W O R L D W I D E
wwPDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 05:26 PM GMT

PDB ID	:	4IC8
Title	:	Crystal structure of the apo ERK5 kinase domain
Authors	:	Gogl, G.; Remenyi, A.
Deposited on	:	2012-12-10
Resolution	:	2.80 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
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)	:	trunk26865
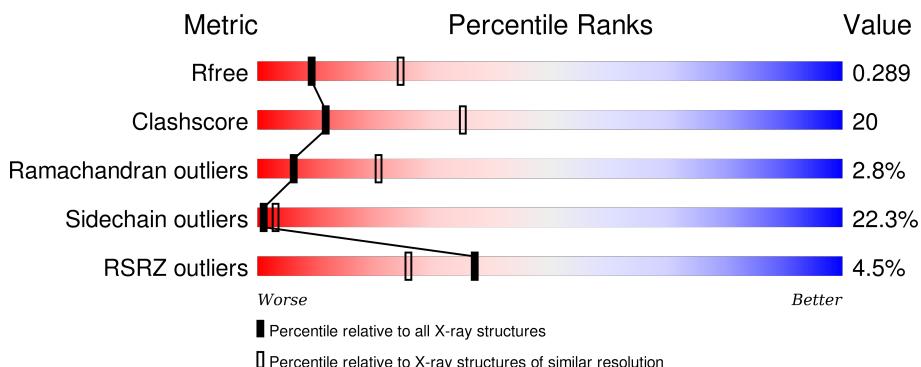
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION
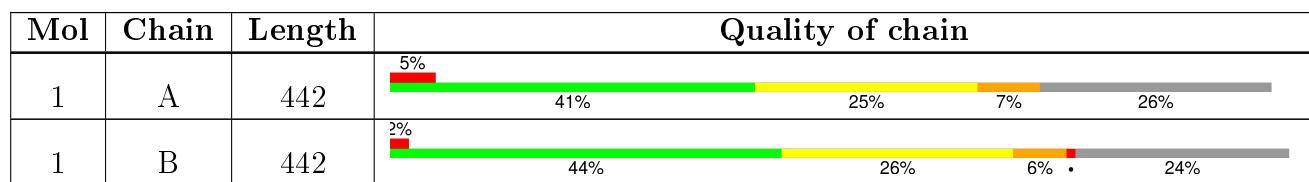
The reported resolution of this entry is 2.80 Å.

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	Percentile Ranks	Value
Rfree		0.289
Clashscore		20
Ramachandran outliers		2.8%
Sidechain outliers		22.3%
RSRZ outliers		4.5%

Worse   *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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.

