



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:25 PM GMT

PDB ID : 3ZDT
Title : Crystal structure of basic patch mutant FAK FERM domain FAK31- 405 K216A, K218A, R221A, K222A
Authors : Goni, G.M.; Epifano, C.; Boskovic, J.; Camacho-Artacho, M.; Zhou, J.; Martin, M.T.; Eck, M.J.; Kremer, L.; Graeter, F.; Gervasio, F.L.; Perez-Moreno, M.; Lietha, D.
Deposited on : 2012-11-30
Resolution : 3.15 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) : 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

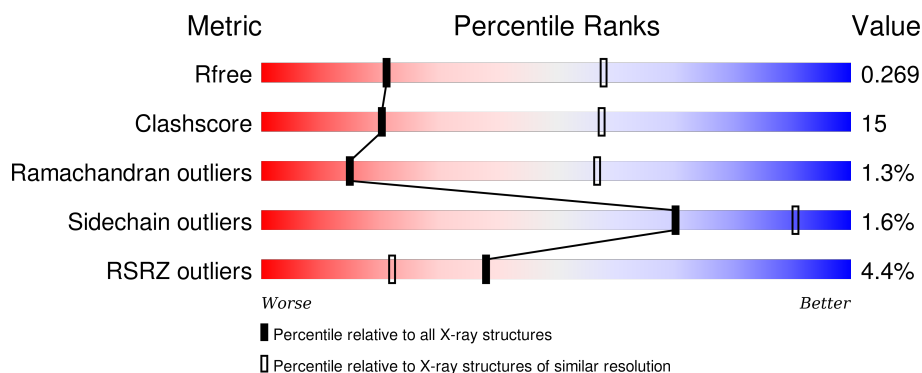
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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}	91344	1112 (3.20-3.12)
Clashscore	102246	1249 (3.20-3.12)
Ramachandran outliers	100387	1222 (3.20-3.12)
Sidechain outliers	100360	1221 (3.20-3.12)
RSRZ outliers	91569	1117 (3.20-3.12)

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 $\leq 5\%$. 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	377	<div> <div>2%</div> <div>54%</div> <div>31%</div> <div>•</div> <div>14%</div> </div>
1	B	377	<div> <div>5%</div> <div>59%</div> <div>22%</div> <div>•</div> <div>16%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5192 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 FOCAL ADHESION KINASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	0	0
			2624	1678	447	489	10			
1	B	317	Total	C	N	O	S	0	0	0
			2561	1639	436	476	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	GLY	-	EXPRESSION TAG	UNP Q00944
A	30	SER	-	EXPRESSION TAG	UNP Q00944
A	216	ALA	LYS	ENGINEERED MUTATION	UNP Q00944
A	218	ALA	LYS	ENGINEERED MUTATION	UNP Q00944
A	221	ALA	ARG	ENGINEERED MUTATION	UNP Q00944
A	222	ALA	LYS	ENGINEERED MUTATION	UNP Q00944
B	29	GLY	-	EXPRESSION TAG	UNP Q00944
B	30	SER	-	EXPRESSION TAG	UNP Q00944
B	216	ALA	LYS	ENGINEERED MUTATION	UNP Q00944
B	218	ALA	LYS	ENGINEERED MUTATION	UNP Q00944
B	221	ALA	ARG	ENGINEERED MUTATION	UNP Q00944
B	222	ALA	LYS	ENGINEERED MUTATION	UNP Q00944

