



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:45 PM UTC

PDB ID : 4IC8 / pdb_00004ic8
Title : Crystal structure of the apo ERK5 kinase domain
Authors : Gogl, G.; Remenyi, A.
Deposited on : 2012-12-10
Resolution : 2.80 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

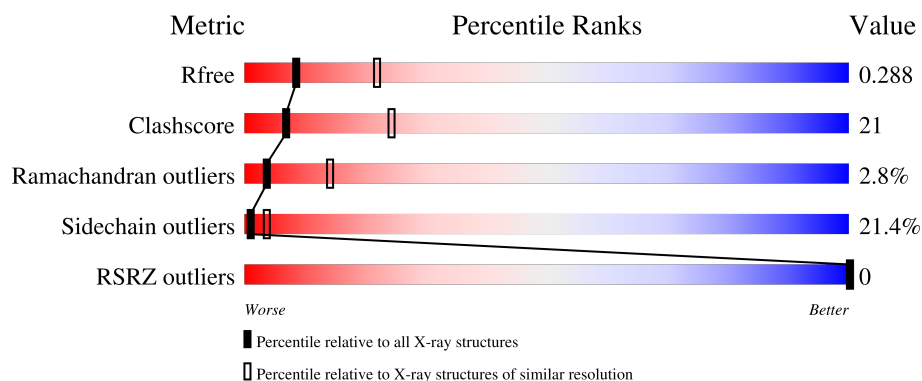
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	442	
1	B	442	

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	C	N	O	S	0	0	0
			2375	1536	403	427	9			
1	B	336	Total	C	N	O	S	0	0	0
			2432	1566	421	436	9			

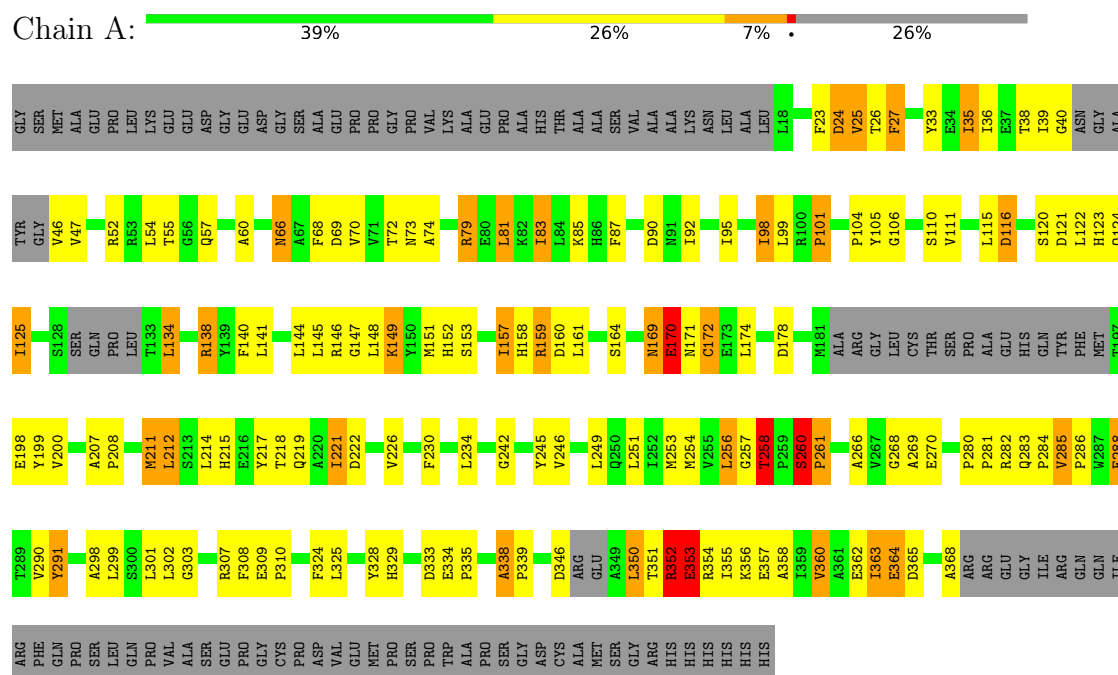
There are 22 discrepancies between the modelled and reference sequences:

