%)
2	B	0.33	0/2823	0.64	2/3837 (0.1%)
All	All	0.31	0/6313	0.61	4/8590 (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	2
2	B	0	7
All	All	0	9

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	438	LEU	N-CA-C	-8.98	86.76	111.00
1	A	33	ARG	CG-CD-NE	6.32	125.07	111.80
2	B	630	ARG	CB-CA-C	5.32	121.04	110.40
1	A	33	ARG	NE-CZ-NH1	-5.04	117.78	120.30

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	170	SER	Peptide
1	A	33	ARG	Peptide

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Mol	Chain	Res	Type	Group
2	B	436	ASP	Peptide
2	B	437	GLU	Peptide
2	B	438	LEU	Peptide
2	B	439	LYS	Peptide
2	B	440	PRO	Peptide
2	B	630	ARG	Peptide
2	B	753	GLN	Peptide

## 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	A	3418	0	3363	75	0
2	B	2750	0	2763	76	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
All	All	6170	0	6126	146	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 (146) 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)
2:B:756:ASN:N	2:B:756:ASN:HD22	1.68	0.92
2:B:756:ASN:H	2:B:756:ASN:HD22	1.18	0.90
2:B:612:ARG:HG3	2:B:630:ARG:HG3	1.57	0.84
1:A:77:GLU:HA	1:A:80:LEU:HG	1.59	0.82
2:B:612:ARG:CG	2:B:630:ARG:HG3	2.10	0.82
2:B:672:PRO:HG3	2:B:677:ILE:HD11	1.62	0.81
1:A:31:SER:HA	1:A:33:ARG:HD2	1.66	0.77
2:B:631:LYS:NZ	2:B:665:GLU:OE2	2.19	0.76
1:A:230:TRP:HB3	1:A:243:ALA:HB3	1.75	0.69
2:B:660:ASP:OD2	2:B:663:LYS:NZ	2.28	0.67
2:B:756:ASN:ND2	2:B:756:ASN:N	2.42	0.67
2:B:459:VAL:HG13	2:B:791:ALA:HB2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:THR:HG23	1:A:190:ARG:H	1.60	0.65
2:B:540:ARG:HG2	2:B:582:LEU:HD11	1.78	0.64
2:B:459:VAL:HG12	2:B:470:THR:HG22	1.80	0.64
2:B:569:TRP:HE1	2:B:625:THR:HG23	1.63	0.64
2:B:768:HIS:ND1	2:B:794:ASP:OD2	2.31	0.63
2:B:708:ARG:HG2	2:B:709:PRO:HD2	1.80	0.62
2:B:612:ARG:HH12	2:B:632:LEU:HB2	1.63	0.62
2:B:523:LEU:HB2	2:B:583:LEU:HB2	1.81	0.61
1:A:308:ARG:NH1	1:A:354:THR:HA	2.16	0.60
2:B:519:GLU:OE2	2:B:589:SER:N	2.34	0.60
1:A:67:ILE:HG12	1:A:93:LEU:HD22	1.83	0.60
2:B:510:THR:O	2:B:539:SER:OG	2.19	0.60
1:A:42:ARG:NH2	1:A:73:ARG:O	2.35	0.59
2:B:612:ARG:NH1	2:B:632:LEU:HB2	2.18	0.59
1:A:197:ASP:OD2	1:A:201:ARG:NH1	2.35	0.58
2:B:438:LEU:O	2:B:439:LYS:HB2	2.03	0.58
2:B:753:GLN:NE2	2:B:754:LEU:H	2.02	0.58
2:B:612:ARG:HD2	2:B:630:ARG:O	2.04	0.57
1:A:426:LYS:HB2	1:A:427:GLU:OE1	2.05	0.57
1:A:116:ALA:HB3	1:A:149:ALA:HB3	1.87	0.56
1:A:109:GLU:OE1	1:A:109:GLU:N	2.38	0.56
1:A:51:ASN:HB3	1:A:59:GLY:HA2	1.87	0.56
1:A:76:LEU:O	1:A:79:TYR:HB3	2.05	0.56
