



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:16 AM GMT

PDB ID : 3OF0
Title : crystal structure of the L317I mutant of the chicken c-Src tyrosine kinase domain
Authors : Boubeva, R.; Pernot, L.; Perozzo, R.; Scapozza, L.
Deposited on : 2010-08-13
Resolution : 2.70 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

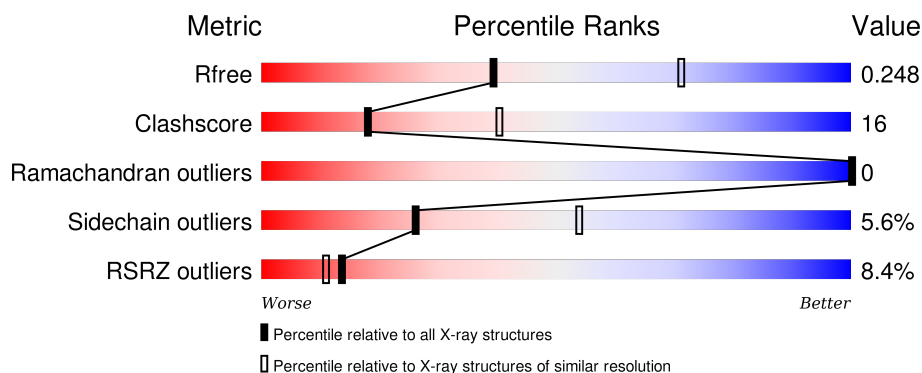
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	286	<div> <div>8%</div> <div>61%</div> <div>28%</div> <div>9%</div> </div>
1	B	286	<div> <div>7%</div> <div>57%</div> <div>29%</div> <div>12%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4297 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 Proto-oncogene tyrosine-protein kinase Src.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	0	0
			2066	1325	348	377	16			
1	B	251	Total	C	N	O	S	0	0	0
			1990	1277	332	365	16			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	248	GLY	-	EXPRESSION TAG	UNP P00523
A	249	HIS	-	EXPRESSION TAG	UNP P00523
A	250	MET	-	EXPRESSION TAG	UNP P00523
A	317	ILE	LEU	ENGINEERED MUTATION	UNP P00523
B	248	GLY	-	EXPRESSION TAG	UNP P00523
B	249	HIS	-	EXPRESSION TAG	UNP P00523
B	250	MET	-	EXPRESSION TAG	UNP P00523
B	317	ILE	LEU	ENGINEERED MUTATION	UNP P00523

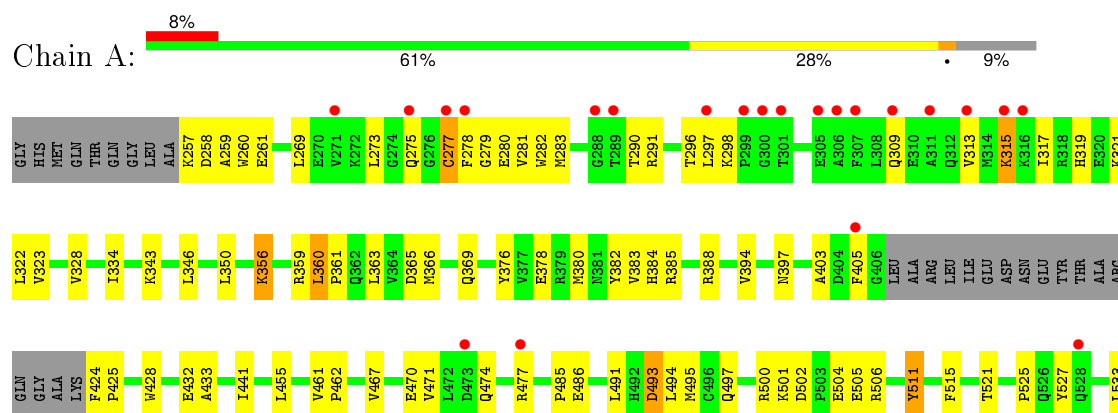
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	108	Total	O	0	0
			108	108		
2	B	133	Total	O	0	0
			133	133		

