



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 01:15 PM GMT

PDB ID : 2D1I
Title : Structure of human Atg4b
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Deposited on : 2005-08-24
Resolution : 2.00 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

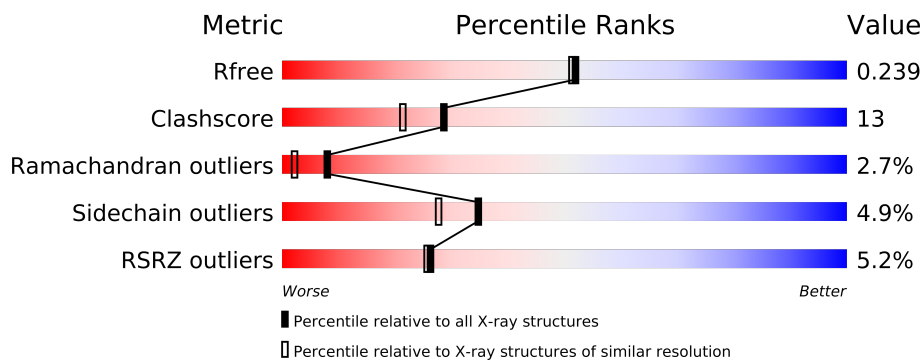
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.00 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	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (2.00-2.00)

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. 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	398	
1	B	398	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5724 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 Cysteine protease APG4B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	0	0
			2693	1725	453	494	21			
1	B	339	Total	C	N	O	S	0	0	0
			2693	1725	453	494	21			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	CLONING ARTIFACT	UNP Q9Y4P1
A	-3	PRO	-	CLONING ARTIFACT	UNP Q9Y4P1
A	-2	LEU	-	CLONING ARTIFACT	UNP Q9Y4P1
A	-1	GLY	-	CLONING ARTIFACT	UNP Q9Y4P1
A	0	SER	-	CLONING ARTIFACT	UNP Q9Y4P1
B	-4	GLY	-	CLONING ARTIFACT	UNP Q9Y4P1
B	-3	PRO	-	CLONING ARTIFACT	UNP Q9Y4P1
B	-2	LEU	-	CLONING ARTIFACT	UNP Q9Y4P1
B	-1	GLY	-	CLONING ARTIFACT	UNP Q9Y4P1
B	0	SER	-	CLONING ARTIFACT	UNP Q9Y4P1

- Molecule 2 is water.

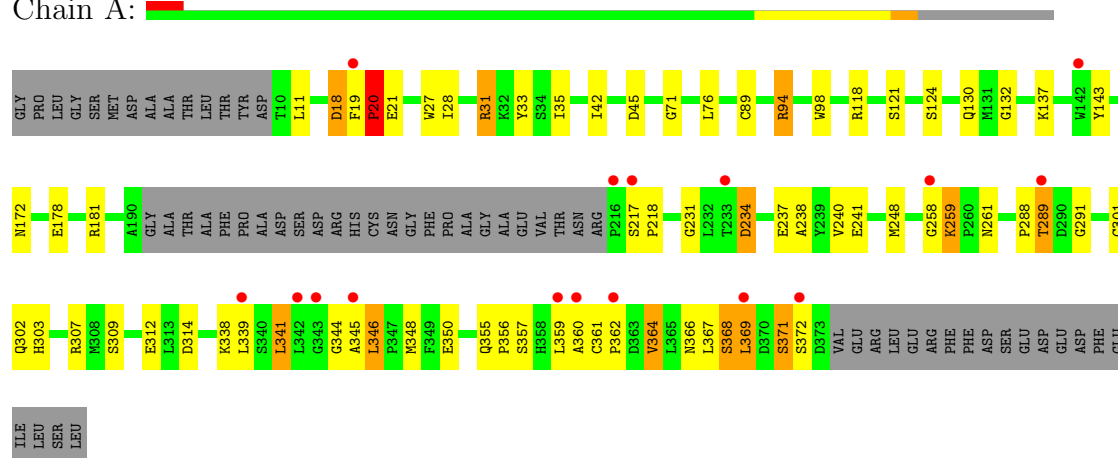
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	171	Total	O	0	0
			171	171		
2	B	167	Total	O	0	0
			167	167		

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.

