



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:46 AM GMT

PDB ID : 3FZR
Title : Crystal structure of PYK2 complexed with PF-431396
Authors : Han,S.
Deposited on : 2009-01-26
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

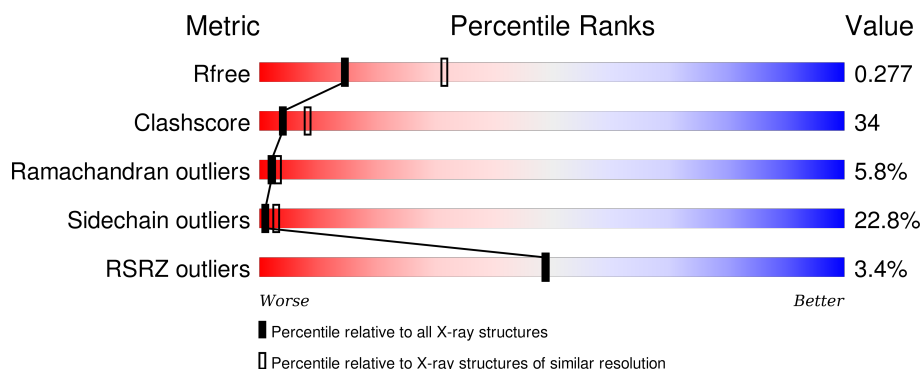
1 Overall quality at a glance

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	277	

2 Entry composition [i](#)

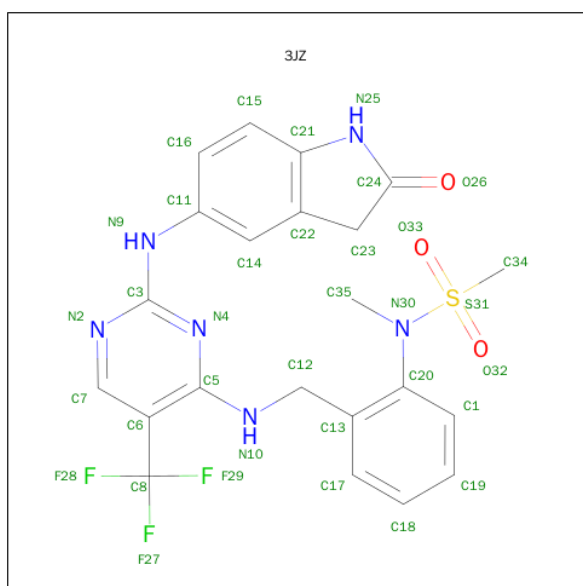
There are 4 unique types of molecules in this entry. The entry contains 2213 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Protein tyrosine kinase 2 beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	0	0
			2114	1365	349	381	19			

- Molecule 2 is N-METHYL-N-{2-[(2-{(2-OXO-2,3-DIHYDRO-1H-INDOL-5-YL)AMINO]-5-(TRIFLUOROMETHYL)PYRIMIDIN-4-YL}AMINO)METHYL]PHENYL}METHANESULFONAMIDE (three-letter code: 3JZ) (formula: C₂₂H₂₁F₃N₆O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			35	22	3	6	3		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		

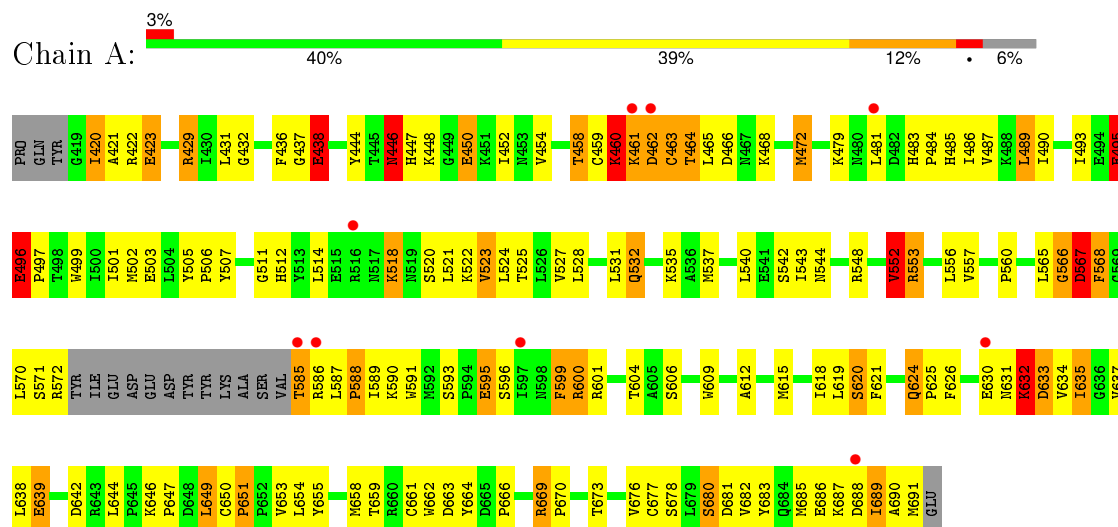
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	59	Total	O	0	0
			59	59		