Mol	Chain	Length	Quality of chain
1	A	442	5% — 41% / 25% / 7% / 26%
1	B	442	2% — 44% / 26% / 6% / • / 24%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 4807 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 Mitogen-activated protein kinase 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	325	Total 2375	C 1536	N 403	O 427	S 9	0	0	0
1	B	336	Total 2432	C 1566	N 421	O 436	S 9	0	0	0
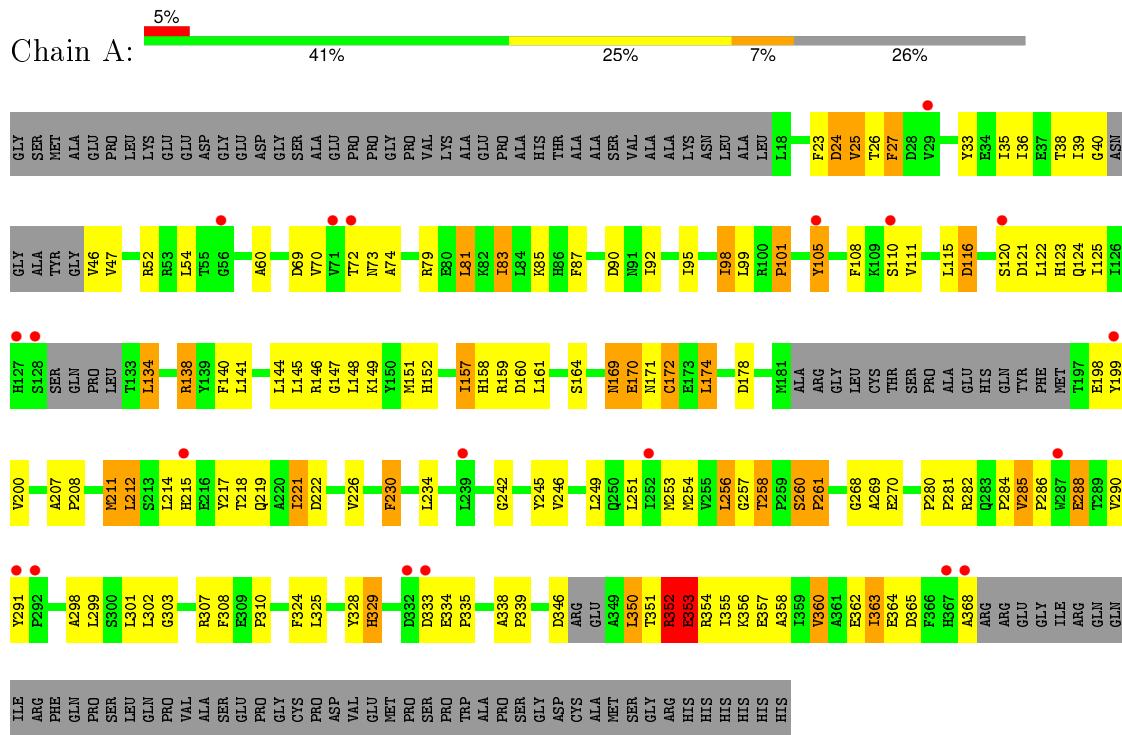
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	GLY	-	EXPRESSION TAG	UNP Q13164
A	-22	SER	-	EXPRESSION TAG	UNP Q13164
A	410	SER	-	EXPRESSION TAG	UNP Q13164
A	411	GLY	-	EXPRESSION TAG	UNP Q13164
A	412	ARG	-	EXPRESSION TAG	UNP Q13164
A	413	HIS	-	EXPRESSION TAG	UNP Q13164
A	414	HIS	-	EXPRESSION TAG	UNP Q13164
A	415	HIS	-	EXPRESSION TAG	UNP Q13164
A	416	HIS	-	EXPRESSION TAG	UNP Q13164
A	417	HIS	-	EXPRESSION TAG	UNP Q13164
A	418	HIS	-	EXPRESSION TAG	UNP Q13164
B	-23	GLY	-	EXPRESSION TAG	UNP Q13164
B	-22	SER	-	EXPRESSION TAG	UNP Q13164
B	410	SER	-	EXPRESSION TAG	UNP Q13164
B	411	GLY	-	EXPRESSION TAG	UNP Q13164
B	412	ARG	-	EXPRESSION TAG	UNP Q13164
B	413	HIS	-	EXPRESSION TAG	UNP Q13164
B	414	HIS	-	EXPRESSION TAG	UNP Q13164
B	415	HIS	-	EXPRESSION TAG	UNP Q13164
B	416	HIS	-	EXPRESSION TAG	UNP Q13164
B	417	HIS	-	EXPRESSION TAG	UNP Q13164
B	418	HIS	-	EXPRESSION TAG	UNP Q13164
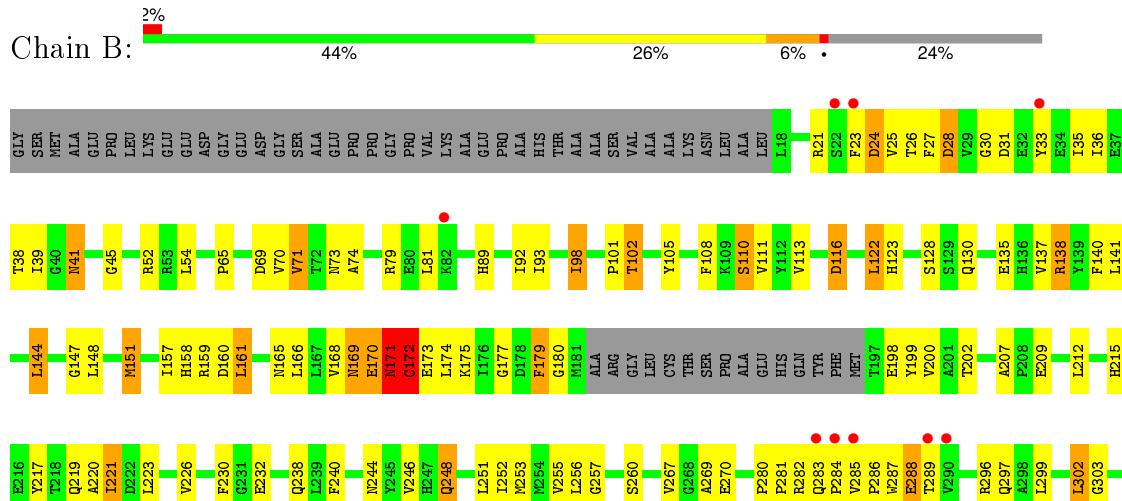
3 Residue-property plots ⓘ
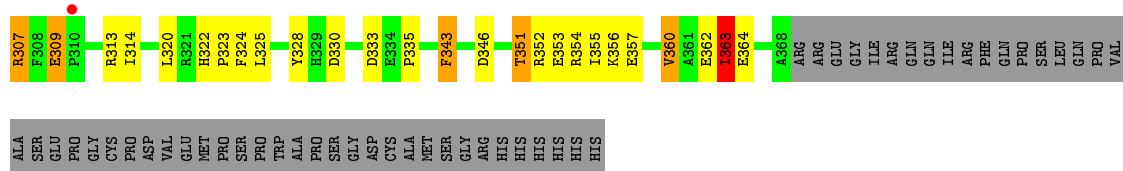
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Mitogen-activated protein kinase 7