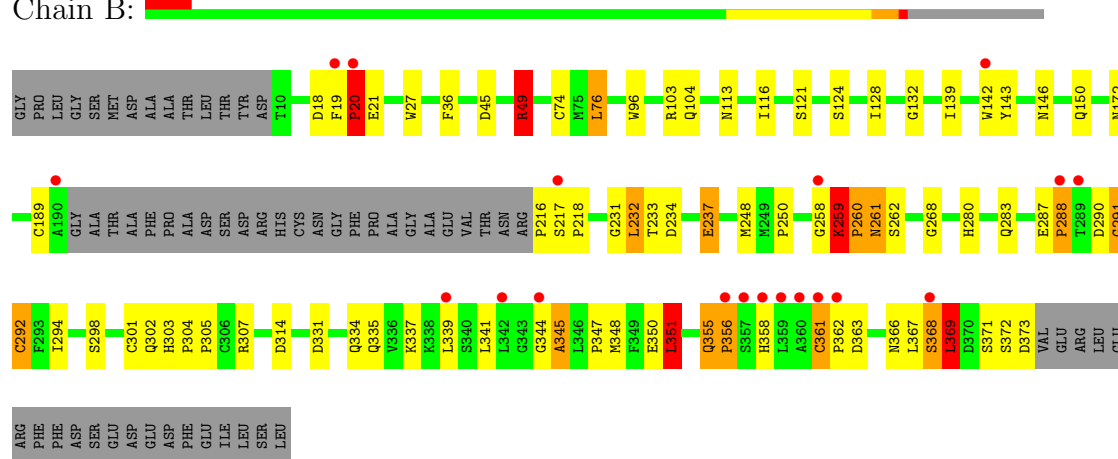
• Molecule 1: Cysteine protease APG4B

Chain A:



• Molecule 1: Cysteine protease APG4B

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.28Å 161.32Å 51.27Å 90.00° 119.58° 90.00°	Depositor
Resolution (Å)	44.59 – 2.00 44.59 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (44.59-2.00) 98.6 (44.59-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.08 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.220 , 0.283 0.204 , 0.239	Depositor DCC
R_{free} test set	2435 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.9	EDS
Estimated twinning fraction	0.015 for l,k,-h-l 0.015 for -h-l,k,h 0.017 for -h-l,-k,l 0.017 for h,-k,-h-l 0.487 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 48760 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5724	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	0.53	0/2769	0.69	2/3764 (0.1%)
1	B	0.52	0/2769	0.70	5/3764 (0.1%)
All	All	0.53	0/5538	0.69	7/7528 (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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	ARG	NE-CZ-NH2	-6.88	116.86	120.30
1	B	49	ARG	NE-CZ-NH2	-6.02	117.29	120.30
1	B	369	LEU	CA-CB-CG	5.95	128.99	115.30
1	B	49	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	B	339	LEU	CA-CB-CG	5.59	128.15	115.30
1	A	369	LEU	CA-CB-CG	5.56	128.08	115.30
1	B	351	LEU	CA-CB-CG	5.13	127.10	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	20	PRO	Peptide
1	B	20	PRO	Peptide

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	2693	0	2622	73	0
1	B	2693	0	2622	60	0
2	A	171	0	0	7	0
2	B	167	0	0	4	0
All	All	5724	0	5244	133	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 13.