1:A:73:ARG:O	1:A:73:ARG:HG3	2.06	0.56
2:B:464:THR:O	2:B:784:ARG:NH2	2.39	0.56
2:B:772:ASN:C	2:B:773:LYS:HG3	2.26	0.55
2:B:753:GLN:CD	2:B:754:LEU:H	2.10	0.55
1:A:103:VAL:HG22	1:A:104:TYR:H	1.72	0.54
1:A:152:ASP:HB3	1:A:154:LEU:HD23	1.89	0.54
2:B:671:GLN:O	2:B:708:ARG:HG3	2.07	0.54
1:A:425:THR:OG1	1:A:426:LYS:N	2.40	0.54
2:B:612:ARG:HG2	2:B:630:ARG:HG3	1.90	0.54
2:B:633[A]:ASN:N	2:B:633[A]:ASN:OD1	2.29	0.54
2:B:756:ASN:H	2:B:756:ASN:ND2	1.96	0.54
1:A:367:ILE:HB	1:A:384:LEU:HB2	1.90	0.54
1:A:196:MET:HB3	2:B:529:PRO:HG3	1.90	0.53
1:A:152:ASP:OD2	1:A:156:ARG:NH2	2.40	0.53
1:A:36:LEU:HD21	1:A:41:ILE:HG12	1.90	0.53
1:A:234:ASP:OD2	1:A:237:SER:HB3	2.09	0.52
2:B:519:GLU:HG2	2:B:590:THR:HA	1.90	0.52
1:A:390:LYS:HE2	2:B:446:GLN:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:447:THR:HB	2:B:799:LEU:HB3	1.92	0.52
2:B:629:PHE:C	2:B:631:LYS:HG2	2.30	0.52
1:A:262:PRO:HD3	1:A:287:ARG:HA	1.93	0.50
2:B:618:HIS:ND1	2:B:625:THR:HG22	2.27	0.50
1:A:427:GLU:N	1:A:427:GLU:OE1	2.45	0.50
2:B:543:LEU:HD12	2:B:582:LEU:HD12	1.94	0.50
2:B:742:LEU:HD21	2:B:790:SER:HB3	1.94	0.49
1:A:387:HIS:HA	1:A:414:ARG:NH1	2.27	0.49
1:A:401:GLU:OE1	1:A:401:GLU:N	2.31	0.49
1:A:389:ASN:HB2	1:A:410:ASP:HB3	1.93	0.49
1:A:147:LEU:HD11	1:A:155:LEU:HD23	1.94	0.49
1:A:225:THR:O	1:A:246:ASP:HB3	2.12	0.49
2:B:435:PRO:HB2	2:B:438:LEU:HG	1.94	0.49
2:B:665:GLU:HG3	2:B:666:LEU:H	1.78	0.49
2:B:735:ASP:OD1	2:B:743:GLN:HB3	2.12	0.49
1:A:175:GLY:HA2	1:A:203:TRP:HH2	1.78	0.49
2:B:611:GLN:CD	2:B:612:ARG:H	2.16	0.49
1:A:51:ASN:OD1	1:A:58:THR:OG1	2.31	0.48
2:B:567:GLY:HA3	2:B:625:THR:HG21	1.94	0.48
1:A:302:ALA:HB3	1:A:316:ALA:HB3	1.95	0.48
2:B:521:ILE:HD13	2:B:605:THR:HG21	1.95	0.48
1:A:113:TRP:CE2	1:A:478:GLU:HG3	2.48	0.48
1:A:256:LYS:O	1:A:287:ARG:NH1	2.41	0.48
2:B:569:TRP:NE1	2:B:625:THR:HG23	2.29	0.48
1:A:265:SER:O	2:B:533:PRO:HG2	2.13	0.47
2:B:628:PRO:HG2	2:B:629:PHE:CE2	2.48	0.47
1:A:31:SER:O	1:A:31:SER:OG	2.29	0.47
1:A:390:LYS:NZ	2:B:483:LEU:O	2.47	0.47
1:A:422:ARG:O	1:A:434:VAL:N	2.44	0.47
2:B:726:HIS:HE1	2:B:730:LEU:HD12	1.79	0.47
1:A:306:ASP:HB3	1:A:309:ASP:O	2.14	0.47
1:A:392:VAL:HG21	1:A:409:HIS:NE2	2.30	0.47
2:B:715:PHE:CZ	2:B:761:PRO:HG3	2.50	0.47
2:B:568:LYS:HE3	2:B:570:ALA:HB2	1.96	0.46
1:A:46:LEU:HB3	1:A:65:PHE:CZ	2.50	0.46
2:B:510:THR:HB	2:B:512:ILE:HG13	1.96	0.46
2:B:612:ARG:HD3	2:B:612:ARG:HA	1.70	0.46
1:A:31:SER:HA	1:A:33:ARG:CD	2.43	0.46
1:A:79:TYR:O	1:A:83:ASN:ND2	2.47	0.46
1:A:198:ARG:HG2	1:A:226:GLY:O	2.16	0.45