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

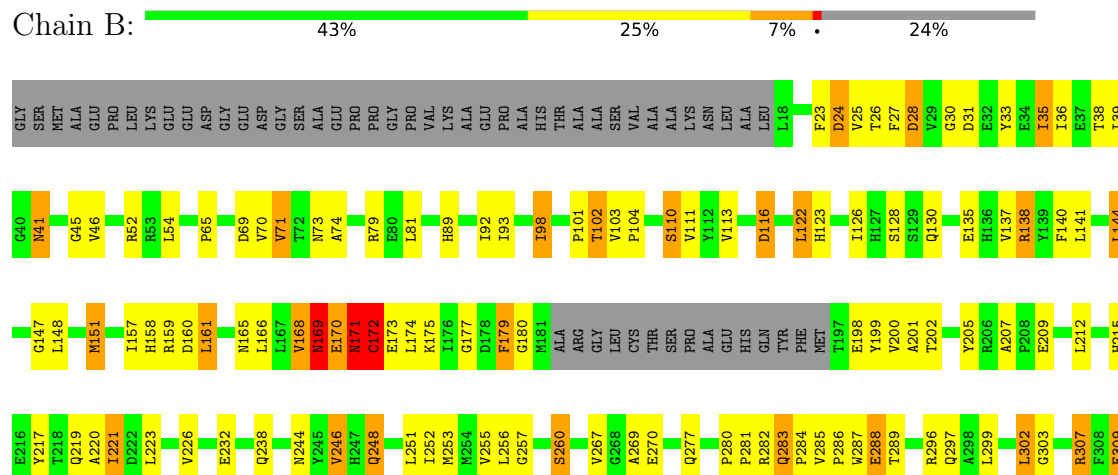
3 Residue-property plots [i](#)

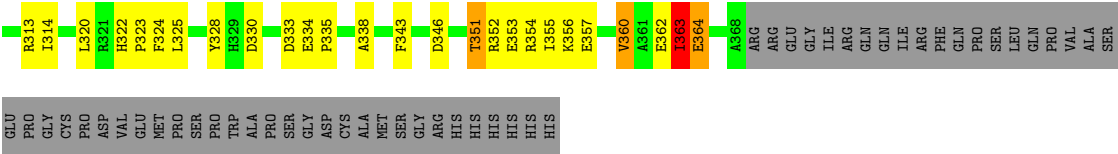
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Mitogen-activated protein kinase 7



• Molecule 1: Mitogen-activated protein kinase 7





GLU
PRO
GLY
CYS
PRO
ASP
VAL
GLU
MET
PRO
SER
PRO
TRP
ALA
PRO
SER
GLY
ASP
CYS
ALA
MET
SER
GLY
ARG
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics

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
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.262 , 0.290 0.262 , 0.288	Depositor DCC
R_{free} test set	948 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	55.0	Xtriage
Anisotropy	0.719	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 79.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.478 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	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.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	0.41	0/2430	1.02	19/3320 (0.6%)
1	B	0.52	3/2490 (0.1%)	1.17	19/3411 (0.6%)
All	All	0.47	3/4920 (0.1%)	1.10	38/6731 (0.6%)

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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	170	GLU	CA-C	10.29	1.67	1.52
1	B	170	GLU	N-CA	5.57	1.53	1.46
1	B	171	ASN	CA-C	5.43	1.64	1.52