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4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	59.90Å　　93.22Å　　69.26Å 90.00°　　89.96°　　90.00°	Depositor
Resolution (Å)	45.29　–　2.80 45.29　–　2.80	Depositor EDS
% Data completeness (in resolution range)	98.1 (45.29-2.80) 92.7 (45.29-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.94 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.262　,　0.290 0.263　,　0.289	Depositor DCC
R_{free} test set	899 reflections (5.42%)	DCC
Wilson B-factor (Å^2)	56.1	Xtriage
Anisotropy	0.705	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 55.6	EDS
Estimated twinning fraction	0.478 for h,-k,-l	Xtriage
L-test for twinning[2]	$< |L| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	2 of 18523 reflections (0.011%)	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	4807	wwPDB-VP
Average B, all atoms (Å^2)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	0/2430	0.61	1/3320 (0.0%)
1	B	0.34	1/2490 (0.0%)	0.78	4/3411 (0.1%)
All	All	0.32	1/4920 (0.0%)	0.70	5/6731 (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	3
1	B	0	3
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	170	GLU	CA-C	5.49	1.67	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	171	ASN	CB-CA-C	13.79	137.97	110.40
1	B	171	ASN	N-CA-C	-13.40	74.83	111.00
1	B	171	ASN	N-CA-CB	-11.53	89.85	110.60
1	B	170	GLU	N-CA-C	7.01	129.91	111.00
1	A	174	LEU	CA-CB-CG	5.95	128.98	115.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	101	PRO	Peptide
1	A	260	SER	Peptide
1	A	35	ILE	Peptide
1	B	102	THR	Peptide
1	B	260	SER	Peptide
1	B	30	GLY	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	2375	0	2154	88	0
1	B	2432	0	2209	99	0
All	All	4807	0	4363	186	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 20.

