



Full wwPDB X-ray Structure Validation Report i

Mar 1, 2014 – 01:13 AM GMT

PDB ID : 3F3U
Title : Kinase domain of cSrc in complex with inhibitor RL37 (Type III)
Authors : Gruetter, C.; Klueter, S.; Getlik, M.; Rauh, D.
Deposited on : 2008-10-31
Resolution : 2.50 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

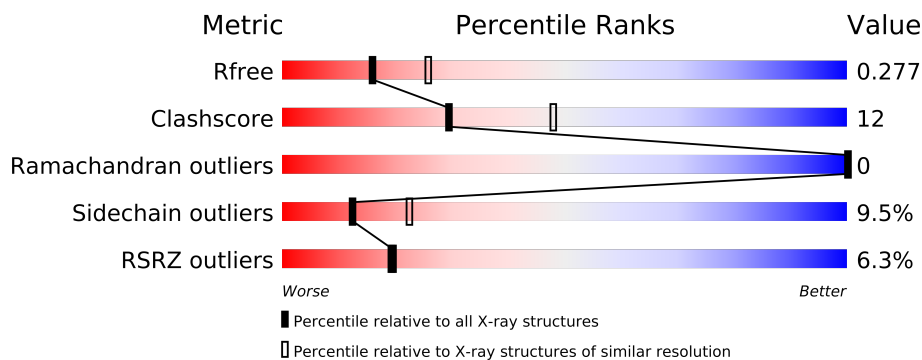
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.50 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}	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	286	
1	B	286	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	1AW	A	534	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4355 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

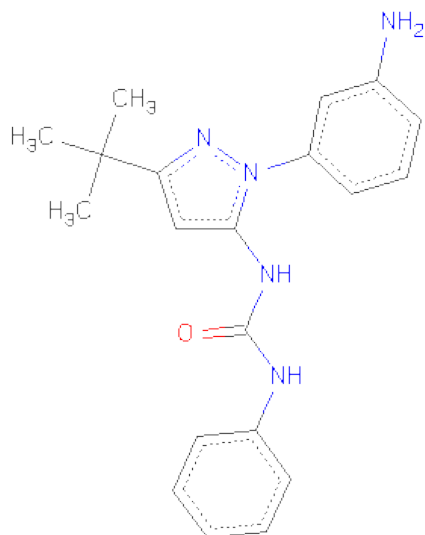
- Molecule 1 is a protein called Proto-oncogene tyrosine-protein kinase Src.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	0	0
			2103	1351	350	384	18			
1	B	259	Total	C	N	O	S	0	0	0
			2088	1342	348	381	17			

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	345	CYS	SER	ENGINEERED	UNP P00523
B	248	GLY	-	EXPRESSION TAG	UNP P00523
B	249	HIS	-	EXPRESSION TAG	UNP P00523
B	250	MET	-	EXPRESSION TAG	UNP P00523
B	345	CYS	SER	ENGINEERED	UNP P00523

- Molecule 2 is 1-[1-(3-AMINOPHENYL)-3-TERT-BUTYL-1H-PYRAZOL-5-YL]-3-PHENYLUREA (three-letter code: 1AW) (formula: C₂₀H₂₃N₅O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			26	20	5	1		
2	A	1	Total	C	N	O	0	0
			26	20	5	1		
2	B	1	Total	C	N	O	0	0
			26	20	5	1		

- Molecule 3 is water.