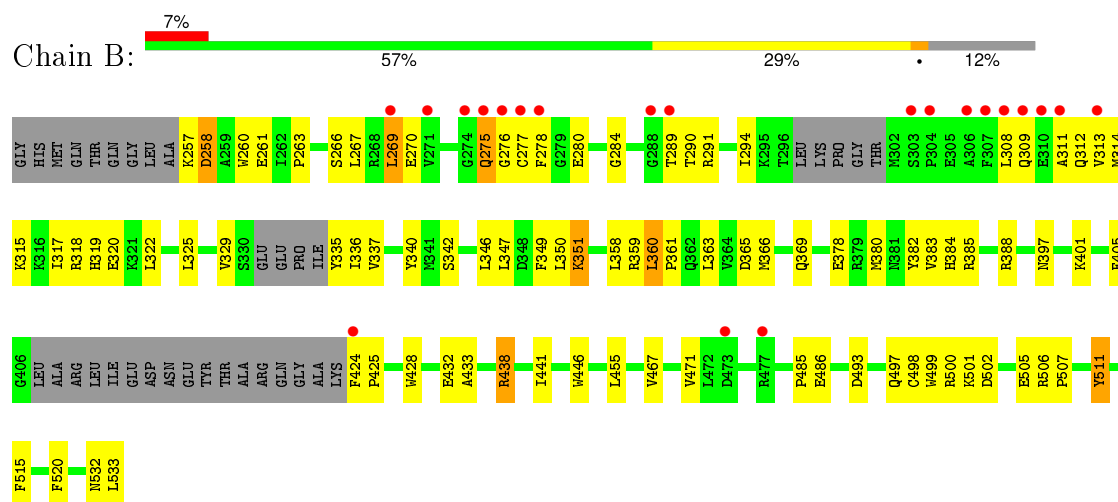
3 Residue-property plots

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: Proto-oncogene tyrosine-protein kinase Src



- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	42.07Å 63.50Å 74.13Å 78.66° 89.41° 90.00°	Depositor
Resolution (Å)	32.78 – 2.70 32.78 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.3 (32.78-2.70) 91.2 (32.78-2.70)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 2.68Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.233 , 0.262 0.218 , 0.248	Depositor DCC
R_{free} test set	977 reflections (4.86%)	DCC
Wilson B-factor (Å ²)	25.8	Xtriage
Anisotropy	0.677	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 54.7	EDS
Estimated twinning fraction	0.030 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 20128 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	4297	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.69% 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	0.26	0/2116	0.43	0/2866
1	B	0.23	0/2036	0.41	0/2755
All	All	0.25	0/4152	0.42	0/5621

There are no bond length outliers.

There are no bond angle outliers.

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	2066	0	2027	63	0
1	B	1990	0	1942	63	0
2	A	108	0	0	3	0
2	B	133	0	0	3	0
All	All	4297	0	3969	126	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 16.