All (186) 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:198:GLU:CB	1:A:199:TYR:HA	1.92	0.98
1:B:169:ASN:O	1:B:172:CYS:N	1.96	0.98
1:B:198:GLU:CB	1:B:199:TYR:HA	1.95	0.95
1:A:98:ILE:HD11	1:A:363:ILE:HG12	1.58	0.84
1:B:98:ILE:HG23	1:B:363:ILE:HG23	1.61	0.82
1:B:138:ARG:HH21	1:B:328:TYR:HD2	1.30	0.78
1:B:269:ALA:HB1	1:B:270:GLU:HA	1.68	0.76
1:B:169:ASN:C	1:B:172:CYS:H	1.89	0.75
1:A:284:PRO:HB2	1:A:285:VAL:HG13	1.67	0.75
1:B:170:GLU:CA	1:B:171:ASN:HB3	2.16	0.74
1:B:284:PRO:HB2	1:B:285:VAL:HB	1.70	0.73
1:B:101:PRO:HG3	1:B:110:SER:O	1.89	0.72
1:B:354:ARG:HG3	1:B:354:ARG:HH11	1.55	0.71
1:B:280:PRO:O	1:B:282:ARG:N	2.23	0.70
1:B:71:VAL:HG13	1:B:352:ARG:HB2	1.73	0.69
1:A:257:GLY:HA3	1:A:284:PRO:HB3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:ALA:HB1	1:A:270:GLU:HA	1.74	0.69
1:B:157:ILE:HB	1:B:159:ARG:HG3	1.76	0.68
1:A:353:GLU:HG3	1:A:356:LYS:HE3	1.76	0.68
1:A:85:LYS:NZ	1:A:362:GLU:OE1	2.28	0.67
1:B:166:LEU:HB3	1:B:174:LEU:HD11	1.77	0.67
1:B:98:ILE:HG12	1:B:113:VAL:HG12	1.76	0.66
1:B:198:GLU:CB	1:B:199:TYR:CA	2.73	0.66
1:A:352:ARG:HA	1:A:352:ARG:NE	2.10	0.66
1:B:362:GLU:C	1:B:364:GLU:H	1.99	0.65
1:B:297:GLN:HG3	1:B:324:PHE:HD1	1.61	0.65
1:A:25:VAL:HG22	1:A:26:THR:H	1.59	0.65
1:B:28:ASP:OD2	1:B:28:ASP:N	2.28	0.64
1:B:352:ARG:HE	1:B:353:GLU:HG2	1.62	0.64
1:A:291:TYR:HB2	1:A:299:LEU:HD21	1.79	0.64
1:A:303:GLY:O	1:A:307:ARG:NH2	2.30	0.63
1:A:116:ASP:OD1	1:A:116:ASP:N	2.32	0.63
1:A:169:ASN:OD1	1:A:169:ASN:N	2.32	0.62
1:A:364:GLU:O	1:A:368:ALA:N	2.33	0.62
1:A:212:LEU:HD21	1:A:249:LEU:HD22	1.82	0.61
1:B:362:GLU:C	1:B:363:ILE:HG13	2.20	0.61
1:B:41:ASN:OD1	1:B:41:ASN:N	2.31	0.61
1:A:354:ARG:O	1:A:358:ALA:N	2.32	0.61
1:B:343:PHE:CG	1:B:346:ASP:HB2	2.36	0.61
1:B:169:ASN:OD1	1:B:171:ASN:ND2	2.33	0.61
1:B:288:GLU:CD	1:B:288:GLU:H	2.04	0.60
1:A:214:LEU:O	1:A:268:GLY:N	2.22	0.60
1:A:351:THR:OG1	1:A:352:ARG:N	2.34	0.60
1:A:157:ILE:HG21	1:A:221:ILE:HD11	1.84	0.60
1:A:170:GLU:HA	1:A:172:CYS:N	2.17	0.59
1:A:352:ARG:NH1	1:A:353:GLU:OE1	2.35	0.59
1:A:123:HIS:HB2	1:A:164:SER:HA	1.84	0.58
