



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:50 PM UTC

PDB ID : 7ANK / pdb_00007ank
Title : Crystal structure of sarcomeric protein FATZ-1 (d91-FATZ-1 construct) in complex with half dimer of alpha-actinin-2
Authors : Sponga, A.; Arolas, J.L.; Rodriguez Chamorro, A.; Mlynek, G.; Hollerl, E.; Schreiner, C.; Pedron, M.; Kostan, J.; Ribeiro, E.A.; Djinovic-Carugo, K.
Deposited on : 2020-10-12
Resolution : 3.20 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

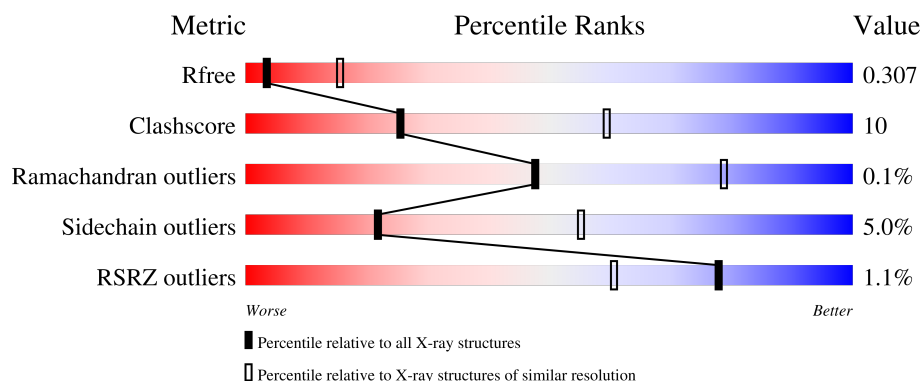
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	535	
2	B	389	
3	C	209	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7319 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 Alpha-actinin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	479	Total	C	N	O	S	71	0	0
			3928	2463	716	728	21			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	508	SER	-	expression tag	UNP P35609
A	509	GLU	-	expression tag	UNP P35609
A	510	ARG	-	expression tag	UNP P35609
A	511	VAL	-	expression tag	UNP P35609
A	512	ARG	-	expression tag	UNP P35609
A	513	ASN	-	expression tag	UNP P35609
A	514	PHE	-	expression tag	UNP P35609
A	515	GLU	-	expression tag	UNP P35609
A	516	ASP	-	expression tag	UNP P35609
A	517	PRO	-	expression tag	UNP P35609
A	518	ALA	-	expression tag	UNP P35609
A	519	ALA	-	expression tag	UNP P35609
A	520	ASN	-	expression tag	UNP P35609
A	521	LYS	-	expression tag	UNP P35609
A	522	ALA	-	expression tag	UNP P35609
A	523	ARG	-	expression tag	UNP P35609
A	524	LYS	-	expression tag	UNP P35609
A	525	GLU	-	expression tag	UNP P35609
A	526	ALA	-	expression tag	UNP P35609
A	527	GLU	-	expression tag	UNP P35609
A	528	LEU	-	expression tag	UNP P35609
A	529	ALA	-	expression tag	UNP P35609
A	530	ALA	-	expression tag	UNP P35609
A	531	ALA	-	expression tag	UNP P35609
A	532	THR	-	expression tag	UNP P35609
A	533	ALA	-	expression tag	UNP P35609
A	534	GLU	-	expression tag	UNP P35609

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Chain	Residue	Modelled	Actual	Comment	Reference
A	535	GLN	-	expression tag	UNP P35609

- Molecule 2 is a protein called Alpha-actinin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	382	Total	C	N	O	S	36	0	0
			3079	1926	538	599	16			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	506	GLY	-	expression tag	UNP P35609
B	507	SER	-	expression tag	UNP P35609
B	508	SER	-	expression tag	UNP P35609

- Molecule 3 is a protein called Myozenin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	38	Total	C	N	O	S	0	0	0
			312	201	52	57	2			