All (126) 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:279:GLY:HA2	1:A:298:LYS:HD3	1.40	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:500:ARG:HD3	1:B:505:GLU:HB3	1.53	0.89
1:A:280:GLU:HG3	1:A:298:LYS:HE2	1.54	0.88
1:A:500:ARG:HD3	1:A:505:GLU:HB3	1.53	0.87
1:A:260:TRP:HE1	1:A:315:LYS:HG2	1.44	0.82
1:A:257:LYS:CG	1:A:258:ASP:H	1.93	0.81
1:B:359:ARG:HD3	2:B:191:HOH:O	1.84	0.77
1:A:260:TRP:HB3	1:A:328:VAL:HG22	1.66	0.77
1:B:257:LYS:HG2	1:B:261:GLU:HG3	1.67	0.77
1:B:311:ALA:HB1	1:B:315:LYS:HE3	1.68	0.76
1:B:329:VAL:HB	1:B:335:TYR:HB2	1.73	0.70
1:A:297:LEU:HD23	1:A:334:ILE:HG13	1.74	0.69
1:A:297:LEU:HD12	1:A:298:LYS:N	2.09	0.67
1:B:309:GLN:O	1:B:313:VAL:HG23	1.95	0.67
1:A:350:LEU:HD21	1:A:455:LEU:HA	1.74	0.67
1:A:359:ARG:HB3	1:A:361:PRO:HD2	1.76	0.67
1:B:257:LYS:CG	1:B:261:GLU:HG3	2.25	0.67
1:B:350:LEU:HD21	1:B:455:LEU:HA	1.76	0.67
1:A:279:GLY:HA3	1:A:296:THR:O	1.96	0.66
1:A:384:HIS:O	1:A:385:ARG:HB2	1.93	0.66
1:A:521:THR:O	1:A:525:PRO:HG3	1.96	0.66
1:B:384:HIS:O	1:B:385:ARG:HB2	1.97	0.63
1:A:257:LYS:HG2	1:A:258:ASP:H	1.62	0.63
1:A:378:GLU:HG3	1:A:441:ILE:HG12	1.81	0.62
1:B:320:GLU:O	1:B:401:LYS:HE2	1.98	0.62
1:B:382:TYR:HB3	1:B:405:PHE:HZ	1.63	0.62
1:A:309:GLN:O	1:A:313:VAL:HG23	1.99	0.61
1:A:257:LYS:CG	1:A:258:ASP:N	2.64	0.60
1:B:351:LYS:HB3	2:B:160:HOH:O	2.01	0.60
1:A:260:TRP:HE1	1:A:315:LYS:CG	2.15	0.59
1:B:267:LEU:HD21	1:B:337:VAL:HG21	1.84	0.58
1:A:467:VAL:HG22	1:A:470:GLU:HG3	1.85	0.58
1:A:380:MET:HB2	1:A:382:TYR:HD2	1.69	0.58
1:A:343:LYS:HB2	1:A:394:VAL:HB	1.86	0.57
1:A:319:HIS:HB3	1:A:322:LEU:HD12	1.85	0.57
1:B:359:ARG:HA	2:B:191:HOH:O	2.04	0.57
1:B:378:GLU:HG3	1:B:441:ILE:HG12	1.87	0.57
1:B:319:HIS:HB3	1:B:322:LEU:HD12	1.86	0.56
1:A:383:VAL:O	1:A:405:PHE:HE1	1.88	0.56
1:A:279:GLY:HA2	1:A:298:LYS:CD	2.28	0.56
1:A:275:GLN:OE1	1:A:280:GLU:HG2	2.07	0.54
1:A:269:LEU:HB3	1:A:282:TRP:CE3	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:GLU:HG3	1:B:284:GLY:HA2	1.91	0.52
1:B:275:GLN:NE2	1:B:280:GLU:HG2	2.24	0.52
1:B:346:LEU:O	1:B:350:LEU:HB2	2.10	0.52
1:A:278:PHE:O	1:A:297:LEU:HA	2.12	0.50
1:A:493:ASP:O	1:A:497:GLN:HG3	2.11	0.50
1:B:383:VAL:HG12	1:B:385:ARG:HG3	1.93	0.50
1:B:267:LEU:HD13	1:B:335:TYR:HD2	1.77	0.50
1:A:511:TYR:C	1:A:511:TYR:CD2	2.85	0.50
1:A:365:ASP:O	1:A:369:GLN:HG3	2.11	0.49
1:B:365:ASP:O	1:B:369:GLN:HG3	2.11	0.49
1:B:446:TRP:CE3	1:B:499:TRP:HA	2.47	0.49
1:B:277:CYS:O	1:B:278:PHE:HD1	1.96	0.49
1:B:313:VAL:HG12	1:B:405:PHE:HE1	1.78	0.49
1:B:380:MET:CB	1:B:382:TYR:HD2	2.26	0.48
1:A:432:GLU:HG2	1:A:433:ALA:N	2.27	0.48
1:B:511:TYR:C	1:B:511:TYR:CD2	2.86	0.48
1:B:276:GLY:C	1:B:278:PHE:H	2.17	0.48
1:A:321:LYS:HE3	2:A:67:HOH:O	2.13	0.48
1:B:269:LEU:HD22	1:B:294:ILE:HD12	1.94	0.48
1:B:363:LEU:HD23	1:B:366:MET:CE	2.44	0.47
1:A:277:CYS:C	1:A:278:PHE:HD1	2.18	0.47
1:B:311:ALA:HB1	1:B:315:LYS:CE	2.43	0.47
1:B:347:LEU:O	1:B:351:LYS:HG2	2.14	0.47
1:B:467:VAL:O	1:B:471:VAL:HG23	2.14	0.47