1:A:211:MET:O	1:A:212:LEU:HB2	2.04	0.57
1:B:170:GLU:HA	1:B:172:CYS:N	2.20	0.57
1:B:69:ASP:N	1:B:69:ASP:OD2	2.39	0.56
1:B:330:ASP:HB3	1:B:333:ASP:HB2	1.86	0.56
1:B:141:LEU:HA	1:B:144:LEU:HB2	1.88	0.55
1:B:232:GLU:HG3	1:B:238:GLN:HA	1.89	0.55
1:A:52:ARG:HG3	1:A:54:LEU:H	1.71	0.55
1:B:170:GLU:N	1:B:171:ASN:HB3	2.23	0.54
1:B:138:ARG:HH22	1:B:325:LEU:HA	1.72	0.54
1:A:169:ASN:CG	1:A:171:ASN:HD21	2.11	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:252:ILE:HG22	1:B:256:LEU:HD11	1.88	0.54
1:A:325:LEU:O	1:A:329:HIS:N	2.40	0.53
1:B:159:ARG:HE	1:B:180:GLY:HA3	1.72	0.53
1:A:157:ILE:HG22	1:A:159:ARG:H	1.74	0.53
1:B:307:ARG:HD3	1:B:309:GLU:HG3	1.90	0.53
1:B:138:ARG:NH2	1:B:325:LEU:HA	2.23	0.53
1:B:45:GLY:HA2	1:B:65:PRO:HD2	1.91	0.53
1:A:350:LEU:N	1:A:351:THR:HA	2.24	0.53
1:A:92:ILE:HD11	1:A:147:GLY:O	2.09	0.53
1:B:52:ARG:HG3	1:B:54:LEU:H	1.72	0.53
1:A:218:THR:O	1:A:221:ILE:HG23	2.09	0.53
1:B:351:THR:HG22	1:B:354:ARG:CZ	2.39	0.52
1:A:269:ALA:CB	1:A:270:GLU:HA	2.39	0.52
1:A:85:LYS:NZ	1:A:365:ASP:OD2	2.38	0.52
1:A:72:THR:O	1:A:74:ALA:N	2.43	0.52
1:A:351:THR:H	1:A:355:ILE:HD11	1.75	0.51
1:A:260:SER:N	1:A:261:PRO:HD3	2.25	0.51
1:B:220:ALA:HB1	1:B:313:ARG:HD2	1.93	0.51
1:B:138:ARG:HB3	1:B:328:TYR:HE2	1.77	0.50
1:A:258:THR:OG1	1:A:282:ARG:N	2.43	0.50
1:A:362:GLU:C	1:A:364:GLU:H	2.14	0.50
1:A:134:LEU:HD23	1:A:138:ARG:HH12	1.76	0.50
1:B:122:LEU:HD13	1:B:168:VAL:HG21	1.93	0.50
1:A:288:GLU:H	1:A:288:GLU:CD	2.13	0.50
1:A:352:ARG:O	1:A:354:ARG:N	2.45	0.49
1:B:357:GLU:O	1:B:360:VAL:HG22	2.13	0.49
1:B:170:GLU:CA	1:B:172:CYS:N	2.76	0.49
1:A:146:ARG:HG2	1:A:334:GLU:HG2	1.94	0.49
1:A:256:LEU:HD13	1:A:308:PHE:CE1	2.47	0.49
1:A:284:PRO:HB2	1:A:285:VAL:CG1	2.39	0.49
1:B:158:HIS:CD2	1:B:161:LEU:HG	2.48	0.49
1:B:25:VAL:HG22	1:B:26:THR:H	1.78	0.49
1:A:269:ALA:HB1	1:A:270:GLU:CA	2.43	0.49
1:A:138:ARG:HG3	1:A:328:TYR:CE2	2.48	0.49
1:B:116:ASP:OD1	1:B:116:ASP:N	2.41	0.48
1:A:352:ARG:O	1:A:355:ILE:HG13	2.13	0.48
1:A:134:LEU:HD23	1:A:138:ARG:NH1	2.28	0.48
1:A:145:LEU:HD21	1:A:226:VAL:HG11	1.95	0.48