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 ($\text{RSRZ} > 2$). 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: Protein tyrosine kinase 2 beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	107.33 Å 107.33 Å 75.79 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.88 – 2.70 29.77 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (17.88-2.70) 98.6 (29.77-2.70)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.70 (at 2.72 Å)	Xtriage
Refinement program	BUSTER-TNT 2.1.1	Depositor
R, R_{free}	0.211 , 0.274 0.213 , 0.277	Depositor DCC
R_{free} test set	601 reflections (5.09%)	DCC
Wilson B-factor (Å ²)	62.6	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 77.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 12460 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2213	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.19% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 3JZ, PO4

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	0.62	0/2163	0.83	2/2926 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	552	VAL	CB-CA-C	6.16	123.10	111.40
1	A	556	LEU	CB-CG-CD1	5.49	120.33	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2114	0	2129	145	1
2	A	35	0	21	5	0
3	A	5	0	0	0	0
4	A	59	0	0	8	1
All	All	2213	0	2150	147	2

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 34.

All (147) 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:429:ARG:HH11	1:A:429:ARG:HB2	1.19	1.07
1:A:635:ILE:HD12	1:A:635:ILE:H	1.27	0.97
1:A:537:MET:CE	1:A:540:LEU:HD12	2.04	0.86
1:A:523:VAL:CG2	1:A:649:LEU:HB3	2.06	0.85
1:A:635:ILE:O	1:A:639:GLU:HG2	1.77	0.84
1:A:429:ARG:NH1	1:A:429:ARG:HB2	1.93	0.83
1:A:647:PRO:HD2	1:A:650:CYS:HB3	1.58	0.83
1:A:537:MET:HE2	1:A:540:LEU:HD12	1.61	0.83
1:A:689:ILE:HG13	1:A:689:ILE:O	1.79	0.82
1:A:523:VAL:HG21	1:A:649:LEU:HB3	1.64	0.80
1:A:464:THR:HG23	1:A:465:LEU:H	1.46	0.79
1:A:587:LEU:O	1:A:589:ILE:HG12	1.83	0.79
1:A:566:GLY:O	1:A:567:ASP:HB3	1.82	0.79
1:A:676:VAL:O	1:A:680:SER:HB2	1.82	0.78
1:A:631:ASN:O	1:A:634:VAL:HG23	1.83	0.77
1:A:632:LYS:O	1:A:632:LYS:HD2	1.87	0.74
1:A:637:VAL:HG12	1:A:642:ASP:HB2	1.69	0.72
1:A:460:LYS:CG	1:A:461:LYS:H	2.03	0.72
1:A:446:ASN:ND2	1:A:452:ILE:HD11	2.05	0.71
1:A:436:PHE:O	1:A:460:LYS:N	2.24	0.70
1:A:528:LEU:O	1:A:532:GLN:HG3	1.92	0.70
1:A:537:MET:HE2	1:A:537:MET:HA	1.74	0.69
1:A:472:MET:CE	1:A:472:MET:HA	2.23	0.69
1:A:635:ILE:N	1:A:635:ILE:HD12	2.04	0.69
1:A:537:MET:HA	1:A:537:MET:CE	2.23	0.68
1:A:685:MET:O	1:A:688:ASP:HB2	1.94	0.68
1:A:464:THR:HG23	1:A:465:LEU:N	2.09	0.68
1:A:459:CYS:SG	1:A:462:ASP:HB3	2.34	0.67