1:A:257:LYS:HD3	1:A:261:GLU:HG3	1.97	0.47
1:B:308:LEU:O	1:B:312:GLN:HG2	2.15	0.47
1:A:388:ARG:HB3	1:A:428:TRP:CD1	2.51	0.46
1:A:527:TYR:OH	1:A:533:LEU:OXT	2.33	0.46
1:A:363:LEU:HD23	1:A:366:MET:CE	2.44	0.46
1:A:257:LYS:HG3	1:A:258:ASP:H	1.75	0.46
1:B:277:CYS:C	1:B:278:PHE:HD1	2.19	0.46
1:A:511:TYR:HE2	1:A:515:PHE:HB2	1.81	0.46
1:A:273:LEU:HB2	1:A:281:VAL:HG12	1.97	0.46
1:A:511:TYR:CE2	1:A:515:PHE:HB2	2.51	0.45
1:B:424:PHE:HA	1:B:425:PRO:HD3	1.79	0.45
1:B:532:ASN:O	1:B:533:LEU:HD23	2.16	0.45
1:B:380:MET:HB3	1:B:382:TYR:CD2	2.51	0.45
1:B:263:PRO:HD2	1:B:266:SER:OG	2.17	0.45
1:B:438:ARG:HD3	1:B:438:ARG:HA	1.68	0.45
1:A:346:LEU:O	1:A:350:LEU:HB2	2.16	0.45
1:A:384:HIS:HA	1:A:405:PHE:CE1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:361:PRO:HA	1:B:520:PHE:CE2	2.51	0.44
1:A:511:TYR:C	1:A:511:TYR:HD2	2.21	0.44
1:A:297:LEU:HD12	1:A:298:LYS:H	1.83	0.44
1:B:493:ASP:O	1:B:497:GLN:HG3	2.18	0.44
1:B:325:LEU:HD12	1:B:337:VAL:O	2.18	0.44
1:A:360:LEU:N	1:A:361:PRO:CD	2.81	0.44
1:A:502:ASP:O	1:A:505:GLU:HB2	2.18	0.44
1:A:380:MET:HB2	1:A:382:TYR:CD2	2.52	0.44
1:B:511:TYR:CE2	1:B:515:PHE:HB2	2.53	0.44
1:B:500:ARG:O	1:B:506:ARG:NH1	2.42	0.43
1:B:502:ASP:O	1:B:505:GLU:HB2	2.18	0.43
1:A:491:LEU:O	1:A:495:MET:HG3	2.18	0.43
1:B:314:MET:O	1:B:317:ILE:HB	2.18	0.43
1:A:494:LEU:HD22	1:A:515:PHE:CE2	2.54	0.43
1:B:446:TRP:HA	1:B:498:CYS:O	2.18	0.43
1:A:424:PHE:HA	1:A:425:PRO:HD3	1.84	0.43
1:B:340:TYR:CE2	1:B:342:SER:HA	2.54	0.43
1:B:485:PRO:O	1:B:486:GLU:HB2	2.19	0.43
1:B:276:GLY:C	1:B:278:PHE:N	2.72	0.43
1:A:258:ASP:OD1	1:A:259:ALA:N	2.52	0.43
1:A:501:LYS:HE3	1:A:501:LYS:HB2	1.60	0.42
1:B:380:MET:HB3	1:B:382:TYR:HD2	1.84	0.42
1:B:360:LEU:N	1:B:361:PRO:CD	2.82	0.42
1:B:506:ARG:HA	1:B:507:PRO:HD3	1.87	0.42
1:A:467:VAL:O	1:A:471:VAL:HG23	2.19	0.42
1:B:432:GLU:HG2	1:B:433:ALA:N	2.35	0.42
1:A:277:CYS:HA	2:A:163:HOH:O	2.18	0.42
1:A:356:LYS:HB3	1:A:356:LYS:NZ	2.34	0.42
1:B:309:GLN:C	1:B:311:ALA:N	2.71	0.42
1:A:485:PRO:O	1:A:486:GLU:HB2	2.19	0.42
1:A:317:ILE:HG23	1:A:376:TYR:HE2	1.85	0.41
1:B:349:PHE:CE2	1:B:358:LEU:HD11	2.55	0.41
1:A:323:VAL:HG21	1:A:403:ALA:HB2	2.02	0.41
1:A:432:GLU:OE2	1:A:506:ARG:NH2	2.53	0.41
1:B:511:TYR:HE2	1:B:515:PHE:HB2	1.85	0.41
1:B:382:TYR:HB3	1:B:405:PHE:CZ	2.49	0.41
1:A:504:GLU:HB2	2:A:38:HOH:O	2.21	0.41
1:A:283:MET:HG2	1:A:291:ARG:HH11	1.85	0.41
1:B:388:ARG:HB3	1:B:428:TRP:CD1	2.56	0.41
1:B:258:ASP:OD1	1:B:260:TRP:HD1	2.04	0.41
1:A:461:VAL:HA	1:A:462:PRO:HD3	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:511:TYR:HD2	1:B:511:TYR:C	2.25	0.40
1:B:497:GLN:O	1:B:506:ARG:HG3	2.22	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	256/286 (90%)	242 (94%)	14 (6%)	0	100	100
1	B	243/286 (85%)	228 (94%)	15 (6%)	0	100	100
All	All	499/572 (87%)	470 (94%)	29 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	217/245 (89%)	207 (95%)	10 (5%)	33	64
1	B	209/245 (85%)	195 (93%)	14 (7%)	20	44
All	All	426/490 (87%)	402 (94%)	24 (6%)	26	54