1:B:287:TRP:CZ2	1:B:303:GLY:HA2	2.49	0.48
1:A:157:ILE:HD11	1:A:219:GLN:HG2	1.96	0.48
1:A:170:GLU:HA	1:A:172:CYS:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:362:GLU:HA	1:A:365:ASP:HB3	1.97	0.47
1:B:286:PRO:O	1:B:289:THR:OG1	2.28	0.47
1:A:222:ASP:O	1:A:226:VAL:HG23	2.15	0.47
1:A:87:PHE:HE2	1:A:151:MET:HG3	1.78	0.47
1:A:338:ALA:HB3	1:A:339:PRO:HD3	1.95	0.47
1:B:169:ASN:OD1	1:B:171:ASN:CG	2.53	0.47
1:B:320:LEU:HA	1:B:325:LEU:HD12	1.97	0.47
1:B:158:HIS:NE2	1:B:160:ASP:O	2.47	0.47
1:A:198:GLU:CB	1:A:199:TYR:CA	2.75	0.47
1:A:242:GLY:HA2	1:A:251:LEU:HD12	1.97	0.47
1:A:230:PHE:HE2	1:A:301:LEU:HD23	1.80	0.46
1:A:286:PRO:O	1:A:290:VAL:HG23	2.16	0.46
1:B:89:HIS:CD2	1:B:335:PRO:HD2	2.51	0.46
1:A:357:GLU:O	1:A:360:VAL:HG22	2.16	0.46
1:B:74:ALA:HB1	1:B:355:ILE:HG21	1.98	0.46
1:B:138:ARG:HB3	1:B:328:TYR:CE2	2.50	0.46
1:B:269:ALA:CB	1:B:270:GLU:HA	2.43	0.46
1:A:79:ARG:O	1:A:83:ILE:HB	2.16	0.45
1:A:101:PRO:HG3	1:A:110:SER:O	2.15	0.45
1:B:171:ASN:O	1:B:172:CYS:HB2	2.16	0.45
1:B:215:HIS:HB3	1:B:267:VAL:HA	1.99	0.45
1:B:256:LEU:C	1:B:284:PRO:HB3	2.37	0.45
1:A:121:ASP:OD1	1:A:124:GLN:HG2	2.16	0.45
1:B:248:GLN:O	1:B:252:ILE:HG13	2.16	0.45
1:B:135:GLU:HA	1:B:138:ARG:HB2	1.99	0.45
1:A:282:ARG:O	1:A:284:PRO:HD3	2.17	0.45
1:B:253:MET:O	1:B:257:GLY:N	2.50	0.45
1:B:209:GLU:HG3	1:B:217:TYR:HB3	1.98	0.45
1:B:296:ARG:HA	1:B:299:LEU:HD12	1.97	0.45
1:A:60:ALA:N	1:A:115:LEU:O	2.42	0.44
1:B:283:GLN:HA	1:B:284:PRO:HD2	1.76	0.44
1:B:170:GLU:N	1:B:171:ASN:CB	2.80	0.44
1:B:165:ASN:O	1:B:177:GLY:N	2.31	0.44
1:B:322:HIS:CG	1:B:323:PRO:HD2	2.53	0.44
1:B:157:ILE:HD11	1:B:219:GLN:HG2	2.00	0.44
1:A:25:VAL:HG21	1:B:288:GLU:CD	2.38	0.44
1:A:333:ASP:O	1:A:335:PRO:HD3	2.18	0.43
1:B:92:ILE:HD11	1:B:147:GLY:HA2	2.00	0.43
1:A:79:ARG:NH1	1:A:346:ASP:HA	2.33	0.43
1:A:352:ARG:O	1:A:355:ILE:N	2.37	0.43
1:A:280:PRO:HA	1:A:281:PRO:HD3	1.92	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:LYS:O	1:B:360:VAL:HG13	2.18	0.43
1:A:120:SER:OG	1:A:121:ASP:N	2.52	0.43
1:A:27:PHE:N	1:A:27:PHE:CD2	2.86	0.43
