Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:30 PM GMT

PDB ID	:	1PBW
Title	:	STRUCTURE OF BCR-HOMOLOGY (BH) DOMAIN
Authors	:	Musacchio, A.; Cantley, L.C.; Harrison, S.C.
Deposited on	:	1996-10-17
Resolution	:	2.00 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:

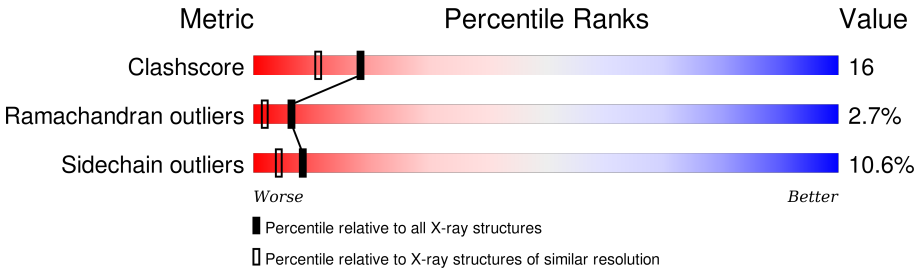
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

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))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (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. 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 <=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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	216	55% 21% 6% • 15%
1	B	216	59% 21% 9% • 10%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3284 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 PHOSPHATIDYLINOSITOL 3-KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	184	Total	C	N	O	S	0	0	0
			1469	953	234	277	5			
1	B	195	Total	C	N	O	S	0	0	0
			1548	1003	250	290	5			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	124	Total	O	0	0
			124	124		
2	B	143	Total	O	0	0
			143	143		

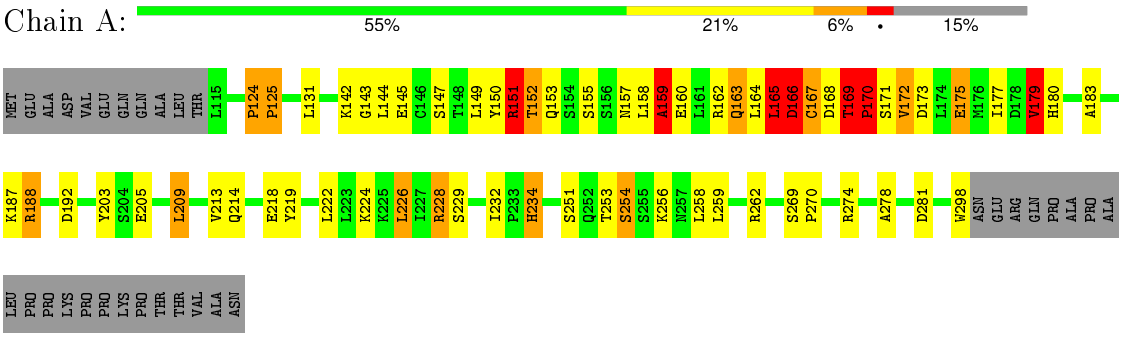
3 Residue-property plots (i)

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.

Note EDS was not executed.

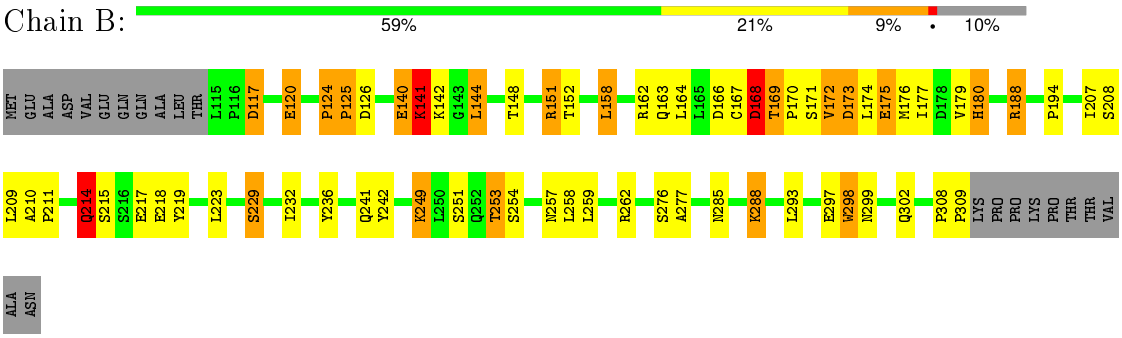
- Molecule 1: PHOSPHATIDYLINOSITOL 3-KINASE