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	171	ASN	CB-CA-C	14.67	137.97	110.10
1	B	170	GLU	N-CA-C	13.51	129.91	113.16
1	B	171	ASN	N-CA-C	-12.92	74.83	111.00
1	B	171	ASN	N-CA-CB	-12.15	89.85	110.50
1	B	283	GLN	CA-C-N	8.97	131.06	119.84
1	B	283	GLN	C-N-CA	8.97	131.06	119.84
1	B	364	GLU	N-CA-C	-7.14	103.59	112.72
1	A	258	THR	CA-C-N	6.94	128.51	119.84
1	A	258	THR	C-N-CA	6.94	128.51	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	283	GLN	CA-C-N	6.74	128.26	119.84
1	A	283	GLN	C-N-CA	6.74	128.26	119.84
1	B	169	ASN	N-CA-C	-6.61	97.51	108.34
1	B	260	SER	CA-C-N	6.55	128.03	119.84
1	B	260	SER	C-N-CA	6.55	128.03	119.84
1	A	125	ILE	N-CA-C	6.28	119.05	112.83
1	A	364	GLU	N-CA-C	-6.08	103.81	112.13
1	B	338	ALA	CA-C-N	-6.02	114.18	120.38
1	B	338	ALA	C-N-CA	-6.02	114.18	120.38
1	A	260	SER	CA-C-N	5.95	127.27	119.84
1	A	260	SER	C-N-CA	5.95	127.27	119.84
1	B	283	GLN	N-CA-C	5.95	117.56	110.07
1	B	103	VAL	N-CA-C	5.82	121.44	108.88
1	A	309	GLU	CA-C-N	5.73	126.12	119.47
1	A	309	GLU	C-N-CA	5.73	126.12	119.47
1	A	170	GLU	N-CA-C	5.68	118.14	108.02
1	A	266	ALA	N-CA-C	-5.49	106.58	113.28
1	B	169	ASN	CB-CA-C	5.48	118.90	110.14
1	A	291	TYR	CA-C-N	5.34	124.67	118.85
1	A	291	TYR	C-N-CA	5.34	124.67	118.85
1	A	338	ALA	CA-C-N	-5.31	114.91	120.38
1	A	338	ALA	C-N-CA	-5.31	114.91	120.38
1	A	66	ASN	CB-CA-C	-5.24	110.11	117.23
1	A	35	ILE	CA-C-N	5.13	130.93	121.70
1	A	35	ILE	C-N-CA	5.13	130.93	121.70
1	B	168	VAL	N-CA-C	5.11	115.33	108.17
1	B	126	ILE	N-CA-C	5.08	115.81	110.62
1	B	35	ILE	CA-C-N	5.04	130.78	121.70
1	B	35	ILE	C-N-CA	5.04	130.78	121.70

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 ⓘ

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	92	0
1	B	2432	0	2209	103	0
All	All	4807	0	4363	194	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 21.