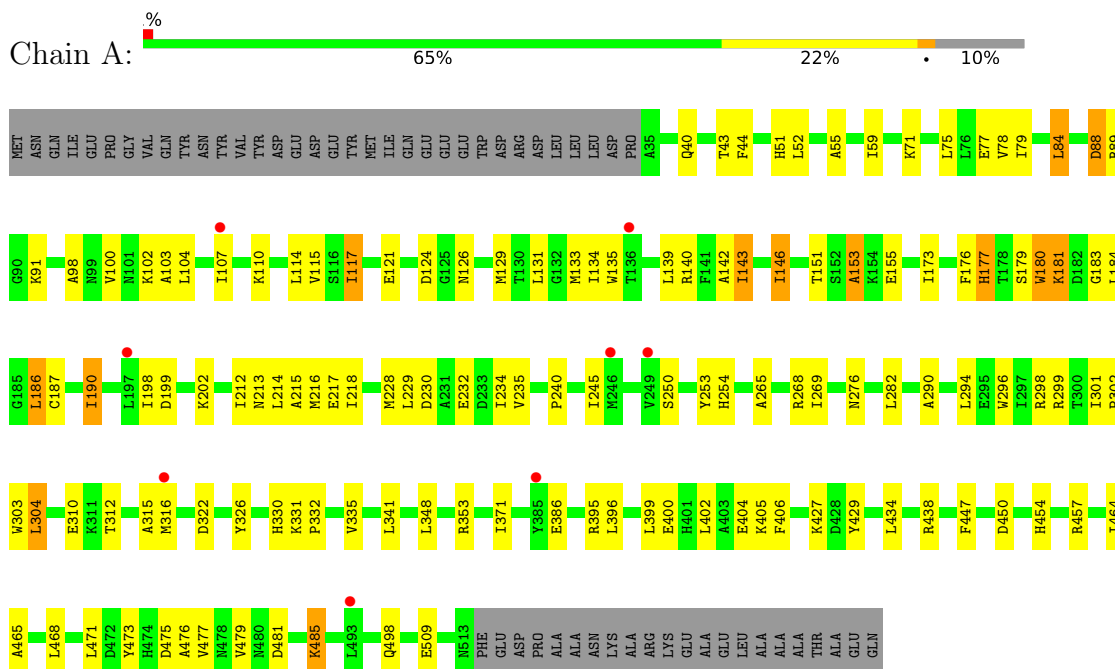
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	91	GLY	-	expression tag	UNP Q9NP98