Chain A:



- Molecule 1: PHOSPHATIDYLINOSITOL 3-KINASE

Chain B:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	39.05Å 90.51Å 69.28Å 90.00° 97.19° 90.00°	Depositor
Resolution (Å)	8.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.00)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	ARP/WARP, X-PLOR 3.1	Depositor
R, R_{free}	0.184 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3284	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

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	0.75	2/1501 (0.1%)	2.09	40/2044 (2.0%)
1	B	0.66	2/1584 (0.1%)	1.81	34/2161 (1.6%)
All	All	0.71	4/3085 (0.1%)	1.95	74/4205 (1.8%)

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
1	B	0	2
All	All	0	4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	125	PRO	N-CD	11.49	1.64	1.47
1	A	170	PRO	N-CD	9.60	1.61	1.47
1	B	125	PRO	N-CD	5.67	1.55	1.47
1	B	309	PRO	N-CD	5.37	1.55	1.47

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	125	PRO	CA-N-CD	-20.54	82.75	111.50
1	A	170	PRO	N-CA-CB	20.35	127.72	103.30
1	A	125	PRO	N-CA-CB	20.29	127.65	103.30
1	A	170	PRO	CA-N-CD	-19.92	83.61	111.50
1	B	151	ARG	CD-NE-CZ	19.55	150.97	123.60
1	A	274	ARG	CD-NE-CZ	17.23	147.72	123.60
1	A	188	ARG	CD-NE-CZ	17.22	147.71	123.60
1	B	125	PRO	CA-N-CD	-16.65	88.19	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	188	ARG	NE-CZ-NH1	15.48	128.04	120.30
1	A	124	PRO	O-C-N	15.33	150.23	121.10
1	A	124	PRO	C-N-CD	-14.85	87.94	120.60
1	A	228	ARG	NE-CZ-NH1	13.68	127.14	120.30
1	A	169	THR	O-C-N	13.55	146.84	121.10
1	B	125	PRO	N-CA-CB	13.30	119.27	103.30
1	A	169	THR	C-N-CD	-11.99	94.23	120.60
1	B	124	PRO	C-N-CD	-11.86	94.50	120.60
1	A	169	THR	C-N-CA	11.69	171.08	122.00
1	B	125	PRO	N-CD-CG	11.16	119.94	103.20
1	B	188	ARG	NE-CZ-NH2	-11.02	114.79	120.30
1	A	151	ARG	NE-CZ-NH1	10.46	125.53	120.30
1	A	124	PRO	C-N-CA	9.63	162.45	122.00
1	A	165	LEU	C-N-CA	9.60	145.71	121.70
1	A	125	PRO	N-CD-CG	9.22	117.04	103.20
1	B	188	ARG	CD-NE-CZ	8.24	135.14	123.60
1	B	124	PRO	O-C-N	8.19	136.67	121.10
1	A	188	ARG	NE-CZ-NH2	8.14	124.37	120.30
1	B	163	GLN	CB-CG-CD	7.99	132.38	111.60
1	A	262	ARG	NE-CZ-NH1	7.99	124.29	120.30
1	B	151	ARG	CG-CD-NE	-7.90	95.20	111.80
1	A	228	ARG	CG-CD-NE	7.84	128.25	111.80
1	B	124	PRO	C-N-CA	7.52	153.60	122.00
1	A	228	ARG	NE-CZ-NH2	-7.52	116.54	120.30
1	A	170	PRO	N-CD-CG	7.22	114.03	103.20
1	B	126	ASP	CB-CG-OD2	7.14	124.73	118.30
1	A	153	GLN	CB-CG-CD	7.12	130.12	111.60
1	B	141	LYS	CA-CB-CG	7.00	128.79	113.40
1	B	298	TRP	CA-CB-CG	6.90	126.80	113.70
1	A	179	VAL	CB-CA-C	-6.82	98.45	111.40
1	A	159	ALA	N-CA-CB	6.72	119.50	110.10
1	B	262	ARG	NE-CZ-NH2	-6.66	116.97	120.30
1	A	124	PRO	CA-C-N	-6.54	98.79	117.10
1	A	151	ARG	CD-NE-CZ	6.49	132.69	123.60
1	B	236	TYR	CB-CG-CD1	6.44	124.86	121.00
1	B	173	ASP	N-CA-CB	6.24	121.84	110.60
1	B	229	SER	N-CA-CB	-6.20	101.20	110.50
1	A	166	ASP	CB-CG-OD1	6.09	123.78	118.30
1	B	120	GLU	CB-CG-CD	-6.07	97.82	114.20
1	B	277	ALA	N-CA-CB	6.01	118.51	110.10
1	A	170	PRO	CA-CB-CG	-5.90	92.79	104.00
1	A	152	THR	N-CA-CB	5.89	121.48	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	151	ARG	NE-CZ-NH2	-5.88	117.36	120.30
1	B	180	HIS	CA-CB-CG	-5.67	103.97	113.60
1	A	162	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	B	117	ASP	CB-CG-OD2	-5.60	113.26	118.30
1	A	124	PRO	CA-C-O	-5.50	107.00	120.20
1	B	162	ARG	CD-NE-CZ	5.48	131.27	123.60
1	B	164	LEU	CA-CB-CG	5.48	127.89	115.30
1	A	192	ASP	CB-CG-OD1	5.45	123.21	118.30
1	A	153	GLN	N-CA-CB	5.42	120.36	110.60
1	A	192	ASP	CB-CG-OD2	-5.39	113.45	118.30
1	A	274	ARG	CG-CD-NE	-5.38	100.50	111.80
1	A	188	ARG	NH1-CZ-NH2	-5.36	113.51	119.40
1	B	276	SER	N-CA-CB	-5.35	102.48	110.50
1	A	169	THR	CA-C-N	-5.26	102.38	117.10
1	B	308	PRO	C-N-CD	5.25	139.42	128.40
1	B	124	PRO	CA-C-N	-5.23	102.45	117.10
1	B	241	GLN	OE1-CD-NE2	5.18	133.81	121.90
1	A	169	THR	CA-C-O	-5.12	109.34	120.10
1	B	242	TYR	CB-CG-CD1	-5.12	117.93	121.00
1	B	236	TYR	CB-CG-CD2	-5.11	117.94	121.00
1	B	120	GLU	CB-CA-C	-5.04	100.31	110.40
1	B	140	GLU	OE1-CD-OE2	-5.04	117.25	123.30
1	B	242	TYR	CB-CG-CD2	5.04	124.02	121.00
1	A	143	GLY	CA-C-O	-5.02	111.56	120.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	124	PRO	Peptide
1	A	169	THR	Peptide
1	B	124	PRO	Mainchain,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	1469	0	1505	49	0
1	B	1548	0	1584	48	0
2	A	124	0	0	10	1
2	B	143	0	0	13	1
All	All	3284	0	3089	95	1