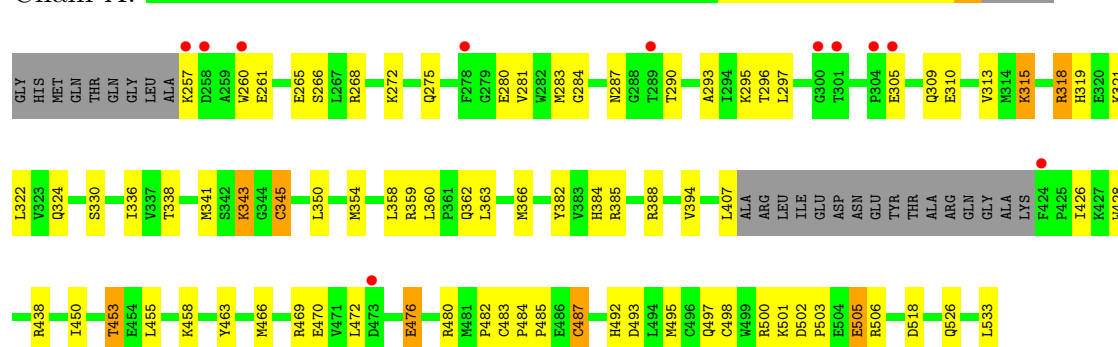
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	41	Total	O	0	0
			41	41		
3	B	45	Total	O	0	0
			45	45		

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.

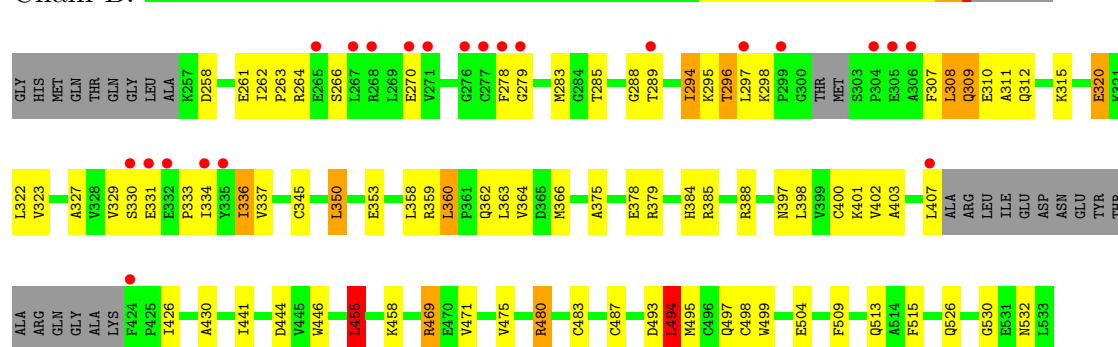
- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

Chain A:



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

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	42.09Å 63.53Å 73.99Å 78.94° 89.37° 90.06°	Depositor
Resolution (Å)	36.59 – 2.50 36.59 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (36.59-2.50) 97.3 (36.59-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.03 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.222 , 0.281 0.220 , 0.277	Depositor DCC
R_{free} test set	1014 reflections (4.17%)	DCC
Wilson B-factor (Å ²)	31.1	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 35.8	EDS
Estimated twinning fraction	0.045 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 25330 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4355	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1AW

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	0.82	1/2155 (0.0%)	0.83	2/2917 (0.1%)
1	B	0.83	2/2139 (0.1%)	0.87	6/2894 (0.2%)
All	All	0.82	3/4294 (0.1%)	0.85	8/5811 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	345	CYS	CB-SG	-7.71	1.69	1.82
1	A	505	GLU	CG-CD	6.03	1.60	1.51
1	B	400	CYS	CB-SG	-5.99	1.72	1.82

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	480	ARG	NE-CZ-NH1	7.74	124.17	120.30
1	A	480	ARG	NE-CZ-NH1	6.90	123.75	120.30
1	B	480	ARG	NE-CZ-NH2	-6.89	116.86	120.30
1	B	350	LEU	CA-CB-CG	6.06	129.25	115.30
1	B	494	LEU	CA-CB-CG	5.61	128.21	115.30
1	A	480	ARG	NE-CZ-NH2	-5.37	117.62	120.30
1	B	444	ASP	CB-CG-OD2	-5.18	113.64	118.30
1	B	455	LEU	CA-CB-CG	5.05	126.92	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2103	0	2089	47	0
1	B	2088	0	2072	54	0
2	A	52	0	46	7	0
2	B	26	0	23	3	0
3	A	41	0	0	3	0
3	B	45	0	0	3	0
All	All	4355	0	4230	104	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