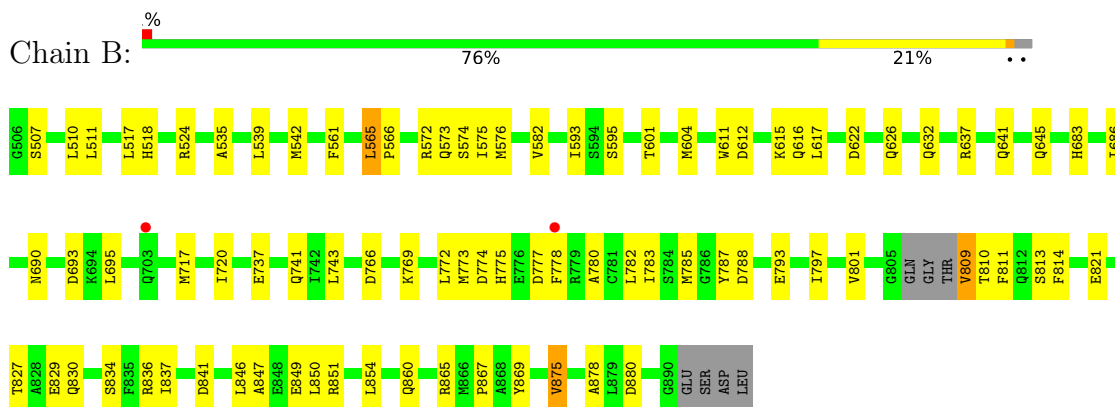
3 Residue-property plots

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: Alpha-actinin-2



• Molecule 2: Alpha-actinin-2



• Molecule 3: Myozenin-1



ASP GLY GLU THR GLU GLU LEU	K233	ALA	SER	LYS	ARG	MET	THR	PHE	GLN	MET	PRO	PHE	ASP	LEU	GLY	PRO	LEU	LEU	SER	GLU	PRO	LEU	VAL	LEU	TYR	ASN	GLN	ASN	LEU	SER	ASN	ARG	PRO	SER	PHE	ASN	ARG	THR	PRO	ILE	TRP	LEU	SER	SER	GLY	GLU	PRO	VAL	ASP	TYR	ASN	VAL	ASP	ILE	GLY	ILE	PRO	LEU																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.60Å 56.92Å 209.38Å 90.00° 94.56° 90.00°	Depositor
Resolution (Å)	46.94 – 3.20 46.94 – 3.20	Depositor EDS
% Data completeness (in resolution range)	98.9 (46.94-3.20) 98.9 (46.94-3.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 3.19Å)	Xtriage
Refinement program	BUSTER 2.10.3 (6-FEB-2020)	Depositor
R, R_{free}	0.255 , 0.284 0.281 , 0.307	Depositor DCC
R_{free} test set	1288 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	127.5	Xtriage
Anisotropy	0.516	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 185.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7319	wwPDB-VP
Average B, all atoms (Å ²)	206.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.92% 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	0.69	1/3999 (0.0%)	1.11	7/5386 (0.1%)
2	B	0.66	0/3134	1.08	6/4232 (0.1%)
3	C	0.53	0/321	0.86	0/431
All	All	0.67	1/7454 (0.0%)	1.08	13/10049 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	153	ALA	CA-C	7.43	1.62	1.52

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	386	GLU	CA-C-N	8.41	133.44	120.82
1	A	386	GLU	C-N-CA	8.41	133.44	120.82
1	A	450	ASP	CA-CB-CG	7.46	120.06	112.60
2	B	827	THR	CA-C-N	6.07	128.70	120.38
2	B	827	THR	C-N-CA	6.07	128.70	120.38
1	A	322	ASP	CA-CB-CG	6.03	118.63	112.60
1	A	180	TRP	CA-C-N	5.67	128.15	120.38
1	A	180	TRP	C-N-CA	5.67	128.15	120.38
1	A	88	ASP	CA-CB-CG	5.56	118.16	112.60
2	B	787	TYR	CA-C-N	5.53	132.10	121.54
2	B	787	TYR	C-N-CA	5.53	132.10	121.54
2	B	847	ALA	CA-C-N	5.21	127.26	120.28
2	B	847	ALA	C-N-CA	5.21	127.26	120.28

There are no chirality outliers.

There are no planarity outliers.

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	3928	0	3937	87	0
2	B	3079	0	3001	57	0
3	C	312	0	300	4	0
All	All	7319	0	7238	138	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 10.