All (194) 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:169:ASN:C	1:B:172:CYS:H	1.89	0.80
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: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:HH11	1:B:354:ARG:HG3	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
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:B:362:GLU:C	1:B:364:GLU:H	1.99	0.67
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:362:GLU:C	1:B:363:ILE:HG13	2.20	0.66
1:A:352:ARG:NE	1:A:352:ARG:HA	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:GLU:CB	1:B:199:TYR:CA	2.73	0.66
1:A:25:VAL:HG22	1:A:26:THR:H	1.59	0.65
1:B:297:GLN:HG3	1:B:324:PHE:HD1	1.61	0.65
1:B:28:ASP:OD2	1:B:28:ASP:N	2.28	0.64
1:B:288:GLU:H	1:B:288:GLU:CD	2.04	0.64
1:A:291:TYR:HB2	1:A:299:LEU:HD21	1.79	0.64
1:B:352:ARG:HE	1:B:353:GLU:HG2	1.62	0.64
1:A:303:GLY:O	1:A:307:ARG:NH2	2.30	0.63
1:A:116:ASP:N	1:A:116:ASP:OD1	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:41:ASN:N	1:B:41:ASN:OD1	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:A:214:LEU:O	1:A:268:GLY:N	2.22	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:169:ASN:CG	1:A:171:ASN:HD21	2.11	0.58
1:A:123:HIS:HB2	1:A:164:SER:HA	1.84	0.58
1:A:351:THR:OG1	1:A:352:ARG:N	2.34	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:OD2	1:B:69:ASP:N	2.39	0.56
1:A:288:GLU:CD	1:A:288:GLU:H	2.13	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:A:362:GLU:C	1:A:364:GLU:H	2.14	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:ILE:HD11	1:A:147:GLY:O	2.09	0.53
1:A:350:LEU:N	1:A:351:THR:HA	2.24	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:72:THR:O	1:A:74:ALA:N	2.43	0.52
1:A:85:LYS:NZ	1:A:365:ASP:OD2	2.38	0.52
1:B:169:ASN:OD1	1:B:171:ASN:CG	2.53	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:A:134:LEU:HD23	1:A:138:ARG:HH12	1.76	0.50
1:A:258:THR:OG1	1:A:282:ARG:N	2.43	0.50
1:B:138:ARG:HB3	1:B:328:TYR:HE2	1.77	0.50
1:B:122:LEU:HD13	1:B:168:VAL:HG21	1.93	0.50
1:B:256:LEU:C	1:B:284:PRO:HB3	2.37	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:A:146:ARG:HG2	1:A:334:GLU:HG2	1.94	0.49
1:B:170:GLU:CA	1:B:172:CYS:N	2.76	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:25:VAL:HG22	1:B:26:THR:H	1.78	0.49
1:B:158:HIS:CD2	1:B:161:LEU:HG	2.48	0.49
1:B:205:TYR:OH	1:B:232:GLU:OE1	2.29	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:25:VAL:HG21	1:B:288:GLU:CD	2.38	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:B:101:PRO:O	1:B:102:THR:C	2.56	0.48
1:A:170:GLU:HA	1:A:172:CYS:H	1.79	0.48
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:ALA:HB3	1:A:339:PRO:HD3	1.95	0.47
1:B:158:HIS:NE2	1:B:160:ASP:O	2.47	0.47
1:B:320:LEU:HA	1:B:325:LEU:HD12	1.97	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:333:ASP:C	1:A:335:PRO:HD3	2.41	0.46
1:A:170:GLU:HA	1:A:171:ASN:C	2.40	0.46
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:A:40:GLY:C	1:A:47:VAL:H	2.23	0.46
1:A:357:GLU:O	1:A:360:VAL:HG22	2.16	0.46
1:B:89:HIS:CD2	1:B:335:PRO:HD2	2.51	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:A:121:ASP:OD1	1:A:124:GLN:HG2	2.16	0.45
1:A:158:HIS:C	1:A:160:ASP:H	2.24	0.45
1:B:248:GLN:O	1:B:252:ILE:HG13	2.16	0.45
1:B:128:SER:C	1:B:130:GLN:H	2.24	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:209:GLU:HG3	1:B:217:TYR:HB3	1.98	0.45
1:B:253:MET:O	1:B:257:GLY:N	2.50	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:362:GLU:C	1:B:364:GLU:N	2.70	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:157:ILE:HD11	1:B:219:GLN:HG2	2.00	0.44
1:B:322:HIS:CG	1:B:323:PRO:HD2	2.53	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
1:B:356:LYS:O	1:B:360:VAL:HG13	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:PHE:CD2	1:A:27:PHE:N	2.86	0.43
1:A:120:SER:OG	1:A:121:ASP:N	2.52	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:A:207:ALA:HA	1:A:208:PRO:HD3	1.91	0.42
1:B:158:HIS:HD2	1:B:161:LEU:HG	1.84	0.42
1:A:215:HIS:NE2	1:A:310:PRO:HD2	2.34	0.42
1:A:66:ASN:C	1:A:68:PHE:H	2.28	0.42
1:A:55:THR:C	1:A:57:GLN:H	2.27	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:249:LEU:O	1:A:253:MET:N	2.53	0.41
1:B:174:LEU:HD12	1:B:175:LYS:N	2.35	0.41
1:B:354:ARG:HH11	1:B:354:ARG:CG	2.29	0.41
1:B:23:PHE:HA	1:B:24:ASP:HA	1.91	0.41
1:B:179:PHE:HD2	1:B:179:PHE:HA	1.76	0.41
1:B:269:ALA:HB1	1:B:270:GLU:CA	2.44	0.41
1:B:314:ILE:HD12	1:B:314:ILE:HA	1.95	0.41
1:A:122:LEU:HA	1:A:122:LEU:HD12	1.85	0.41
1:B:144:LEU:HD22	1:B:226:VAL:HG22	2.02	0.41
1:B:297:GLN:HE22	1:B:323:PRO:HB2	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:A:148:LEU:HD12	1:A:148:LEU:HA	1.84	0.41
1:A:298:ALA:HB2	1:A:324:PHE:CE1	2.56	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:151:MET:HE3	1:B:151:MET:HB3	1.67	0.41
1:B:244:ASN:HB3	1:B:246:VAL:HG12	2.01	0.41
1:A:105:TYR:O	1:A:105:TYR:HD2	2.04	0.40
1:A:258:THR:HB	1:A:281:PRO:HA	2.03	0.40
1:A:27:PHE:N	1:A:27:PHE:HD2	2.20	0.40
1:A:149:LYS:O	1:A:153:SER:OG	2.36	0.40
1:A:152:HIS:HB3	1:A:219:GLN:OE1	2.21	0.40
1:A:23:PHE:HA	1:A:24:ASP:HA	1.89	0.40
1:B:45:GLY:HA2	1:B:65:PRO:CD	2.51	0.40
1:B:79:ARG:NH1	1:B:346:ASP:OD2	2.51	0.40
1:B:102:THR:C	1:B:104:PRO:HD2	2.46	0.40
1:B:138:ARG:NH1	1:B:324:PHE:O	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:199:TYR:C	1:B:201:ALA:H	2.30	0.40
1:B:302:LEU:HD12	1:B:302:LEU:HA	1.83	0.40
1:B:351:THR:OG1	1:B:355:ILE:HG13	2.21	0.40
1:B:93:ILE:HD12	1:B:93:ILE:HA	2.00	0.40
1:A:104:PRO:C	1:A:106:GLY:H	2.30	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%)	3	11
1	B	332/442 (75%)	292 (88%)	32 (10%)	8 (2%)	4	17
All	All	647/884 (73%)	562 (87%)	67 (10%)	18 (3%)	4	14