All (104) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:345:CYS:SG	2:A:534:1AW:NAD	2.32	1.01
1:B:294:ILE:HG23	1:B:337:VAL:HG22	1.52	0.90
1:B:285:THR:HG22	1:B:288:GLY:HA2	1.57	0.86
1:A:363:LEU:HD13	1:A:455:LEU:O	1.77	0.85
1:B:263:PRO:HD2	1:B:266:SER:OG	1.83	0.79
1:B:359:ARG:H	1:B:362:GLN:HE21	1.33	0.76
1:B:469:ARG:CG	1:B:469:ARG:HH11	1.98	0.74
1:B:310:GLU:HG3	2:B:1:1AW:CAV	2.18	0.74
1:A:453:THR:HG23	3:A:18:HOH:O	1.87	0.74
1:B:493:ASP:O	1:B:497:GLN:HG3	1.88	0.74
1:B:469:ARG:HH11	1:B:469:ARG:HG2	1.53	0.73
1:B:285:THR:CG2	1:B:288:GLY:HA2	2.19	0.73
1:A:322:LEU:HD13	2:A:1:1AW:HAB	1.72	0.72
1:A:266:SER:HB2	1:A:287:ASN:HD22	1.58	0.69
1:B:298:LYS:HB3	1:B:333:PRO:HB3	1.73	0.68
1:B:526:GLN:HG2	3:B:8:HOH:O	1.94	0.68
1:A:500:ARG:HD3	1:A:505:GLU:HB3	1.76	0.67
1:B:494:LEU:HG	1:B:515:PHE:CE1	2.30	0.67
1:A:313:VAL:HG11	1:A:382:TYR:OH	1.94	0.67
1:A:388:ARG:HB3	1:A:428:TRP:CD1	2.31	0.65
1:B:359:ARG:H	1:B:362:GLN:NE2	1.94	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:476:GLU:OE1	1:A:476:GLU:HA	1.97	0.64
1:B:323:VAL:HG21	1:B:403:ALA:HB2	1.81	0.62
1:A:281:VAL:HG23	2:A:534:1AW:HABB	1.84	0.60
1:B:310:GLU:HG3	2:B:1:1AW:CAP	2.35	0.57
1:B:323:VAL:HG23	1:B:402:VAL:O	2.05	0.57
1:A:450:ILE:O	1:A:453:THR:HG22	2.06	0.56
1:A:426:ILE:HD11	1:A:472:LEU:HD21	1.87	0.56
1:A:518:ASP:OD2	3:A:85:HOH:O	2.18	0.54
1:A:280:GLU:H	1:A:296:THR:HB	1.72	0.54
1:A:260:TRP:CZ2	1:A:315:LYS:HG2	2.43	0.54
1:B:378:GLU:HB2	1:B:441:ILE:HG12	1.89	0.54
1:B:322:LEU:HD22	1:B:402:VAL:HB	1.90	0.53
1:B:363:LEU:HD13	1:B:455:LEU:O	2.09	0.53
1:B:430:ALA:HB2	1:B:446:TRP:CB	2.38	0.53
1:A:463:TYR:HA	3:A:48:HOH:O	2.08	0.52
1:B:320:GLU:O	1:B:401:LYS:HE2	2.10	0.52
1:A:319:HIS:CD2	1:A:321:LYS:H	2.28	0.52
1:A:266:SER:HB2	1:A:287:ASN:ND2	2.25	0.51
1:B:469:ARG:CG	1:B:469:ARG:NH1	2.64	0.51
1:B:261:GLU:OE1	1:B:330:SER:HB2	2.11	0.51
1:B:311:ALA:O	1:B:315:LYS:HG3	2.11	0.50
1:B:264:ARG:HE	1:B:329:VAL:HG11	1.76	0.50
1:B:279:GLY:HA3	1:B:296:THR:O	2.12	0.50
1:A:438:ARG:HH21	1:A:503:PRO:HG2	1.75	0.50
1:A:261:GLU:OE1	1:A:330:SER:HB2	2.11	0.49
1:B:307:PHE:HE2	1:B:334:ILE:CD1	2.25	0.49
1:B:309:GLN:HA	1:B:312:GLN:HG2	1.93	0.49
1:B:397:ASN:O	1:B:398:LEU:HB2	2.11	0.49
1:A:384:HIS:O	1:A:385:ARG:HB2	2.12	0.49
1:A:309:GLN:NE2	1:A:309:GLN:HA	2.27	0.49
1:B:359:ARG:HB2	1:B:362:GLN:HE22	1.78	0.49
1:B:310:GLU:OE1	1:B:336:ILE:HD12	2.13	0.49
2:B:1:1AW:HAP	2:B:1:1AW:NAT	2.28	0.49
1:A:341:MET:H	2:A:534:1AW:HAN	1.76	0.48