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 16.

All (95) 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:A:172:VAL:HG22	1:B:172:VAL:HG21	1.52	0.92
1:A:131:LEU:HD13	1:A:166:ASP:HB2	1.58	0.85
1:B:166:ASP:HB3	2:B:386:HOH:O	1.82	0.79
1:B:210:ALA:HB3	1:B:211:PRO:HD3	1.66	0.76
1:A:163:GLN:HG3	1:A:170:PRO:HG2	1.68	0.74
1:B:144:LEU:HD13	1:B:253:THR:HG21	1.68	0.74
2:A:354:HOH:O	1:B:179:VAL:HG23	1.89	0.72
1:A:232:ILE:O	2:A:338:HOH:O	2.11	0.68
1:B:180:HIS:HB3	2:B:451:HOH:O	1.94	0.67
1:A:155:SER:HB3	2:A:441:HOH:O	1.94	0.67
1:A:151:ARG:HG3	1:A:151:ARG:HH11	1.59	0.66
1:A:251:SER:O	1:A:254:SER:HB2	1.95	0.66
1:B:120:GLU:OE1	2:B:413:HOH:O	2.13	0.66
1:A:234:HIS:HB2	2:A:427:HOH:O	1.95	0.65
1:B:297:GLU:O	2:B:379:HOH:O	2.14	0.65
1:A:142:LYS:HD2	1:A:175:GLU:OE1	1.98	0.63
1:A:158:LEU:O	1:A:159:ALA:CB	2.46	0.63
1:A:145:GLU:HG2	1:A:256:LYS:HD2	1.80	0.62
1:B:299:ASN:ND2	2:B:419:HOH:O	2.32	0.62
1:A:158:LEU:O	1:A:159:ALA:HB3	2.01	0.61
1:A:253:THR:HG22	1:A:253:THR:O	2.02	0.59
1:B:170:PRO:O	1:B:171:SER:HB3	2.03	0.59
1:B:214:GLN:OE1	1:B:218:GLU:HB3	2.02	0.59
1:A:253:THR:HG22	1:A:256:LYS:HB2	1.85	0.58
1:A:224:LYS:O	1:A:228:ARG:HD3	2.03	0.58
1:B:293:LEU:O	1:B:297:GLU:HG2	2.04	0.57
1:B:232:ILE:O	2:B:335:HOH:O	2.17	0.57
1:B:297:GLU:HA	2:B:424:HOH:O	2.05	0.57
1:B:167:CYS:O	1:B:168:ASP:HB3	2.06	0.56
1:A:151:ARG:NH2	1:A:258:LEU:HB2	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:LEU:HG	1:A:226:LEU:HD22	1.88	0.55
1:B:249:LYS:HZ3	1:B:249:LYS:HB2	1.71	0.55
1:B:253:THR:HG23	1:B:257:ASN:ND2	2.21	0.54
1:A:164:LEU:O	1:A:166:ASP:OD1	2.25	0.54
1:A:214:GLN:HB2	1:A:218:GLU:OE1	2.08	0.54
1:A:157:ASN:HB3	2:A:350:HOH:O	2.06	0.54
1:A:151:ARG:HG3	1:A:151:ARG:NH1	2.20	0.53
1:B:140:GLU:OE1	1:B:249:LYS:HE2	2.09	0.53
1:A:183:ALA:O	1:A:187:LYS:HG3	2.09	0.53
1:B:251:SER:HA	1:B:259:LEU:O	2.09	0.52
1:A:214:GLN:CD	1:A:214:GLN:H	2.08	0.52
1:A:167:CYS:SG	1:A:168:ASP:N	2.83	0.51
1:A:164:LEU:O	1:A:166:ASP:N	2.43	0.51
1:B:214:GLN:CD	1:B:214:GLN:H	2.13	0.51
1:B:144:LEU:CD1	1:B:253:THR:HG21	2.38	0.51
1:B:180:HIS:HD2	2:B:322:HOH:O	1.93	0.51
1:B:141:LYS:HE3	1:B:175:GLU:OE2	2.10	0.50