1:A:432:GLY:HA3	2:A:999:3JZ:H34B	1.75	0.67
1:A:690:ALA:HA	4:A:35:HOH:O	1.94	0.67
1:A:514:LEU:HD11	1:A:618:ILE:HA	1.78	0.66
1:A:495:GLU:OE1	1:A:495:GLU:HA	1.96	0.66
1:A:587:LEU:O	1:A:589:ILE:N	2.29	0.66
1:A:463:CYS:O	1:A:464:THR:O	2.14	0.66
1:A:544:ASN:O	1:A:572:ARG:HG2	1.96	0.65
1:A:619:LEU:HD12	1:A:658:MET:CE	2.28	0.64
1:A:432:GLY:CA	2:A:999:3JZ:H34B	2.28	0.64
1:A:511:GLY:HA2	1:A:552:VAL:HG13	1.81	0.63
1:A:647:PRO:HD2	1:A:650:CYS:CB	2.28	0.62
1:A:637:VAL:CG1	1:A:642:ASP:HB2	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:GLY:CA	1:A:552:VAL:HG13	2.28	0.62
1:A:461:LYS:O	1:A:461:LYS:HD2	1.99	0.61
1:A:666:PRO:O	1:A:669:ARG:HG3	2.00	0.60
1:A:537:MET:HE1	1:A:540:LEU:HD12	1.81	0.60
1:A:630:GLU:HG2	1:A:633:ASP:OD2	2.02	0.60
1:A:495:GLU:O	1:A:496:GLU:HB2	2.02	0.60
1:A:619:LEU:HD12	1:A:658:MET:HE1	1.82	0.60
1:A:472:MET:HE2	1:A:472:MET:HA	1.83	0.60
1:A:489:LEU:O	1:A:489:LEU:HD23	2.03	0.59
1:A:633:ASP:O	1:A:637:VAL:HG23	2.03	0.58
1:A:531:LEU:O	1:A:535:LYS:HG3	2.03	0.58
1:A:567:ASP:O	1:A:568:PHE:HB2	2.04	0.58
1:A:678:SER:O	1:A:682:VAL:HG23	2.04	0.58
1:A:460:LYS:CG	1:A:461:LYS:N	2.66	0.57
1:A:481:LEU:HD22	1:A:543:ILE:HD11	1.87	0.57
1:A:631:ASN:O	1:A:633:ASP:N	2.38	0.57
1:A:646:LYS:HG3	1:A:655:TYR:CG	2.39	0.57
2:A:999:3JZ:N4	2:A:999:3JZ:C16	2.68	0.57
1:A:649:LEU:N	1:A:649:LEU:HD22	2.20	0.56
1:A:461:LYS:HD2	1:A:461:LYS:C	2.25	0.56
1:A:620:SER:HB3	4:A:38:HOH:O	2.04	0.56
1:A:460:LYS:HG2	1:A:461:LYS:N	2.22	0.55
1:A:523:VAL:HG22	1:A:649:LEU:HB3	1.86	0.55
2:A:999:3JZ:H16	2:A:999:3JZ:N4	2.21	0.55
1:A:522:LYS:HG3	4:A:25:HOH:O	2.08	0.54
1:A:522:LYS:O	1:A:524:LEU:N	2.41	0.54
1:A:588:PRO:HB2	1:A:591:TRP:HB2	1.90	0.54
1:A:420:ILE:CD1	1:A:501:ILE:HD13	2.38	0.53
1:A:615:MET:HE1	1:A:658:MET:HG3	1.91	0.52
1:A:462:ASP:OD2	1:A:462:ASP:O	2.28	0.52
1:A:593:SER:OG	1:A:606:SER:HB2	2.09	0.52
1:A:686:GLU:HA	1:A:689:ILE:HG23	1.90	0.52
1:A:685:MET:HB3	4:A:700:HOH:O	2.08	0.52
1:A:682:VAL:O	1:A:682:VAL:HG12	2.09	0.52
1:A:567:ASP:O	1:A:567:ASP:CG	2.47	0.52
1:A:512:HIS:HB3	4:A:30:HOH:O	2.10	0.52
1:A:527:VAL:HG12	1:A:683:TYR:HB2	1.93	0.51
1:A:485:HIS:CE1	1:A:532:GLN:NE2	2.79	0.51
1:A:487:VAL:HG21	1:A:567:ASP:HB3	1.93	0.51
1:A:458:THR:HG23	1:A:459:CYS:N	2.26	0.51
1:A:609:TRP:CE3	1:A:662:TRP:HA	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:521:LEU:CD2	1:A:525:THR:HG21	2.42	0.50
1:A:446:ASN:HD22	1:A:452:ILE:HD11	1.76	0.50
1:A:463:CYS:SG	1:A:466:ASP:HB2	2.52	0.49
1:A:649:LEU:N	1:A:649:LEU:CD2	2.75	0.49
1:A:481:LEU:HD22	1:A:543:ILE:CD1	2.42	0.49
1:A:565:LEU:HD12	1:A:566:GLY:H	1.76	0.49
1:A:485:HIS:CE1	1:A:532:GLN:HE21	2.31	0.49