All (138) 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)
2:B:611:TRP:HE1	2:B:615:LYS:HE2	1.22	1.04
1:A:405:LYS:HZ3	2:B:542:MET:HB2	1.26	1.00
2:B:772:LEU:HB2	2:B:811:PHE:HA	1.42	0.99
1:A:139:LEU:HA	1:A:143:ILE:HG13	1.53	0.88
1:A:282:LEU:HB3	1:A:348:LEU:HD21	1.54	0.87
2:B:810:THR:HB	2:B:813:SER:HB3	1.57	0.86
1:A:146:ILE:HD11	1:A:254:HIS:CE1	2.11	0.85
2:B:810:THR:HB	2:B:813:SER:CB	2.07	0.84
2:B:611:TRP:NE1	2:B:615:LYS:HE2	1.93	0.84
1:A:199:ASP:HB3	1:A:202:LYS:HZ3	1.49	0.78
1:A:399:LEU:HD21	1:A:471:LEU:HB3	1.66	0.77
1:A:176:PHE:HA	1:A:180:TRP:CD1	2.21	0.76
1:A:282:LEU:CB	1:A:348:LEU:HD21	2.17	0.74
1:A:110:LYS:HB3	1:A:140:ARG:HE	1.53	0.73
2:B:683:HIS:ND1	2:B:686:ILE:HD11	2.04	0.72
1:A:454:HIS:HA	1:A:457:ARG:HG2	1.71	0.71
1:A:341:LEU:HD21	1:A:371:ILE:HD13	1.73	0.71
2:B:780:ALA:HA	2:B:783:ILE:CD1	2.20	0.71
1:A:190:ILE:HB	1:A:198:ILE:HD12	1.75	0.69
1:A:186:LEU:N	1:A:186:LEU:HD23	2.08	0.68
2:B:851:ARG:HH21	2:B:860:GLN:HE22	1.43	0.66
2:B:524:ARG:NH2	2:B:574:SER:OG	2.31	0.64
2:B:573:GLN:HA	2:B:576:MET:HG2	1.80	0.64
1:A:183:GLY:HA3	1:A:212:ILE:HG12	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:611:TRP:HE1	2:B:615:LYS:CE	2.06	0.63
1:A:139:LEU:HD11	1:A:153:ALA:HB1	1.81	0.62
2:B:875:VAL:HG13	2:B:878:ALA:HB2	1.83	0.61
1:A:146:ILE:HD11	1:A:254:HIS:NE2	2.15	0.61
2:B:772:LEU:HD12	2:B:809:VAL:HG22	1.81	0.61
1:A:405:LYS:NZ	2:B:542:MET:HB2	2.08	0.61
1:A:396:LEU:O	1:A:400:GLU:HG2	2.01	0.60
2:B:810:THR:HB	2:B:813:SER:HB2	1.81	0.60
1:A:402:LEU:HB3	1:A:468:LEU:HD21	1.82	0.60
1:A:43:THR:HA	1:A:228:MET:HB3	1.84	0.59
1:A:353:ARG:HH12	3:C:190:ARG:HH12	1.52	0.58
1:A:173:ILE:HA	1:A:179:SER:HB3	1.86	0.57
1:A:399:LEU:HD21	1:A:471:LEU:CB	2.33	0.57
1:A:40:GLN:HB3	1:A:131:LEU:HD22	1.87	0.56
1:A:139:LEU:HA	1:A:143:ILE:CG1	2.32	0.56
1:A:183:GLY:HA2	1:A:186:LEU:HD21	1.87	0.56
2:B:535:ALA:O	2:B:539:LEU:HB2	2.06	0.55
1:A:186:LEU:HD23	1:A:186:LEU:H	1.68	0.55
2:B:683:HIS:HA	2:B:686:ILE:HG12	1.89	0.54
2:B:572:ARG:HH12	2:B:573:GLN:HE21	1.54	0.54
1:A:59:ILE:HG22	1:A:71:LYS:HD2	1.89	0.53
1:A:121:GLU:HA	1:A:124:ASP:HB3	1.89	0.53
1:A:181:LYS:HG3	1:A:240:PRO:HG3	1.90	0.53
1:A:240:PRO:HB2	1:A:245:ILE:HD11	1.91	0.53
1:A:230:ASP:O	1:A:234:ILE:HG12	2.09	0.52
1:A:121:GLU:HB2	1:A:129:MET:SD	2.49	0.52
1:A:476:ALA:HA	1:A:479:VAL:HG22	1.92	0.52
2:B:737:GLU:O	2:B:741:GLN:HG2	2.10	0.52
1:A:190:ILE:HB	1:A:198:ILE:CD1	2.40	0.52
1:A:199:ASP:HB3	1:A:202:LYS:NZ	2.21	0.52
1:A:265:ALA:O	1:A:269:ILE:HG12	2.10	0.52
1:A:151:THR:HB	1:A:155:GLU:HB2	1.92	0.51
1:A:353:ARG:NH1	3:C:190:ARG:HH12	2.09	0.51
1:A:434:LEU:O	1:A:438:ARG:HG2	2.11	0.51
1:A:114:LEU:HB2	1:A:117:ILE:CG2	2.41	0.50
1:A:142:ALA:O	1:A:250:SER:HB2	2.10	0.50
1:A:98:ALA:O	1:A:102:LYS:HG3	2.12	0.50
1:A:110:LYS:HB3	1:A:140:ARG:NE	2.25	0.50
1:A:117:ILE:HD12	1:A:129:MET:CG	2.42	0.50
2:B:869:TYR:HA	2:B:880:ASP:HB2	1.94	0.49
2:B:518:HIS:NE2	2:B:582:VAL:HG11	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:TRP:HD1	1:A:299:ARG:NH2	2.10	0.49
1:A:276:ASN:ND2	2:B:865:ARG:HH12	2.10	0.48
2:B:850:LEU:O	2:B:854:LEU:HB2	2.13	0.48
1:A:126:ASN:HB3	1:A:129:MET:HB3	1.95	0.48
2:B:780:ALA:HA	2:B:783:ILE:HD11	1.96	0.48
1:A:214:LEU:O	1:A:218:ILE:HG12	2.14	0.48