1:B:101:PRO:O	1:B:102:THR:C	2.56	0.43
1:B:207:ALA:HB3	1:B:221:ILE:HG12	2.00	0.43
1:B:169:ASN:ND2	1:B:173:GLU:HB2	2.34	0.43
1:B:158:HIS:HD2	1:B:161:LEU:HG	1.84	0.42
1:A:207:ALA:HA	1:A:208:PRO:HD3	1.91	0.42
1:A:215:HIS:NE2	1:A:310:PRO:HD2	2.34	0.42
1:A:87:PHE:HD2	1:A:92:ILE:HG21	1.85	0.42
1:B:257:GLY:HA3	1:B:284:PRO:HD3	2.02	0.42
1:A:333:ASP:C	1:A:335:PRO:HD3	2.41	0.42
1:B:354:ARG:HH11	1:B:354:ARG:CG	2.29	0.41
1:B:174:LEU:HD12	1:B:175:LYS:N	2.35	0.41
1:A:249:LEU:O	1:A:253:MET:N	2.53	0.41
1:B:269:ALA:HB1	1:B:270:GLU:CA	2.44	0.41
1:A:170:GLU:HA	1:A:171:ASN:C	2.40	0.41
1:B:23:PHE:HA	1:B:24:ASP:HA	1.91	0.41
1:B:314:ILE:HA	1:B:314:ILE:HD12	1.95	0.41
1:B:179:PHE:HD2	1:B:179:PHE:HA	1.76	0.41
1:B:297:GLN:HE22	1:B:323:PRO:HB2	1.85	0.41
1:B:144:LEU:HD22	1:B:226:VAL:HG22	2.02	0.41
1:A:40:GLY:C	1:A:47:VAL:H	2.23	0.41
1:A:122:LEU:HD12	1:A:122:LEU:HA	1.85	0.41
1:B:159:ARG:HE	1:B:180:GLY:CA	2.33	0.41
1:B:333:ASP:O	1:B:335:PRO:HD3	2.21	0.41
1:B:24:ASP:HA	1:B:25:VAL:HA	1.76	0.41
1:B:151:MET:HE3	1:B:151:MET:HB3	1.94	0.41
1:A:298:ALA:HB2	1:A:324:PHE:CE1	2.56	0.41
1:A:148:LEU:HA	1:A:148:LEU:HD12	1.84	0.41
1:B:158:HIS:CD2	1:B:160:ASP:O	2.74	0.41
1:B:287:TRP:CE2	1:B:303:GLY:HA2	2.56	0.41
1:A:81:LEU:HD21	1:A:98:ILE:HD12	2.03	0.41
1:B:244:ASN:HB3	1:B:246:VAL:HG12	2.01	0.41
1:A:258:THR:HB	1:A:281:PRO:HA	2.03	0.40
1:A:105:TYR:HD2	1:A:105:TYR:O	2.04	0.40
1:A:152:HIS:HB3	1:A:219:GLN:OE1	2.21	0.40
1:A:27:PHE:N	1:A:27:PHE:HD2	2.20	0.40
1:B:138:ARG:NH1	1:B:324:PHE:O	2.54	0.40
1:B:351:THR:OG1	1:B:355:ILE:HG13	2.21	0.40
1:B:79:ARG:NH1	1:B:346:ASP:OD2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:GLY:HA2	1:B:65:PRO:CD	2.51	0.40
1:B:128:SER:C	1:B:130:GLN:H	2.24	0.40
1:A:158:HIS:C	1:A:160:ASP:H	2.24	0.40
1:A:23:PHE:HA	1:A:24:ASP:HA	1.89	0.40
1:B:302:LEU:HA	1:B:302:LEU:HD12	1.83	0.40
1:B:93:ILE:HD12	1:B:93:ILE:HA	2.00	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	315/442 (71%)	270 (86%)	35 (11%)	10 (3%)	5	17
1	B	332/442 (75%)	292 (88%)	32 (10%)	8 (2%)	7	25
All	All	647/884 (73%)	562 (87%)	67 (10%)	18 (3%)	6	21