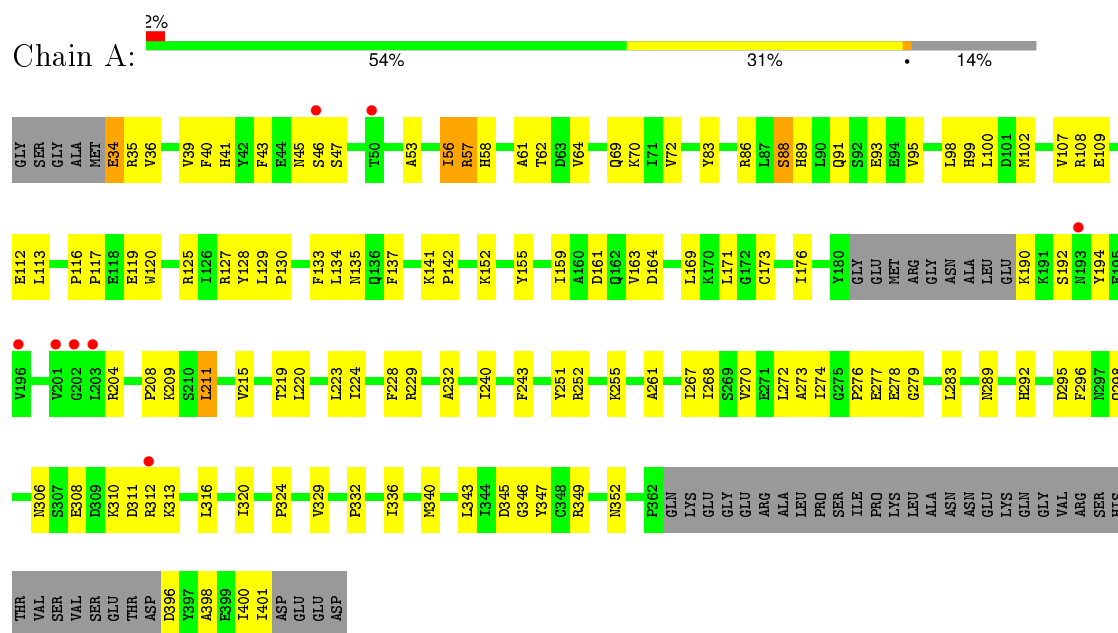
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	O	0	0
			4	4		
2	B	3	Total	O	0	0
			3	3		

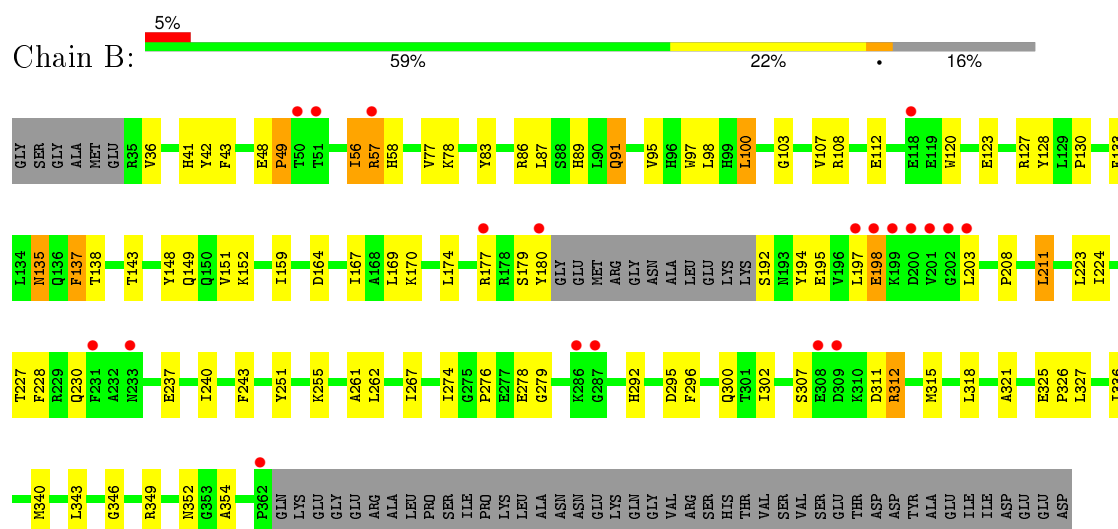
3 Residue-property plots [i](#)

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.