2:B:793:GLU:O	2:B:797:ILE:HG12	2.14	0.48
1:A:117:ILE:HD12	1:A:129:MET:HG3	1.95	0.48
1:A:404:GLU:HG3	2:B:542:MET:HE1	1.96	0.48
2:B:778:PHE:HE2	2:B:797:ILE:HG13	1.79	0.48
1:A:40:GLN:OE1	1:A:131:LEU:HB3	2.14	0.48
1:A:296:TRP:CD1	1:A:299:ARG:NH2	2.82	0.48
2:B:565:LEU:N	2:B:566:PRO:HD2	2.29	0.48
1:A:44:PHE:HB3	1:A:134:ILE:HG21	1.95	0.47
1:A:55:ALA:HB2	1:A:78:VAL:HG21	1.96	0.47
1:A:454:HIS:HA	1:A:457:ARG:CG	2.42	0.47
1:A:51:HIS:ND1	1:A:79:ILE:HG22	2.29	0.47
1:A:303:TRP:CZ3	1:A:304:LEU:HD13	2.49	0.47
1:A:326:TYR:HA	1:A:330:HIS:HB2	1.96	0.47
1:A:187:CYS:SG	1:A:215:ALA:HB2	2.55	0.46
2:B:717:MET:HE3	2:B:720:ILE:HB	1.97	0.46
1:A:100:VAL:O	1:A:104:LEU:HG	2.16	0.46
1:A:103:ALA:O	1:A:107:ILE:HG12	2.16	0.46
1:A:331:LYS:N	1:A:332:PRO:HD2	2.31	0.46
2:B:867:PRO:HG2	2:B:880:ASP:HB3	1.96	0.46
1:A:177:HIS:HB2	1:A:240:PRO:HD2	1.97	0.46
1:A:117:ILE:HD13	1:A:133:MET:HB2	1.98	0.46
2:B:612:ASP:O	2:B:616:GLN:HG2	2.16	0.46
2:B:774:ASP:OD1	2:B:775:HIS:NE2	2.49	0.46
2:B:772:LEU:HD12	2:B:809:VAL:CG2	2.46	0.45
1:A:427:LYS:HG3	1:A:429:TYR:HE1	1.81	0.45
2:B:782:LEU:O	2:B:785:MET:O	2.34	0.45
1:A:447:PHE:HE1	2:B:601:THR:HG21	1.82	0.45
2:B:778:PHE:CD1	2:B:814:PHE:HE1	2.34	0.45
1:A:481:ASP:O	1:A:485:LYS:HG2	2.16	0.45
1:A:77:GLU:HG2	1:A:84:LEU:HB2	1.99	0.45
1:A:406:PHE:HA	1:A:464:ILE:HD11	1.99	0.45
2:B:573:GLN:HA	2:B:576:MET:CG	2.45	0.45
2:B:572:ARG:HH12	2:B:573:GLN:NE2	2.16	0.44
1:A:181:LYS:NZ	1:A:235:VAL:HA	2.32	0.44
2:B:645:GLN:HB2	2:B:695:LEU:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:836:ARG:HG2	2:B:841:ASP:HA	1.98	0.44
3:C:188:TRP:CD1	3:C:192:MET:CE	3.00	0.44
1:A:216:MET:SD	1:A:229:LEU:O	2.76	0.44
2:B:772:LEU:HB2	2:B:811:PHE:CA	2.30	0.44
2:B:507:SER:HA	2:B:510:LEU:HD12	1.98	0.44
2:B:637:ARG:O	2:B:641:GLN:HG2	2.17	0.44
1:A:176:PHE:HA	1:A:180:TRP:HD1	1.80	0.44
1:A:406:PHE:CE2	1:A:465:ALA:HB2	2.52	0.44
1:A:135:TRP:CZ2	1:A:139:LEU:HD13	2.53	0.43
2:B:846:LEU:HB2	2:B:849:GLU:HG3	2.00	0.43
2:B:778:PHE:CE2	2:B:797:ILE:HG13	2.53	0.43
2:B:801:VAL:HG22	2:B:809:VAL:HG12	1.99	0.43
2:B:539:LEU:HD23	2:B:617:LEU:HB2	2.00	0.43
2:B:766:ASP:HA	2:B:773:MET:HB3	2.00	0.43
1:A:405:LYS:NZ	2:B:542:MET:H	2.16	0.43
1:A:143:ILE:HD13	1:A:250:SER:HB3	2.00	0.43
1:A:52:LEU:HG	1:A:75:LEU:HD13	2.01	0.42
1:A:265:ALA:HA	2:B:834:SER:OG	2.18	0.42
1:A:473:TYR:CE2	1:A:475:ASP:HB3	2.54	0.42
1:A:199:ASP:CB	1:A:202:LYS:HZ3	2.27	0.42
2:B:622:ASP:O	2:B:626:GLN:HG2	2.20	0.42
2:B:780:ALA:HA	2:B:783:ILE:HG12	2.01	0.42
1:A:294:LEU:O	1:A:298:ARG:HG3	2.20	0.42
1:A:301:ILE:N	1:A:302:PRO:HD2	2.34	0.42
1:A:312:THR:HG23	1:A:315:ALA:H	1.84	0.42
2:B:575:ILE:HG22	2:B:604:MET:HE1	2.02	0.42
1:A:213:ASN:O	1:A:217:GLU:HG2	2.19	0.41
2:B:593:ILE:HG23	2:B:595:SER:H	1.84	0.41
2:B:561:PHE:HA	3:C:227:PRO:HB3	2.03	0.41
1:A:290:ALA:O	1:A:294:LEU:HB2	2.21	0.41
1:A:146:ILE:HG13	1:A:253:TYR:CE1	2.55	0.40
2:B:773:MET:HG3	2:B:777:ASP:CB	2.52	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	477/535 (89%)	467 (98%)	10 (2%)	0	100	100
2	B	378/389 (97%)	359 (95%)	18 (5%)	1 (0%)	36	68
3	C	34/209 (16%)	32 (94%)	2 (6%)	0	100	100
All	All	889/1133 (78%)	858 (96%)	30 (3%)	1 (0%)	48	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	788	ASP