1:B:168:ASP:OD2	1:B:169:THR:HG22	2.12	0.49
1:B:171:SER:HA	2:B:440:HOH:O	2.12	0.49
1:A:167:CYS:HB3	2:A:420:HOH:O	2.12	0.49
1:B:254:SER:O	1:B:258:LEU:HA	2.13	0.49
1:A:160:GLU:HG3	2:A:350:HOH:O	2.12	0.49
1:A:205:GLU:O	1:A:209:LEU:HB2	2.13	0.49
1:B:298:TRP:CZ3	1:B:302:GLN:HG3	2.48	0.49
1:B:249:LYS:HB2	1:B:249:LYS:NZ	2.28	0.48
1:B:158:LEU:CD1	1:B:188:ARG:HD3	2.43	0.48
1:A:163:GLN:HG3	1:A:170:PRO:CG	2.42	0.48
1:A:149:LEU:O	1:A:150:TYR:HB2	2.13	0.48
1:B:249:LYS:CB	1:B:249:LYS:HZ3	2.26	0.48
1:A:224:LYS:HB3	1:A:228:ARG:HH11	1.77	0.48
1:A:160:GLU:HB3	1:B:176:MET:HE3	1.95	0.47
1:A:172:VAL:CG2	1:A:177:ILE:HD11	2.44	0.47
1:A:131:LEU:HD21	1:A:165:LEU:HD12	1.96	0.47
1:A:151:ARG:HH21	1:A:258:LEU:HB2	1.80	0.47
1:A:222:LEU:O	1:A:226:LEU:HB2	2.16	0.46
1:B:158:LEU:HD13	1:B:188:ARG:HD3	1.97	0.46
1:B:180:HIS:CB	2:B:451:HOH:O	2.60	0.46
1:A:142:LYS:HB3	1:A:179:VAL:HG13	1.99	0.45
1:B:214:GLN:HG2	1:B:215:SER:H	1.80	0.45
1:B:141:LYS:HE3	1:B:175:GLU:HG2	1.99	0.45
1:A:224:LYS:HB3	1:A:228:ARG:NH1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:285:ASN:HB2	2:B:448:HOH:O	2.16	0.44
1:B:117:ASP:HA	1:B:194:PRO:HG2	1.99	0.44
1:B:142:LYS:HE2	1:B:177:ILE:O	2.18	0.44
1:A:269:SER:N	1:A:270:PRO:CD	2.81	0.44
1:A:251:SER:HA	1:A:259:LEU:O	2.18	0.43
1:B:208:SER:O	1:B:211:PRO:HD2	2.18	0.43
1:A:180:HIS:HD2	2:A:320:HOH:O	2.01	0.43
1:A:203:TYR:OH	1:A:278:ALA:HB2	2.18	0.42
1:A:213:VAL:O	2:A:443:HOH:O	2.22	0.42
1:B:288:LYS:HD3	1:B:288:LYS:HA	1.84	0.42
1:B:148:THR:HB	1:B:152:THR:HG23	2.00	0.42
1:A:169:THR:HG22	1:A:170:PRO:O	2.20	0.42
1:A:147:SER:HB2	1:A:258:LEU:HG	2.01	0.42
1:B:144:LEU:HB2	2:B:360:HOH:O	2.19	0.41
1:B:293:LEU:HD23	1:B:293:LEU:HA	1.91	0.41
1:B:214:GLN:HG2	1:B:218:GLU:HB2	2.01	0.41
1:B:167:CYS:O	1:B:168:ASP:CB	2.67	0.41
1:A:144:LEU:HD13	2:A:414:HOH:O	2.19	0.41
1:B:254:SER:HA	1:B:257:ASN:OD1	2.21	0.41
1:B:167:CYS:HA	2:B:458:HOH:O	2.21	0.41
1:A:145:GLU:HG2	1:A:256:LYS:CD	2.48	0.40
1:B:298:TRP:HZ3	1:B:302:GLN:HG3	1.86	0.40
1:A:173:ASP:OD1	1:A:175:GLU:HB2	2.21	0.40
1:A:172:VAL:HB	1:A:173:ASP:H	1.58	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:403:HOH:O	2:B:418:HOH:O[2_555]	2.00	0.20