All (133) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:31:ARG:NH2	1:A:94:ARG:HD2	1.53	1.23
1:A:20:PRO:HB3	1:A:35:ILE:HG12	1.24	1.19
1:A:31:ARG:HH21	1:A:94:ARG:CD	1.65	1.09
1:A:31:ARG:HH21	1:A:94:ARG:HD2	0.93	1.05
1:B:258:GLY:HA2	1:B:259:LYS:HB2	1.31	1.04
1:A:367:LEU:HA	1:A:368:SER:HB2	1.42	0.97
1:A:31:ARG:CZ	2:A:514:HOH:O	2.13	0.95
1:B:344:GLY:HA2	1:B:345:ALA:HB3	1.54	0.88
1:A:258:GLY:HA2	1:A:259:LYS:HB2	1.55	0.88
1:A:20:PRO:HB3	1:A:35:ILE:CG1	2.06	0.85
1:B:367:LEU:HA	1:B:368:SER:HB2	1.59	0.84
1:A:258:GLY:HA2	1:A:259:LYS:CB	2.08	0.82
1:A:118:ARG:HE	1:A:288:PRO:HG3	1.44	0.81
1:B:262:SER:HB2	1:B:280:HIS:CE1	2.21	0.76
1:A:367:LEU:HA	1:A:368:SER:CB	2.16	0.75
1:B:18:ASP:HB3	1:B:19:PHE:C	2.05	0.75
1:A:130:GLN:HG3	2:A:440:HOH:O	1.88	0.74
1:A:31:ARG:NH2	1:A:94:ARG:CD	2.33	0.74
1:A:132:GLY:HA3	1:A:143:TYR:OH	1.90	0.72
1:B:258:GLY:CA	1:B:259:LYS:HB2	2.14	0.71
1:A:20:PRO:HB2	1:A:21:GLU:HA	1.72	0.71
1:A:20:PRO:HB2	1:A:21:GLU:HG2	1.72	0.71
1:A:20:PRO:HB2	1:A:21:GLU:CA	2.20	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:344:GLY:HA2	1:A:345:ALA:C	2.12	0.70
1:A:218:PRO:HB2	2:A:453:HOH:O	1.91	0.70
1:A:238:ALA:HB1	1:A:346:LEU:HG	1.74	0.70
1:B:142:TRP:CD2	1:B:260:PRO:HB3	2.26	0.70
1:A:217:SER:HB2	1:A:218:PRO:HD2	1.74	0.70
1:B:355:GLN:H	1:B:356:PRO:HD2	1.58	0.68
1:B:18:ASP:HB3	1:B:19:PHE:CA	2.25	0.66
1:B:287:GLU:HB3	1:B:288:PRO:HD2	1.78	0.65
1:A:361:CYS:HB3	1:A:364:VAL:HG22	1.78	0.65
1:B:292:CYS:O	1:B:294:ILE:HD12	1.97	0.65
1:A:259:LYS:HD3	1:A:314:ASP:HB2	1.79	0.65
1:A:237:GLU:HB2	2:A:439:HOH:O	1.96	0.65
1:B:45:ASP:O	1:B:49:ARG:HD2	1.97	0.64
1:B:361:CYS:HB2	1:B:363:ASP:H	1.63	0.64
1:B:231:GLY:HA3	1:B:234:ASP:O	1.98	0.63
1:A:217:SER:HB2	1:A:218:PRO:CD	2.29	0.62
1:A:18:ASP:C	1:A:20:PRO:HD3	2.20	0.62
1:A:20:PRO:CB	1:A:21:GLU:HA	2.30	0.61
1:A:367:LEU:CA	1:A:368:SER:HB2	2.25	0.61
1:A:19:PHE:HB3	1:A:307:ARG:NH2	2.15	0.61
1:A:178:GLU:HG2	1:A:181:ARG:HH12	1.64	0.61
1:A:258:GLY:CA	1:A:259:LYS:CB	2.80	0.60
1:B:259:LYS:HE2	1:B:262:SER:H	1.66	0.59
1:B:287:GLU:CB	1:B:288:PRO:HD2	2.33	0.59
1:B:367:LEU:HA	1:B:368:SER:CB	2.32	0.59
1:A:231:GLY:HA3	1:A:234:ASP:O	2.02	0.59
1:A:98:TRP:HZ3	1:A:302:GLN:HE21	1.52	0.58
1:A:20:PRO:HB2	1:A:21:GLU:CG	2.33	0.58
1:B:369:LEU:HB2	1:B:373:ASP:CB	2.34	0.57
1:A:31:ARG:HH21	1:A:94:ARG:CG	2.15	0.57
1:A:31:ARG:NH2	2:A:514:HOH:O	2.28	0.57
1:A:118:ARG:NE	1:A:288:PRO:HG3	2.18	0.57
1:A:339:LEU:O	1:A:345:ALA:HB3	2.05	0.57
1:B:19:PHE:HB2	1:B:307:ARG:CZ	2.34	0.57
1:B:258:GLY:HA2	1:B:259:LYS:CB	2.20	0.56
1:B:232:LEU:HD23	1:B:233:THR:H	1.71	0.56
1:B:345:ALA:HA	1:B:347:PRO:HD3	1.87	0.55
1:B:366:ASN:HB3	2:B:400:HOH:O	2.06	0.54
1:B:172:ASN:HD21	1:B:366:ASN:H	1.56	0.54
1:B:337:LYS:HE2	1:B:351:LEU:HD11	1.90	0.54
1:A:172:ASN:HD21	1:A:366:ASN:H	1.55	0.54
1:B:361:CYS:HB2	1:B:363:ASP:N	2.23	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:142:TRP:CE2	1:B:260:PRO:HB3	2.43	0.53
1:A:28:ILE:HD11	1:A:42:ILE:HG23	1.90	0.53
1:A:289:THR:HG22	1:A:291:GLY:O	2.08	0.53