1:A:527:VAL:CG1	1:A:683:TYR:HB2	2.43	0.48
1:A:571:SER:OG	1:A:572:ARG:N	2.46	0.48
1:A:438:GLU:HG2	1:A:438:GLU:H	1.47	0.48
1:A:595:GLU:OE2	1:A:669:ARG:NH1	2.43	0.47
1:A:496:GLU:HA	1:A:497:PRO:HA	1.44	0.47
1:A:567:ASP:O	1:A:568:PHE:CB	2.57	0.47
1:A:664:TYR:O	1:A:666:PRO:HD3	2.14	0.47
1:A:599:PHE:CD2	1:A:599:PHE:N	2.80	0.47
1:A:460:LYS:CD	1:A:461:LYS:H	2.28	0.47
1:A:599:PHE:O	1:A:601:ARG:N	2.48	0.46
1:A:493:ILE:HB	1:A:499:TRP:HB2	1.97	0.46
1:A:624:GLN:HG3	1:A:625:PRO:HD2	1.98	0.46
1:A:626:PHE:CZ	1:A:644:LEU:HG	2.50	0.46
1:A:484:PRO:HD3	4:A:702:HOH:O	2.15	0.46
1:A:437:GLY:HA3	1:A:460:LYS:H	1.81	0.45
1:A:446:ASN:HB3	1:A:448:LYS:H	1.80	0.45
1:A:537:MET:HE1	1:A:565:LEU:HD21	1.98	0.45
1:A:472:MET:CE	1:A:472:MET:CA	2.94	0.45
1:A:490:ILE:HD12	1:A:503:GLU:N	2.32	0.45
1:A:505:TYR:HA	1:A:506:PRO:HD3	1.55	0.45
1:A:468:LYS:O	1:A:472:MET:HG2	2.17	0.45
1:A:661:CYS:HA	1:A:669:ARG:HB3	1.98	0.45
1:A:483:HIS:HB3	1:A:486:ILE:HG13	1.99	0.45
1:A:502:MET:HE2	1:A:567:ASP:CG	2.37	0.45
1:A:593:SER:HB2	1:A:595:GLU:OE2	2.17	0.44
1:A:446:ASN:HB2	1:A:450:GLU:H	1.83	0.44
1:A:635:ILE:CD1	1:A:635:ILE:H	2.03	0.44
1:A:567:ASP:HA	1:A:570:LEU:HD12	1.99	0.44
1:A:650:CYS:SG	1:A:654:LEU:HB3	2.57	0.44
1:A:444:TYR:CD2	1:A:452:ILE:HD12	2.52	0.44
1:A:481:LEU:CD2	1:A:543:ILE:CD1	2.96	0.44
1:A:619:LEU:HD12	1:A:658:MET:HE3	2.00	0.43
1:A:537:MET:CA	1:A:537:MET:CE	2.94	0.43
1:A:444:TYR:HD2	1:A:452:ILE:HD12	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:THR:CG2	1:A:459:CYS:N	2.79	0.43
1:A:615:MET:O	1:A:619:LEU:HG	2.18	0.43
1:A:647:PRO:HB3	4:A:38:HOH:O	2.18	0.43
1:A:553:ARG:CG	1:A:553:ARG:HH11	2.32	0.43
1:A:688:ASP:C	1:A:690:ALA:H	2.23	0.43
1:A:688:ASP:C	1:A:690:ALA:N	2.73	0.43
1:A:503:GLU:O	2:A:999:3JZ:H7	2.19	0.42
1:A:595:GLU:H	1:A:595:GLU:HG3	1.39	0.42
1:A:524:LEU:O	1:A:524:LEU:HG	2.18	0.42
1:A:518:LYS:HB3	1:A:518:LYS:HE3	1.38	0.42
1:A:496:GLU:HG3	1:A:497:PRO:HA	2.01	0.42
1:A:649:LEU:O	1:A:651:PRO:HD3	2.19	0.42
1:A:649:LEU:CD2	1:A:649:LEU:H	2.33	0.42
1:A:612:ALA:HB3	1:A:662:TRP:NE1	2.35	0.42
1:A:489:LEU:HD23	1:A:489:LEU:C	2.40	0.41
1:A:423:GLU:H	1:A:423:GLU:HG3	1.66	0.41
1:A:678:SER:O	1:A:681:ASP:HB2	2.19	0.41
1:A:420:ILE:HG12	1:A:421:ALA:N	2.34	0.41
1:A:683:TYR:HA	1:A:686:GLU:HB2	2.02	0.41
1:A:669:ARG:HA	1:A:670:PRO:HD3	1.84	0.41
1:A:507:TYR:HB2	1:A:557:VAL:O	2.21	0.41
1:A:688:ASP:O	1:A:690:ALA:N	2.54	0.41
1:A:646:LYS:HE3	1:A:650:CYS:O	2.21	0.40
1:A:514:LEU:HD13	1:A:621:PHE:HA	2.03	0.40
1:A:585:THR:HA	4:A:33:HOH:O	2.21	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:20:HOH:O	4:A:20:HOH:O[8_666]	1.67	0.53
1:A:688:ASP:OD2	1:A:688:ASP:OD2[7_555]	1.86	0.34