• Molecule 1: FOCAL ADHESION KINASE 1



• Molecule 1: FOCAL ADHESION KINASE 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	41.57Å 175.53Å 60.03Å 90.00° 93.94° 90.00°	Depositor
Resolution (Å)	43.88 – 3.15 43.88 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.6 (43.88-3.15) 99.6 (43.88-3.15)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.214 , 0.278 0.208 , 0.269	Depositor DCC
R_{free} test set	742 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	74.7	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 46.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 14762 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5192	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.74% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	1.10	13/2679 (0.5%)	0.88	8/3622 (0.2%)
1	B	0.99	9/2617 (0.3%)	0.85	5/3541 (0.1%)
All	All	1.05	22/5296 (0.4%)	0.86	13/7163 (0.2%)

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	B	0	1

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	34	GLU	CD-OE1	16.21	1.43	1.25
1	A	192	SER	CB-OG	13.87	1.60	1.42
1	A	312	ARG	CZ-NH1	-12.87	1.16	1.33
1	B	198	GLU	CD-OE1	11.26	1.38	1.25
1	B	195	GLU	CD-OE2	8.83	1.35	1.25
1	A	308	GLU	CD-OE2	-8.81	1.16	1.25
1	A	88	SER	CB-OG	8.76	1.53	1.42
1	B	312	ARG	CZ-NH2	7.83	1.43	1.33
1	B	177	ARG	CZ-NH1	7.51	1.42	1.33
1	B	195	GLU	CD-OE1	7.17	1.33	1.25
1	B	78	LYS	CD-CE	6.69	1.68	1.51
1	A	308	GLU	CD-OE1	6.48	1.32	1.25
1	A	312	ARG	CZ-NH2	6.48	1.41	1.33
1	A	34	GLU	CD-OE2	6.35	1.32	1.25
1	A	57	ARG	CZ-NH2	-6.29	1.24	1.33
1	A	113	LEU	CB-CG	6.05	1.70	1.52
1	A	109	GLU	CD-OE2	5.86	1.32	1.25
1	A	312	ARG	CD-NE	5.65	1.56	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	192	SER	CB-OG	5.63	1.49	1.42
1	B	312	ARG	CD-NE	5.47	1.55	1.46
1	B	137	PHE	CG-CD2	5.41	1.46	1.38
1	A	57	ARG	NE-CZ	5.36	1.40	1.33

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	312	ARG	NE-CZ-NH2	-18.29	111.16	120.30
1	A	312	ARG	NE-CZ-NH2	-11.49	114.56	120.30
1	A	57	ARG	NE-CZ-NH2	9.32	124.96	120.30
1	A	113	LEU	CB-CG-CD2	9.31	126.84	111.00
1	B	57	ARG	NE-CZ-NH2	-8.34	116.13	120.30
1	A	34	GLU	OE1-CD-OE2	6.16	130.69	123.30
1	A	211	LEU	CA-CB-CG	6.14	129.42	115.30
1	A	312	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	A	310	LYS	CD-CE-NZ	-5.50	99.05	111.70
1	B	312	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	A	57	ARG	NH1-CZ-NH2	-5.16	113.73	119.40
1	B	211	LEU	CA-CB-CG	5.07	126.96	115.30
1	B	312	ARG	CD-NE-CZ	-5.04	116.54	123.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	91	GLN	Sidechain

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	2624	0	2599	85	0
1	B	2561	0	2542	66	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
All	All	5192	0	5141	151	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 15.