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	ILE
1	A	363	ILE
1	B	36	ILE
1	B	363	ILE
1	A	172	CYS
1	A	200	VAL
1	B	200	VAL
1	A	73	ASN
1	A	353	GLU
1	A	352	ARG
1	B	172	CYS
1	B	171	ASN

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Mol	Chain	Res	Type
1	B	31	ASP
1	B	281	PRO
1	A	70	VAL
1	A	261	PRO
1	A	25	VAL
1	B	35	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	213/373 (57%)	164 (77%)	49 (23%)	1	3
1	B	217/373 (58%)	170 (78%)	47 (22%)	1	3
All	All	430/746 (58%)	334 (78%)	96 (22%)	1	3

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASP
1	A	27	PHE
1	A	33	TYR
1	A	38	THR
1	A	39	ILE
1	A	46	VAL
1	A	69	ASP
1	A	81	LEU
1	A	83	ILE
1	A	90	ASP
1	A	95	ILE
1	A	98	ILE
1	A	99	LEU
1	A	105	TYR
1	A	108	PHE
1	A	111	VAL
1	A	116	ASP

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Mol	Chain	Res	Type
1	A	125	ILE
1	A	134	LEU
1	A	138	ARG
1	A	140	PHE
1	A	141	LEU
1	A	144	LEU
1	A	149	LYS
1	A	157	ILE
1	A	161	LEU
1	A	169	ASN
1	A	170	GLU
1	A	174	LEU
1	A	178	ASP
1	A	211	MET
1	A	212	LEU
1	A	217	TYR
1	A	221	ILE
1	A	230	PHE
1	A	234	LEU
1	A	245	TYR
1	A	246	VAL
1	A	254	MET
1	A	256	LEU
1	A	258	THR
1	A	285	VAL
1	A	288	GLU
1	A	302	LEU
1	A	329	HIS
1	A	350	LEU
1	A	352	ARG
1	A	353	GLU
1	A	360	VAL
1	B	21	ARG
1	B	24	ASP
1	B	27	PHE
1	B	28	ASP
1	B	33	TYR
1	B	38	THR
1	B	39	ILE
1	B	41	ASN
1	B	70	VAL
1	B	71	VAL

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Mol	Chain	Res	Type
1	B	73	ASN
1	B	81	LEU
1	B	98	ILE
1	B	105	TYR
1	B	108	PHE
1	B	110	SER
1	B	111	VAL
1	B	116	ASP
1	B	122	LEU
1	B	123	HIS
1	B	137	VAL
1	B	138	ARG
1	B	140	PHE
1	B	144	LEU
1	B	148	LEU
1	B	151	MET
1	B	161	LEU
1	B	169	ASN
1	B	172	CYS
1	B	179	PHE
1	B	202	THR
1	B	212	LEU
1	B	221	ILE
1	B	223	LEU
1	B	230	PHE
1	B	240	PHE
1	B	248	GLN
1	B	251	LEU
1	B	255	VAL
1	B	288	GLU
1	B	302	LEU
1	B	307	ARG
1	B	309	GLU
1	B	343	PHE
1	B	351	THR
1	B	360	VAL
1	B	363	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	HIS

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Mol	Chain	Res	Type
1	A	238	GLN
1	B	58	GLN
1	B	91	ASN
1	B	143	GLN
1	B	165	ASN
1	B	248	GLN

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)

There are no ligands in this entry.

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, 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	325/442 (73%)	0.19	20 (6%)	24	15	51, 89, 148, 327	0
1	B	336/442 (76%)	-0.01	10 (2%)	54	41	40, 81, 149, 267	0
All	All	661/884 (74%)	0.09	30 (4%)	37	26	40, 84, 149, 327	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	284	PRO	9.1
1	A	128	SER	7.6
1	A	333	ASP	7.0
1	A	215	HIS	6.2
1	A	127	HIS	5.8
1	A	72	THR	5.7
1	A	292	PRO	5.1
1	A	332	ASP	4.5
1	B	22	SER	4.4
1	A	368	ALA	4.4
1	A	199	TYR	4.3
1	A	29	VAL	3.8
1	A	105	TYR	3.8
1	A	367	HIS	3.8
1	B	283	GLN	3.0
1	B	290	VAL	3.0
1	A	291	TYR	2.8
1	B	33	TYR	2.7
1	B	310	PRO	2.6
1	A	56	GLY	2.5
1	B	285	VAL	2.5
1	A	239	LEU	2.4
1	A	120	SER	2.4
1	A	287	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	23	PHE	2.3
1	B	289	THR	2.3
1	B	82	LYS	2.1
1	A	71	VAL	2.1
1	A	252	ILE	2.0
1	A	110	SER	2.0

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.