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	420/467 (90%)	396 (94%)	24 (6%)	18	51
2	B	332/338 (98%)	318 (96%)	14 (4%)	26	60
3	C	32/151 (21%)	31 (97%)	1 (3%)	35	66
All	All	784/956 (82%)	745 (95%)	39 (5%)	22	55

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	84	LEU
1	A	88	ASP
1	A	89	ARG
1	A	91	LYS
1	A	115	VAL
1	A	117	ILE
1	A	143	ILE
1	A	146	ILE

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Mol	Chain	Res	Type
1	A	177	HIS
1	A	181	LYS
1	A	184	LEU
1	A	186	LEU
1	A	190	ILE
1	A	232	GLU
1	A	268	ARG
1	A	304	LEU
1	A	310	GLU
1	A	316	MET
1	A	335	VAL
1	A	395	ARG
1	A	477	VAL
1	A	485	LYS
1	A	498	GLN
1	A	509	GLU
2	B	511	LEU
2	B	517	LEU
2	B	565	LEU
2	B	632	GLN
2	B	690	ASN
2	B	693	ASP
2	B	743	LEU
2	B	769	LYS
2	B	809	VAL
2	B	821	GLU
2	B	829	GLU
2	B	830	GLN
2	B	837	ILE
2	B	875	VAL
3	C	215	LEU

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

Mol	Chain	Res	Type
1	A	276	ASN
1	A	336	GLN
1	A	422	GLN
1	A	444	HIS
1	A	466	GLN
1	A	484	GLN
2	B	546	HIS

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Mol	Chain	Res	Type
2	B	573	GLN
2	B	579	GLN
2	B	632	GLN
2	B	655	ASN
2	B	684	ASN
2	B	699	HIS
2	B	710	ASN
2	B	754	GLN
2	B	860	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 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	470/535 (87%)	-0.04	8 (1%) 69 49	134, 206, 270, 286	0
2	B	377/389 (96%)	-0.29	2 (0%) 87 76	145, 191, 288, 295	0
3	C	38/209 (18%)	0.04	0 100 100	186, 222, 241, 246	0
All	All	885/1133 (78%)	-0.14	10 (1%) 78 61	134, 196, 277, 295	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	778	PHE	3.1
1	A	493	LEU	2.7
1	A	136	THR	2.6
1	A	197	LEU	2.5
2	B	703	GLN	2.4
1	A	249	VAL	2.3
1	A	316	MET	2.3
1	A	246	MET	2.0
1	A	107	ILE	2.0
1	A	385	TYR	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 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.