All (151) 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:41:HIS:HD2	1:A:43:PHE:H	1.16	0.91
1:B:41:HIS:HD2	1:B:43:PHE:H	1.21	0.85
1:A:204:ARG:HE	1:A:209:LYS:HD3	1.41	0.84
1:B:89:HIS:NE2	1:B:91:GLN:HB3	1.93	0.84
1:A:133:PHE:HB2	1:A:137:PHE:CE2	2.13	0.81
1:A:61:ALA:HB3	1:A:396:ASP:N	1.96	0.81
1:A:211:LEU:O	1:A:215:VAL:HG12	1.81	0.81
1:A:89:HIS:CD2	1:A:91:GLN:HB3	2.16	0.81
1:B:194:TYR:HA	1:B:197:LEU:HD12	1.62	0.80
1:B:128:TYR:CE1	1:B:346:GLY:HA3	2.18	0.77
1:A:35:ARG:HD2	1:A:108:ARG:NH2	1.99	0.77
1:B:133:PHE:HB2	1:B:137:PHE:CE2	2.22	0.75
1:A:70:LYS:HG3	1:A:398:ALA:HB3	1.68	0.75
1:A:35:ARG:HD2	1:A:108:ARG:HH22	1.49	0.75
1:B:159:ILE:HD11	1:B:251:TYR:HB2	1.73	0.71
1:B:262:LEU:HD22	1:B:327:LEU:HD11	1.73	0.70
1:B:86:ARG:HD2	1:B:95:VAL:HG13	1.73	0.70
1:B:41:HIS:CD2	1:B:43:PHE:H	2.07	0.70
1:B:279:GLY:HA2	1:B:296:PHE:CE2	2.28	0.69
1:B:56:ILE:H	1:B:56:ILE:HD13	1.57	0.69
1:B:164:ASP:HB2	1:B:167:ILE:HG12	1.75	0.68
1:B:128:TYR:CD1	1:B:346:GLY:HA3	2.28	0.68
1:A:41:HIS:CD2	1:A:43:PHE:H	2.07	0.68
1:A:133:PHE:HB2	1:A:137:PHE:HE2	1.56	0.68
1:A:240:ILE:O	1:A:243:PHE:HB3	1.93	0.68
1:A:86:ARG:HD2	1:A:95:VAL:CG1	2.24	0.67
1:A:346:GLY:HA2	1:A:349:ARG:HD2	1.77	0.66
1:B:170:LYS:O	1:B:174:LEU:HG	1.95	0.65
1:A:219:THR:O	1:A:223:LEU:HG	1.97	0.65
1:A:128:TYR:CD1	1:A:346:GLY:HA3	2.31	0.65
1:A:129:LEU:HB2	1:A:276:PRO:HG3	1.79	0.65
1:A:127:ARG:NH2	1:A:343:LEU:HB2	2.12	0.65
1:A:86:ARG:HD2	1:A:95:VAL:HG11	1.78	0.65
1:A:99:HIS:NE2	1:A:349:ARG:NH2	2.46	0.64
1:B:292:HIS:HE1	1:B:295:ASP:OD1	1.80	0.64
1:B:41:HIS:HD2	1:B:43:PHE:N	1.93	0.64
1:B:311:ASP:OD1	1:B:312:ARG:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:LEU:HD22	1:B:107:VAL:HG21	1.79	0.63
1:A:98:LEU:HD22	1:A:107:VAL:HG21	1.80	0.63
1:A:161:ASP:OD1	1:A:208:PRO:HB2	1.98	0.63
1:A:311:ASP:OD2	1:A:313:LYS:HE2	1.99	0.63
1:A:128:TYR:CE1	1:A:346:GLY:HA3	2.33	0.63
1:A:278:GLU:N	1:A:278:GLU:OE1	2.31	0.63
1:B:261:ALA:HB1	1:B:267:ILE:HG23	1.81	0.63
1:B:86:ARG:NH2	1:B:123:GLU:OE2	2.29	0.63
1:B:86:ARG:HD2	1:B:95:VAL:CG1	2.27	0.62
1:B:103:GLY:O	1:B:107:VAL:HG12	2.00	0.62
1:B:240:ILE:O	1:B:243:PHE:HB3	1.99	0.62
1:A:36:VAL:O	1:A:108:ARG:NH1	2.33	0.61
1:A:277:GLU:HB2	1:A:278:GLU:OE1	2.01	0.60
1:B:97:TRP:CE2	1:B:127:ARG:HD2	2.37	0.59