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	182/216 (84%)	169 (93%)	7 (4%)	6 (3%)	5 1
1	B	193/216 (89%)	182 (94%)	7 (4%)	4 (2%)	9 3
All	All	375/432 (87%)	351 (94%)	14 (4%)	10 (3%)	6 2

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	125	PRO
1	A	159	ALA
1	A	170	PRO
1	A	171	SER
1	B	125	PRO
1	B	168	ASP
1	B	173	ASP
1	A	166	ASP
1	A	169	THR
1	B	214	GLN

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	170/197 (86%)	152 (89%)	18 (11%)	8 4
1	B	178/197 (90%)	159 (89%)	19 (11%)	8 4
All	All	348/394 (88%)	311 (89%)	37 (11%)	8 4

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	151	ARG
1	A	152	THR
1	A	163	GLN
1	A	165	LEU

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Mol	Chain	Res	Type
1	A	167	CYS
1	A	169	THR
1	A	172	VAL
1	A	175	GLU
1	A	179	VAL
1	A	188	ARG
1	A	209	LEU
1	A	219	TYR
1	A	226	LEU
1	A	229	SER
1	A	234	HIS
1	A	254	SER
1	A	281	ASP
1	A	298	TRP
1	B	141	LYS
1	B	144	LEU
1	B	151	ARG
1	B	158	LEU
1	B	168	ASP
1	B	169	THR
1	B	172	VAL
1	B	174	LEU
1	B	175	GLU
1	B	207	ILE
1	B	209	LEU
1	B	214	GLN
1	B	217	GLU
1	B	219	TYR
1	B	223	LEU
1	B	229	SER
1	B	249	LYS
1	B	253	THR
1	B	288	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	180	HIS
1	A	221	GLN
1	B	180	HIS

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

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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.