1:A:493:ASP:O	1:A:497:GLN:HG3	2.13	0.48
1:B:307:PHE:CE2	1:B:334:ILE:HD11	2.49	0.48
1:A:318:ARG:NH1	1:A:318:ARG:HB3	2.28	0.48
2:A:1:1AW:HAL	2:A:1:1AW:OAE	2.14	0.48
1:B:285:THR:HG22	1:B:288:GLY:CA	2.35	0.48
1:B:358:LEU:O	1:B:458:LYS:NZ	2.46	0.47
1:B:307:PHE:HE2	1:B:334:ILE:HD11	1.78	0.47
1:B:526:GLN:CG	3:B:8:HOH:O	2.57	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:483:CYS:SG	1:A:487:CYS:O	2.72	0.47
1:A:426:ILE:CD1	1:A:472:LEU:HD21	2.45	0.47
1:A:260:TRP:HE1	1:A:315:LYS:HD2	1.80	0.46
1:B:530:GLY:HA3	3:B:77:HOH:O	2.15	0.46
1:A:492:HIS:O	1:A:495:MET:HB2	2.16	0.46
1:A:426:ILE:O	1:A:426:ILE:HG13	2.15	0.46
1:A:319:HIS:HD2	1:A:321:LYS:H	1.63	0.46
1:A:283:MET:HG2	1:A:284:GLY:N	2.30	0.45
1:A:358:LEU:O	1:A:458:LYS:NZ	2.49	0.45
1:A:272:LYS:CE	1:A:275:GLN:HB3	2.47	0.45
1:A:295:LYS:HB3	1:A:336:ILE:HB	1.99	0.45
1:A:293:ALA:HB3	1:A:338:THR:OG1	2.16	0.45
1:B:471:VAL:O	1:B:475:VAL:HG13	2.17	0.44
1:B:362:GLN:O	1:B:366:MET:HG3	2.18	0.44
1:B:308:LEU:HD22	1:B:308:LEU:HA	1.80	0.44
1:B:295:LYS:HE2	1:B:307:PHE:HZ	1.82	0.43
1:B:480:ARG:NH2	1:B:499:TRP:O	2.50	0.43
1:A:482:PRO:O	1:A:484:PRO:HD3	2.18	0.43
1:B:262:ILE:HG12	1:B:327:ALA:HB1	2.00	0.43
1:A:343:LYS:HB2	1:A:394:VAL:O	2.18	0.43
1:A:358:LEU:O	1:A:359:ARG:NH1	2.40	0.43
1:B:384:HIS:O	1:B:385:ARG:HB2	2.19	0.43
2:A:534:1AW:OAE	2:A:534:1AW:HAL	2.18	0.43
1:B:334:ILE:HD12	1:B:334:ILE:C	2.39	0.43
1:B:458:LYS:NZ	1:B:532:ASN:O	2.52	0.42
1:A:466:MET:HA	1:A:470:GLU:OE1	2.19	0.42
1:A:485:PRO:O	1:A:533:LEU:HD12	2.19	0.42
1:B:495:MET:O	1:B:498:CYS:HB2	2.19	0.42
1:A:318:ARG:NH2	1:A:324:GLN:NE2	2.67	0.42
1:B:294:ILE:CG2	1:B:337:VAL:HG22	2.35	0.42
1:B:483:CYS:SG	1:B:487:CYS:O	2.78	0.42
1:B:509:PHE:O	1:B:513:GLN:N	2.45	0.41
1:A:310:GLU:HA	2:A:1:1AW:CAH	2.50	0.41
1:A:502:ASP:HB3	1:A:505:GLU:OE1	2.19	0.41
1:A:426:ILE:HD11	1:A:472:LEU:CD2	2.51	0.41
1:B:375:ALA:O	1:B:379:ARG:HG3	2.21	0.41
1:A:498:CYS:O	1:A:506:ARG:HD3	2.19	0.41
1:A:362:GLN:O	1:A:366:MET:HG3	2.21	0.40
1:B:262:ILE:HD12	1:B:266:SER:HB2	2.04	0.40
1:B:360:LEU:HD22	1:B:364:VAL:HG23	2.04	0.40
1:B:378:GLU:HB2	1:B:441:ILE:CD1	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	257/286 (90%)	242 (94%)	15 (6%)	0	100	100
1	B	253/286 (88%)	235 (93%)	18 (7%)	0	100	100
All	All	510/572 (89%)	477 (94%)	33 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	227/245 (93%)	207 (91%)	20 (9%)	14	26
1	B	225/245 (92%)	202 (90%)	23 (10%)	11	19
All	All	452/490 (92%)	409 (90%)	43 (10%)	12	22