1:A:159:ILE:CD1	1:A:251:TYR:HB2	2.33	0.59
1:B:108:ARG:HG2	1:B:112:GLU:OE2	2.03	0.59
1:A:99:HIS:NE2	1:A:345:ASP:OD2	2.24	0.58
1:B:148:TYR:HE1	1:B:243:PHE:CG	2.21	0.58
1:A:278:GLU:CD	1:A:278:GLU:H	2.05	0.58
1:B:159:ILE:CD1	1:B:251:TYR:HB2	2.34	0.57
1:B:307:SER:HA	1:B:315:MET:HG2	1.85	0.57
1:A:159:ILE:HD13	1:A:251:TYR:HB2	1.86	0.57
1:B:325:GLU:HG2	1:B:326:PRO:HD2	1.87	0.57
1:A:161:ASP:OD1	1:A:208:PRO:CB	2.54	0.56
1:A:56:ILE:HG22	1:A:400:ILE:HA	1.88	0.56
1:A:277:GLU:OE1	1:A:277:GLU:HA	2.06	0.55
1:B:56:ILE:N	1:B:56:ILE:HD13	2.21	0.55
1:A:173:CYS:HA	1:A:176:ILE:HD12	1.88	0.55
1:B:352:ASN:C	1:B:354:ALA:H	2.10	0.54
1:B:100:LEU:H	1:B:100:LEU:HD22	1.73	0.54
1:B:36:VAL:O	1:B:108:ARG:NH2	2.40	0.54
1:A:89:HIS:NE2	1:A:91:GLN:HB3	2.22	0.54
1:A:349:ARG:O	1:A:352:ASN:O	2.26	0.53
1:A:194:TYR:CD1	1:A:194:TYR:C	2.81	0.53
1:A:298:GLN:HB3	1:A:320:ILE:HG23	1.92	0.52
1:A:267:ILE:O	1:A:268:ILE:HD13	2.10	0.51
1:B:292:HIS:CE1	1:B:295:ASP:OD1	2.62	0.51
1:A:292:HIS:CE1	1:A:295:ASP:OD1	2.63	0.51
1:A:279:GLY:HA2	1:A:296:PHE:CE2	2.45	0.51
1:A:35:ARG:HG3	1:A:108:ARG:NH1	2.27	0.50
1:A:316:LEU:HB3	1:A:329:VAL:HB	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:ARG:HH21	1:A:209:LYS:NZ	2.08	0.49
1:A:62:THR:HA	1:A:396:ASP:HA	1.94	0.49
1:A:343:LEU:HD11	1:A:347:TYR:HE2	1.76	0.49
1:B:97:TRP:CD2	1:B:127:ARG:HD2	2.47	0.49
1:B:48:GLU:CD	1:B:49:PRO:HD2	2.33	0.49
1:B:336:ILE:O	1:B:340:MET:HG3	2.13	0.49
1:A:133:PHE:CE2	1:A:134:LEU:HG	2.47	0.48
1:B:58:HIS:HE1	1:B:108:ARG:HH11	1.60	0.48
1:A:99:HIS:CE1	1:A:349:ARG:HH22	2.31	0.47
1:B:274:ILE:HA	1:B:279:GLY:O	2.15	0.47
1:A:86:ARG:HD2	1:A:95:VAL:HG13	1.95	0.47
1:A:163:VAL:HG22	1:A:164:ASP:N	2.29	0.47
1:B:89:HIS:CD2	1:B:91:GLN:HB3	2.49	0.47
1:A:45:ASN:O	1:A:47:SER:N	2.48	0.47
1:B:300:GLN:HE21	1:B:321:ALA:HB2	1.80	0.47
1:A:99:HIS:CE1	1:A:349:ARG:NH2	2.82	0.47
1:B:255:LYS:HE2	1:B:278:GLU:OE2	2.14	0.46
1:A:141:LYS:HB2	1:A:142:PRO:HD3	1.98	0.46
1:A:273:ALA:HB2	1:A:283:LEU:HD11	1.96	0.46
1:B:179:SER:HB3	1:B:180:TYR:CD1	2.51	0.46
1:B:100:LEU:H	1:B:100:LEU:CD2	2.29	0.46
1:A:274:ILE:HA	1:A:279:GLY:O	2.16	0.46
1:A:69:GLN:HA	1:A:72:VAL:HG22	1.96	0.46
1:B:138:THR:HG23	1:B:237:GLU:OE2	2.15	0.46
1:A:155:TYR:CZ	1:A:171:LEU:HD12	2.51	0.46