1:A:341:PRO:HG2	1:A:363:SER:OG	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:389:ASN:HA	2:B:446:GLN:HE22	1.82	0.45
2:B:726:HIS:ND1	2:B:730:LEU:HB2	2.32	0.45
2:B:435:PRO:HG3	2:B:441:PHE:HE1	1.80	0.45
1:A:261:GLU:HG3	1:A:262:PRO:HD2	1.97	0.45
1:A:308:ARG:HH12	1:A:354:THR:HA	1.81	0.45
2:B:747:GLY:HA2	2:B:758:THR:O	2.16	0.45
1:A:121:SER:O	1:A:127:GLY:HA3	2.18	0.44
1:A:412:THR:HG21	1:A:414:ARG:NH1	2.33	0.44
1:A:301:THR:HG21	1:A:343:LEU:HA	1.99	0.44
1:A:16:LYS:HA	1:A:35:LEU:HA	1.99	0.44
2:B:589:SER:CB	2:B:610:GLY:HA2	2.47	0.44
1:A:410:ASP:OD1	1:A:412:THR:HG22	2.18	0.43
1:A:97:ARG:HE	1:A:97:ARG:HB2	1.48	0.43
2:B:478:ARG:HG2	2:B:490:SER:HB3	2.00	0.43
1:A:41:ILE:HG13	1:A:46:LEU:HD12	2.00	0.43
1:A:17:VAL:HG23	1:A:93:LEU:HG	2.00	0.43
2:B:519:GLU:OE2	2:B:587:VAL:HG23	2.18	0.43
2:B:726:HIS:CE1	2:B:730:LEU:HD12	2.53	0.43
2:B:440:PRO:CB	2:B:786:PRO:HG3	2.49	0.43
2:B:642:HIS:HA	2:B:643:PRO:HD3	1.90	0.43
2:B:745:PHE:HA	2:B:761:PRO:HA	2.01	0.43
2:B:755:GLU:N	2:B:755:GLU:OE2	2.51	0.43
1:A:407:GLY:HA3	1:A:466:VAL:HG21	2.01	0.43
1:A:38:PRO:HA	1:A:41:ILE:HG21	2.00	0.43
1:A:384:LEU:HB3	1:A:416:TRP:CE3	2.54	0.43
2:B:776:VAL:HA	2:B:792:GLY:HA2	2.01	0.42
1:A:308:ARG:CZ	1:A:354:THR:HA	2.49	0.42
1:A:15:VAL:H	1:A:38:PRO:HD3	1.84	0.42
1:A:320:HIS:CE1	1:A:341:PRO:HD3	2.55	0.42
2:B:567:GLY:HA2	2:B:586:THR:O	2.20	0.42
1:A:155:LEU:HB2	1:A:168:SER:HB3	2.02	0.42
1:A:343:LEU:HD12	1:A:390:LYS:HB3	2.02	0.42
2:B:438:LEU:HD12	2:B:762:VAL:HG12	2.01	0.42
2:B:794:ASP:OD1	2:B:794:ASP:N	2.52	0.42
1:A:237:SER:C	1:A:238:LYS:HG3	2.40	0.42
2:B:665:GLU:HG3	2:B:666:LEU:N	2.34	0.42
1:A:121:SER:HB3	1:A:124:SER:HB3	2.01	0.42
1:A:324:THR:HB	1:A:334:SER:HB3	2.02	0.41
2:B:575:ARG:O	2:B:579:GLU:HG2	2.20	0.41
2:B:714:ARG:HG3	2:B:714:ARG:O	2.20	0.41
1:A:469:ASP:O	1:A:472:GLY:HA2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:672:PRO:HA	2:B:701:HIS:NE2	2.34	0.41
1:A:33:ARG:H	1:A:33:ARG:HG3	1.25	0.41
1:A:48:ARG:HA	1:A:48:ARG:HD3	1.65	0.41
1:A:14:GLN:HA	1:A:38:PRO:HD2	2.02	0.41
2:B:612:ARG:CZ	2:B:632:LEU:H	2.34	0.41
2:B:571:ARG:HG2	2:B:571:ARG:H	1.72	0.41
1:A:241:LEU:HG	1:A:305:PHE:CE2	2.55	0.40
1:A:42:ARG:NH2	1:A:74:SER:HA	2.37	0.40
2:B:631:LYS:HB2	2:B:631:LYS:HE3	1.93	0.40
2:B:522:PHE:CE1	2:B:584:ARG:HD3	2.57	0.40
1:A:31:SER:O	1:A:34:GLN:NE2	2.42	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	440/510 (86%)	417 (95%)	22 (5%)	1 (0%)	49	81
2	B	343/369 (93%)	322 (94%)	21 (6%)	0	100	100
All	All	783/879 (89%)	739 (94%)	43 (6%)	1 (0%)	53	85