1:B:362:PRO:HB3	2:B:456:HOH:O	2.09	0.53
1:A:19:PHE:HB3	1:A:307:ARG:HH22	1.73	0.52
1:A:338:LYS:O	1:A:341:LEU:HG	2.10	0.52
1:B:259:LYS:HG3	1:B:314:ASP:HB2	1.90	0.52
1:A:98:TRP:HZ3	1:A:302:GLN:NE2	2.07	0.52
1:B:96:TRP:HE1	1:B:104:GLN:NE2	2.08	0.51
1:B:290:ASP:O	1:B:291:GLY:C	2.49	0.50
1:A:217:SER:CB	1:A:218:PRO:CD	2.90	0.50
1:A:367:LEU:HB2	2:A:407:HOH:O	2.11	0.49
1:B:121:SER:HB2	1:B:124:SER:HB3	1.93	0.49
1:B:18:ASP:HB3	1:B:20:PRO:N	2.27	0.49
1:B:369:LEU:HB2	1:B:373:ASP:HB2	1.93	0.49
1:B:301:CYS:SG	1:B:303:HIS:CD2	3.06	0.48
1:A:301:CYS:SG	1:A:303:HIS:CD2	3.07	0.48
1:A:20:PRO:CB	1:A:21:GLU:CA	2.90	0.48
1:B:21:GLU:HB3	1:B:36:PHE:CE1	2.48	0.48
1:A:301:CYS:SG	1:A:303:HIS:NE2	2.86	0.48
1:A:118:ARG:HE	1:A:288:PRO:CG	2.22	0.47
1:A:361:CYS:HB3	1:A:362:PRO:HA	1.96	0.47
1:A:71:GLY:O	1:A:261:ASN:ND2	2.47	0.47
1:A:121:SER:HB2	1:A:124:SER:HB3	1.96	0.47
1:A:89:CYS:SG	1:A:94:ARG:CZ	3.03	0.46
1:B:331:ASP:O	1:B:334:GLN:HG2	2.15	0.45
1:B:27:TRP:CD2	1:B:248:MET:HG2	2.50	0.45
1:B:146:ASN:HD21	1:B:150:GLN:HE21	1.64	0.45
1:A:258:GLY:HA2	1:A:259:LYS:HB3	1.95	0.45
1:A:361:CYS:HB3	1:A:362:PRO:CA	2.47	0.45
1:A:237:GLU:HA	1:A:240:VAL:HG23	1.98	0.45
1:A:178:GLU:HG2	1:A:181:ARG:HH22	1.82	0.45
1:B:292:CYS:HB2	2:B:455:HOH:O	2.18	0.44
1:A:31:ARG:HG3	1:A:33:TYR:CE2	2.52	0.44
1:B:76:LEU:HD13	1:B:128:ILE:HG22	2.00	0.44
1:B:96:TRP:HE1	1:B:104:GLN:HE21	1.64	0.44
1:B:132:GLY:HA3	1:B:143:TYR:OH	2.17	0.44
1:A:371:SER:HA	1:A:372:SER:HA	1.65	0.44
1:B:367:LEU:CA	1:B:368:SER:HB2	2.41	0.43
1:A:76:LEU:HD21	1:A:143:TYR:CD2	2.53	0.43
1:B:74:CYS:SG	2:B:428:HOH:O	2.60	0.43
1:B:20:PRO:HB2	1:B:21:GLU:H	1.65	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:283:GLN:NE2	1:B:298:SER:HB2	2.34	0.43
1:A:178:GLU:HG2	1:A:181:ARG:NH1	2.31	0.43
1:B:304:PRO:HA	1:B:305:PRO:HD3	1.93	0.42
1:A:367:LEU:CA	1:A:368:SER:CB	2.92	0.42
1:B:287:GLU:HB3	1:B:288:PRO:CD	2.49	0.42
1:A:309:SER:HB2	1:A:312:GLU:HG2	2.01	0.42
1:B:371:SER:HA	1:B:372:SER:HA	1.78	0.42
1:B:261:ASN:CB	1:B:262:SER:HA	2.50	0.42
1:A:27:TRP:CD2	1:A:248:MET:HG2	2.55	0.42
1:B:237:GLU:HG2	1:B:237:GLU:H	1.62	0.41
1:A:258:GLY:CA	1:A:259:LYS:HB2	2.37	0.41
1:B:301:CYS:SG	1:B:303:HIS:NE2	2.93	0.41
1:A:217:SER:CB	1:A:218:PRO:HD2	2.44	0.41
1:B:27:TRP:O	1:B:268:GLY:HA3	2.21	0.41
1:A:361:CYS:CB	1:A:364:VAL:HG22	2.47	0.41
1:B:216:PRO:HA	1:B:217:SER:HA	1.91	0.41
1:B:344:GLY:CA	1:B:345:ALA:O	2.69	0.41
1:A:241:GLU:HB3	1:A:344:GLY:O	2.20	0.41
1:A:31:ARG:HG3	1:A:33:TYR:CZ	2.56	0.41
1:B:344:GLY:HA3	1:B:345:ALA:O	2.21	0.41
1:A:31:ARG:NH1	1:A:45:ASP:OD2	2.51	0.40
1:B:113:ASN:HA	1:B:116:ILE:HG12	2.03	0.40
1:A:344:GLY:HA2	1:A:345:ALA:O	2.21	0.40
1:B:217:SER:HB2	1:B:218:PRO:HD2	2.03	0.40
1:B:250:PRO:HD2	1:B:335:GLN:HE22	1.86	0.40
1:A:137:LYS:HE2	2:A:564: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	335/398 (84%)	314 (94%)	15 (4%)	6 (2%)	13 5
1	B	335/398 (84%)	312 (93%)	11 (3%)	12 (4%)	5 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	670/796 (84%)	626 (93%)	26 (4%)	18 (3%)	8	2