1:B:302:ILE:HG12	1:B:318:LEU:CD2	2.46	0.46
1:A:34:GLU:CD	1:A:57:ARG:HD2	2.36	0.46
1:B:227:THR:O	1:B:230:GLN:HG2	2.16	0.45
1:B:77:VAL:HG13	1:B:143:THR:OG1	2.15	0.45
1:A:152:LYS:O	1:A:155:TYR:HB3	2.17	0.45
1:A:220:LEU:O	1:A:224:ILE:HG13	2.16	0.45
1:A:261:ALA:HB1	1:A:267:ILE:HG23	1.97	0.45
1:A:272:LEU:HD12	1:A:340:MET:CE	2.47	0.45
1:A:40:PHE:CD1	1:A:53:ALA:HB2	2.52	0.45
1:A:64:VAL:HG23	1:A:102:MET:O	2.17	0.45
1:B:208:PRO:HG2	1:B:211:LEU:HB2	1.99	0.45
1:A:204:ARG:NE	1:A:209:LYS:HD3	2.20	0.45
1:A:93:GLU:N	1:A:93:GLU:OE1	2.50	0.45
1:B:77:VAL:HG11	1:B:83:TYR:HE1	1.81	0.44
1:A:35:ARG:HD3	1:A:36:VAL:H	1.82	0.44
1:B:58:HIS:CE1	1:B:108:ARG:HH11	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:349:ARG:HA	1:B:354:ALA:HB3	1.99	0.44
1:A:100:LEU:HD23	1:A:349:ARG:NH2	2.33	0.43
1:A:261:ALA:HB1	1:A:267:ILE:CG2	2.48	0.43
1:A:108:ARG:HG2	1:A:112:GLU:OE2	2.18	0.43
1:A:332:PRO:HB2	1:A:336:ILE:HD12	2.00	0.43
1:A:83:TYR:HA	1:A:125:ARG:O	2.18	0.43
1:B:127:ARG:NH2	1:B:343:LEU:HB2	2.33	0.43
1:A:159:ILE:HD11	1:A:251:TYR:HB2	2.01	0.43
1:B:198:GLU:HA	1:B:203:LEU:HG	1.99	0.43
1:B:42:TYR:HB3	1:B:149:GLN:HB2	2.00	0.42
1:A:58:HIS:HB2	1:A:62:THR:HB	2.00	0.42
1:B:89:HIS:HB2	1:B:120:TRP:CZ3	2.53	0.42
1:B:224:ILE:O	1:B:228:PHE:HB3	2.19	0.42
1:A:129:LEU:HA	1:A:130:PRO:HD2	1.88	0.42
1:B:97:TRP:CZ2	1:B:127:ARG:HD2	2.55	0.42
1:A:62:THR:CA	1:A:396:ASP:HA	2.48	0.41
1:B:151:VAL:O	1:B:152:LYS:C	2.59	0.41
1:B:135:ASN:HD22	1:B:135:ASN:C	2.24	0.41
1:B:130:PRO:HG2	1:B:133:PHE:HA	2.02	0.41
1:B:302:ILE:HG12	1:B:318:LEU:HD22	2.03	0.41
1:A:57:ARG:HG3	1:A:401:ILE:HD11	2.02	0.41
1:A:127:ARG:CZ	1:A:343:LEU:HB2	2.50	0.41
1:A:229:ARG:O	1:A:232:ALA:CB	2.69	0.41
1:A:252:ARG:HH21	1:A:255:LYS:HE3	1.86	0.41
1:A:93:GLU:O	1:A:95:VAL:HG23	2.21	0.41
1:B:169:LEU:HD11	1:B:223:LEU:HD13	2.02	0.41
1:A:116:PRO:HG2	1:A:119:GLU:HG3	2.02	0.41
1:A:39:VAL:CG2	1:A:56:ILE:HD11	2.51	0.41
1:B:57:ARG:HD2	1:B:57:ARG:N	2.36	0.40
1:B:87:LEU:HD11	1:B:120:TRP:HB3	2.04	0.40
1:A:89:HIS:HB2	1:A:120:TRP:CZ3	2.57	0.40
1:B:279:GLY:HA2	1:B:296:PHE:CZ	2.57	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	320/377 (85%)	286 (89%)	28 (9%)	6 (2%)	10	48
1	B	313/377 (83%)	281 (90%)	30 (10%)	2 (1%)	30	74
All	All	633/754 (84%)	567 (90%)	58 (9%)	8 (1%)	15	57