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	257	LYS
1	A	265	GLU
1	A	268	ARG
1	A	290	THR
1	A	297	LEU
1	A	305	GLU
1	A	315	LYS
1	A	318	ARG
1	A	343	LYS
1	A	345	CYS
1	A	350	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	354	MET
1	A	360	LEU
1	A	407	LEU
1	A	453	THR
1	A	469	ARG
1	A	476	GLU
1	A	487	CYS
1	A	501	LYS
1	A	526	GLN
1	B	258	ASP
1	B	270	GLU
1	B	278	PHE
1	B	283	MET
1	B	289	THR
1	B	294	ILE
1	B	296	THR
1	B	297	LEU
1	B	308	LEU
1	B	309	GLN
1	B	320	GLU
1	B	331	GLU
1	B	336	ILE
1	B	350	LEU
1	B	353	GLU
1	B	360	LEU
1	B	388	ARG
1	B	407	LEU
1	B	426	ILE
1	B	455	LEU
1	B	469	ARG
1	B	494	LEU
1	B	504	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	287	ASN
1	A	309	GLN
1	A	319	HIS
1	A	397	ASN
1	B	362	GLN
1	B	528	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	1AW	A	1	-	28,28,28	2.45	6 (21%)	40,40,40	1.77	7 (17%)
2	1AW	A	534	-	28,28,28	2.28	6 (21%)	40,40,40	1.93	6 (15%)
2	1AW	B	1	-	28,28,28	2.38	6 (21%)	40,40,40	2.47	8 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	1AW	A	1	-	-	0/16/18/18	0/3/3/3
2	1AW	A	534	-	-	0/16/18/18	0/3/3/3
2	1AW	B	1	-	-	0/16/18/18	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	1AW	NAR-NBC	-8.86	1.23	1.39
2	B	1	1AW	NAR-NBC	-8.76	1.23	1.39
2	A	534	1AW	NAR-NBC	-8.35	1.24	1.39
2	B	1	1AW	CAQ-CAY	-4.93	1.33	1.39
2	A	534	1AW	CAW-NBC	-4.60	1.34	1.43
2	A	1	1AW	CAQ-CAY	-4.47	1.33	1.39
2	B	1	1AW	CAW-NBC	-4.33	1.34	1.43
2	A	1	1AW	CAW-NBC	-4.32	1.34	1.43
2	A	1	1AW	CAX-NAS	-4.13	1.33	1.41
2	A	534	1AW	CBD-CAY	3.59	1.58	1.52
2	B	1	1AW	CAZ-NBC	-3.54	1.33	1.36
2	A	534	1AW	CAQ-CAY	-3.46	1.35	1.39
2	A	534	1AW	CAX-NAS	-3.09	1.35	1.41
2	A	1	1AW	CAZ-NBC	-3.06	1.34	1.36
2	B	1	1AW	CAZ-NAT	-2.75	1.34	1.39
2	A	534	1AW	CAZ-NBC	-2.39	1.34	1.36
2	B	1	1AW	CAX-NAS	-2.03	1.37	1.41
2	A	1	1AW	CAP-CAW	2.00	1.41	1.38