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	473	ILE

### 5.3.2 Protein sidechains [i](#)

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	378/423 (89%)	365 (97%)	13 (3%)	40	73
2	B	296/310 (96%)	289 (98%)	7 (2%)	52	80
All	All	674/733 (92%)	654 (97%)	20 (3%)	47	75

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	SER
1	A	33	ARG
1	A	35	LEU
1	A	36	LEU
1	A	43	ARG
1	A	48	ARG
1	A	77	GLU
1	A	170	SER
1	A	280	SER
1	A	294	SER
1	A	354	THR
1	A	362	THR
1	A	373	ARG
2	B	509	ASP
2	B	588	ARG
2	B	633[A]	ASN
2	B	633[B]	ASN
2	B	699	LEU
2	B	756	ASN
2	B	794	ASP

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

Mol	Chain	Res	Type
2	B	446	GLN
2	B	753	GLN
2	B	756	ASN

### 5.3.3 RNA ⓘ

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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, 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	452/510 (88%)	0.18	11 (2%) 59 36	64, 93, 158, 182	2 (0%)
2	B	348/369 (94%)	0.23	7 (2%) 65 43	65, 98, 143, 195	4 (1%)
All	All	800/879 (91%)	0.20	18 (2%) 60 38	64, 95, 154, 195	6 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	13	ALA	3.3
2	B	704	ASP	3.2
1	A	294	SER	3.1
1	A	40	ASP	2.8
1	A	280	SER	2.7
1	A	297	THR	2.7
1	A	281	SER	2.6
1	A	77	GLU	2.6
2	B	754	LEU	2.4
2	B	629	PHE	2.3
2	B	547	PHE	2.3
1	A	246	ASP	2.2
1	A	86	SER	2.2
1	A	411	GLY	2.2
1	A	282	VAL	2.1
2	B	631	LYS	2.1
2	B	588	ARG	2.1
2	B	630	ARG	2.1

### 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. 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	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CL	A	501	1/1	0.89	0.13	98,98,98,98	0
3	CL	B	901	1/1	0.95	0.28	93,93,93,93	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.