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	46	SER
1	A	228	PHE
1	A	324	PRO
1	A	117	PRO
1	A	169	LEU
1	A	270	VAL
1	B	276	PRO
1	B	49	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	285/329 (87%)	279 (98%)	6 (2%)	61	87
1	B	280/329 (85%)	277 (99%)	3 (1%)	80	93
All	All	565/658 (86%)	556 (98%)	9 (2%)	70	90

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	ILE
1	A	88	SER
1	A	135	ASN
1	A	190	LYS

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Mol	Chain	Res	Type
1	A	289	ASN
1	A	306	ASN
1	B	56	ILE
1	B	100	LEU
1	B	135	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	HIS
1	A	58	HIS
1	A	89	HIS
1	A	96	HIS
1	A	135	ASN
1	A	292	HIS
1	A	303	GLN
1	B	41	HIS
1	B	58	HIS
1	B	96	HIS
1	B	99	HIS
1	B	289	ASN
1	B	292	HIS
1	B	300	GLN
1	B	303	GLN
1	B	317	GLN

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 [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 ⓘ

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	326/377 (86%)	0.11	8 (2%) 61 45	33, 69, 133, 167	0
1	B	317/377 (84%)	0.17	20 (6%) 23 12	36, 77, 135, 190	0
All	All	643/754 (85%)	0.14	28 (4%) 38 22	33, 73, 134, 190	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	177	ARG	3.6
1	A	202	GLY	3.6
1	B	286	LYS	3.5
1	B	203	LEU	3.3
1	A	203	LEU	3.3
1	B	202	GLY	3.2
1	B	198	GLU	3.2
1	A	50	THR	3.0
1	B	287	GLY	2.9
1	B	180	TYR	2.8
1	B	233	ASN	2.7
1	B	197	LEU	2.6
1	B	57	ARG	2.6
1	A	193	ASN	2.6
1	A	201	VAL	2.5
1	A	196	VAL	2.4
1	B	309	ASP	2.4
1	B	199	LYS	2.3
1	B	362	PRO	2.3
1	B	50	THR	2.3
1	B	51	THR	2.2
1	B	118	GLU	2.2
1	B	200	ASP	2.2
1	B	308	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	201	VAL	2.2
1	A	46	SER	2.1
1	A	312	ARG	2.1
1	B	231	PHE	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.