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	1AW	CAQ-CAZ-NBC	10.46	108.28	106.68
2	A	534	1AW	CAW-NBC-NAR	8.49	125.42	118.85
2	A	1	1AW	NAT-CAZ-NBC	5.44	126.56	120.99
2	B	1	1AW	CAW-NBC-NAR	5.38	123.02	118.85
2	B	1	1AW	NAT-CAZ-NBC	5.21	126.32	120.99
2	A	534	1AW	CBD-CAY-NAR	4.52	125.38	120.64
2	A	1	1AW	CAW-NBC-NAR	4.37	122.23	118.85
2	B	1	1AW	CBD-CAY-NAR	4.17	125.02	120.64
2	A	1	1AW	CBD-CAY-NAR	3.79	124.61	120.64
2	A	1	1AW	CAQ-CAZ-NBC	3.77	107.26	106.68
2	A	534	1AW	CAW-NBC-CAZ	-3.68	123.50	128.50
2	A	1	1AW	CAP-CAW-NBC	3.33	123.20	119.13
2	B	1	1AW	NAT-CAU-NAS	3.05	117.42	112.57
2	B	1	1AW	CAK-CAW-CAP	-2.95	118.96	121.55
2	B	1	1AW	CAQ-CAY-CBD	-2.82	125.47	128.94
2	A	534	1AW	NAT-CAZ-NBC	2.41	123.45	120.99
2	A	534	1AW	CAQ-CAY-CBD	-2.39	126.01	128.94
2	A	1	1AW	CAY-NAR-NBC	2.33	108.36	105.66
2	A	1	1AW	CAQ-CAY-CBD	-2.27	126.16	128.94
2	A	534	1AW	CAQ-CAZ-NBC	2.26	107.03	106.68
2	B	1	1AW	CAY-NAR-NBC	2.03	108.02	105.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	261/286 (91%)	0.13	11 (4%) 35 36	2, 15, 45, 49	0
1	B	259/286 (90%)	0.33	22 (8%) 11 10	4, 15, 50, 54	0
All	All	520/572 (90%)	0.23	33 (6%) 19 19	2, 15, 48, 54	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	297	LEU	5.0
1	B	278	PHE	4.8
1	B	268	ARG	4.4
1	B	424	PHE	4.1
1	B	331	GLU	3.8
1	B	267	LEU	3.8
1	B	335	TYR	3.6
1	A	300	GLY	3.5
1	B	330	SER	3.5
1	B	289	THR	3.3
1	A	257	LYS	3.2
1	B	276	GLY	3.2
1	B	306	ALA	3.2
1	B	277	CYS	3.0
1	B	305	GLU	2.9
1	B	279	GLY	2.8
1	B	304	PRO	2.7
1	A	424	PHE	2.6
1	A	304	PRO	2.5
1	A	301	THR	2.5
1	A	260	TRP	2.5
1	A	305	GLU	2.5
1	A	289	THR	2.5
1	B	299	PRO	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	258	ASP	2.3
1	A	473	ASP	2.3
1	B	332	GLU	2.3
1	B	334	ILE	2.3
1	A	278	PHE	2.3
1	B	265	GLU	2.2
1	B	270	GLU	2.2
1	B	407	LEU	2.1
1	B	271	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	1AW	A	534	26/26	0.21	2.21	49,54,55,55	0
2	1AW	B	1	26/26	0.23	1.49	57,63,64,64	0
2	1AW	A	1	26/26	0.16	0.06	34,35,41,43	0

6.5 Other polymers ⓘ

There are no such residues in this entry.