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
1	B	31	ASP

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Mol	Chain	Res	Type
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 ⓘ

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%)	166 (78%)	47 (22%)	1	3
1	B	217/373 (58%)	172 (79%)	45 (21%)	1	4
All	All	430/746 (58%)	338 (79%)	92 (21%)	1	4

All (92) 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	79	ARG
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	111	VAL
1	A	116	ASP
1	A	125	ILE
1	A	134	LEU

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Mol	Chain	Res	Type
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	159	ARG
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	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	350	LEU
1	A	352	ARG
1	A	353	GLU
1	A	360	VAL
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	46	VAL
1	B	70	VAL
1	B	71	VAL
1	B	73	ASN
1	B	81	LEU
1	B	98	ILE

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Mol	Chain	Res	Type
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	246	VAL
1	B	248	GLN
1	B	251	LEU
1	B	255	VAL
1	B	277	GLN
1	B	288	GLU
1	B	302	LEU
1	B	307	ARG
1	B	309	GLU
1	B	334	GLU
1	B	351	THR
1	B	360	VAL
1	B	363	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	HIS
1	A	238	GLN
1	B	58	GLN
1	B	165	ASN

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 oligosaccharides 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%)	-1.03	0 100 100	51, 89, 148, 326	0
1	B	336/442 (76%)	-1.08	0 100 100	40, 81, 149, 267	0
All	All	661/884 (74%)	-1.05	0 100 100	40, 84, 149, 326	0

There are no RSRZ outliers to report.

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 oligosaccharides 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.