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	277	CYS
1	A	290	THR
1	A	315	LYS
1	A	356	LYS
1	A	360	LEU
1	A	397	ASN
1	A	474	GLN
1	A	477	ARG
1	A	493	ASP
1	A	511	TYR
1	B	258	ASP
1	B	269	LEU
1	B	275	GLN
1	B	289	THR
1	B	290	THR
1	B	291	ARG
1	B	318	ARG
1	B	336	ILE
1	B	351	LYS
1	B	360	LEU
1	B	397	ASN
1	B	438	ARG
1	B	501	LYS
1	B	511	TYR

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

Mol	Chain	Res	Type
1	A	312	GLN
1	A	397	ASN
1	B	312	GLN
1	B	397	ASN

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 [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 ⓘ

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	260/286 (90%)	0.32	22 (8%) 13 10	11, 32, 104, 124	0
1	B	251/286 (87%)	0.48	21 (8%) 14 11	11, 30, 96, 128	0
All	All	511/572 (89%)	0.40	43 (8%) 14 11	11, 31, 101, 128	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	310	GLU	10.9
1	B	306	ALA	10.0
1	B	303	SER	7.5
1	B	311	ALA	7.5
1	B	278	PHE	6.9
1	B	276	GLY	6.6
1	B	307	PHE	6.4
1	B	277	CYS	5.5
1	A	306	ALA	4.8
1	B	289	THR	4.7
1	B	313	VAL	4.5
1	B	288	GLY	4.2
1	A	300	GLY	4.2
1	A	301	THR	4.1
1	A	297	LEU	3.9
1	A	271	VAL	3.8
1	A	477	ARG	3.8
1	A	473	ASP	3.8
1	A	278	PHE	3.6
1	B	309	GLN	3.6
1	A	311	ALA	3.3
1	A	299	PRO	3.2
1	B	477	ARG	3.2
1	A	316	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	309	GLN	3.0
1	A	277	CYS	2.9
1	B	274	GLY	2.9
1	B	275	GLN	2.9
1	B	308	LEU	2.9
1	B	473	ASP	2.9
1	B	424	PHE	2.9
1	A	313	VAL	2.8
1	B	269	LEU	2.7
1	A	305	GLU	2.7
1	B	271	VAL	2.7
1	B	304	PRO	2.6
1	A	275	GLN	2.4
1	A	405	PHE	2.1
1	A	288	GLY	2.1
1	A	289	THR	2.1
1	A	315	LYS	2.1
1	A	307	PHE	2.1
1	A	528	GLN	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.