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	356	PRO
1	A	20	PRO
1	A	359	LEU
1	A	368	SER
1	B	20	PRO
1	B	288	PRO
1	B	291	GLY
1	B	345	ALA
1	B	355	GLN
1	B	358	HIS
1	B	361	CYS
1	B	368	SER
1	A	259	LYS
1	A	360	ALA
1	B	259	LYS
1	B	139	ILE
1	B	260	PRO
1	A	356	PRO

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	297/344 (86%)	283 (95%)	14 (5%)	36	29
1	B	297/344 (86%)	282 (95%)	15 (5%)	33	26
All	All	594/688 (86%)	565 (95%)	29 (5%)	35	28

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LEU

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Mol	Chain	Res	Type
1	A	18	ASP
1	A	31	ARG
1	A	234	ASP
1	A	289	THR
1	A	341	LEU
1	A	346	LEU
1	A	348	MET
1	A	350	GLU
1	A	355	GLN
1	A	357	SER
1	A	364	VAL
1	A	369	LEU
1	A	371	SER
1	B	49	ARG
1	B	76	LEU
1	B	103	ARG
1	B	189	CYS
1	B	232	LEU
1	B	237	GLU
1	B	259	LYS
1	B	261	ASN
1	B	292	CYS
1	B	302	GLN
1	B	341	LEU
1	B	348	MET
1	B	350	GLU
1	B	351	LEU
1	B	369	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
1	A	283	GLN
1	A	366	ASN
1	B	104	GLN
1	B	141	GLN
1	B	146	ASN
1	B	172	ASN
1	B	245	HIS
1	B	283	GLN
1	B	358	HIS

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Mol	Chain	Res	Type
1	B	366	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no ligands in this entry.

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, 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	339/398 (85%)	0.10	16 (4%) 30 29	22, 38, 66, 78	0
1	B	339/398 (85%)	0.16	19 (5%) 24 23	22, 38, 67, 77	0
All	All	678/796 (85%)	0.13	35 (5%) 26 26	22, 38, 67, 78	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	359	LEU	7.6
1	A	360	ALA	6.0
1	B	339	LEU	6.0
1	B	289	THR	5.8
1	B	344	GLY	4.8
1	B	359	LEU	4.5
1	A	342	LEU	4.2
1	B	19	PHE	3.8
1	B	358	HIS	3.8
1	A	217	SER	3.6
1	A	216	PRO	3.5
1	A	339	LEU	3.4
1	B	342	LEU	3.3
1	B	362	PRO	3.3
1	B	20	PRO	3.3
1	A	362	PRO	3.2
1	B	368	SER	3.2
1	A	258	GLY	3.1
1	A	142	TRP	3.1
1	B	361	CYS	3.0
1	A	343	GLY	2.8
1	A	289	THR	2.8
1	B	357	SER	2.7
1	B	288	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	356	PRO	2.5
1	A	233	THR	2.4
1	B	142	TRP	2.4
1	B	190	ALA	2.4
1	B	258	GLY	2.4
1	A	19	PHE	2.3
1	B	217	SER	2.2
1	A	345	ALA	2.2
1	A	372	SER	2.1
1	A	369	LEU	2.1
1	B	360	ALA	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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.