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	257/277 (93%)	219 (85%)	23 (9%)	15 (6%)	2 3

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	446	ASN
1	A	460	LYS
1	A	464	THR
1	A	495	GLU
1	A	523	VAL
1	A	566	GLY
1	A	567	ASP
1	A	568	PHE
1	A	600	ARG
1	A	632	LYS
1	A	462	ASP
1	A	438	GLU
1	A	496	GLU
1	A	651	PRO
1	A	588	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	237/252 (94%)	183 (77%)	54 (23%)	1 3

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	420	ILE
1	A	422	ARG
1	A	423	GLU
1	A	429	ARG

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Mol	Chain	Res	Type
1	A	431	LEU
1	A	438	GLU
1	A	446	ASN
1	A	447	HIS
1	A	450	GLU
1	A	454	VAL
1	A	458	THR
1	A	460	LYS
1	A	461	LYS
1	A	463	CYS
1	A	472	MET
1	A	479	LYS
1	A	489	LEU
1	A	495	GLU
1	A	496	GLU
1	A	518	LYS
1	A	520	SER
1	A	532	GLN
1	A	542	SER
1	A	548	ARG
1	A	552	VAL
1	A	553	ARG
1	A	560	PRO
1	A	567	ASP
1	A	585	THR
1	A	586	ARG
1	A	590	LYS
1	A	595	GLU
1	A	596	SER
1	A	599	PHE
1	A	600	ARG
1	A	604	THR
1	A	620	SER
1	A	624	GLN
1	A	632	LYS
1	A	633	ASP
1	A	635	ILE
1	A	638	LEU
1	A	639	GLU
1	A	649	LEU
1	A	653	VAL
1	A	659	THR

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Mol	Chain	Res	Type
1	A	663	ASP
1	A	669	ARG
1	A	673	THR
1	A	677	CYS
1	A	680	SER
1	A	687	LYS
1	A	689	ILE
1	A	691	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	446	ASN
1	A	485	HIS
1	A	512	HIS
1	A	554	ASN
1	A	598	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 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	$\# Z > 2$
3	PO4	A	1	-	4,4,4	2.05	1 (25%)	6,6,6	0.28	0
2	3JZ	A	999	-	36,38,38	2.65	17 (47%)	48,57,57	2.75	22 (45%)

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
3	PO4	A	1	-	-	0/0/0/0	0/0/0/0
2	3JZ	A	999	-	-	0/25/33/33	0/4/4/4

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	999	3JZ	O33-S31	-5.45	1.37	1.43
2	A	999	3JZ	C21-C22	-5.26	1.35	1.39
2	A	999	3JZ	C34-S31	-3.47	1.69	1.75
2	A	999	3JZ	C3-N9	-3.30	1.30	1.36
2	A	999	3JZ	C14-C22	-2.43	1.35	1.39
2	A	999	3JZ	C23-C22	2.09	1.54	1.50
2	A	999	3JZ	S31-N30	2.25	1.70	1.65
2	A	999	3JZ	C17-C13	2.30	1.43	1.39
2	A	999	3JZ	O26-C24	2.65	1.28	1.23
2	A	999	3JZ	C24-N25	2.71	1.43	1.36
2	A	999	3JZ	C7-C6	2.78	1.43	1.39
3	A	1	PO4	P-O4	2.82	1.63	1.53
2	A	999	3JZ	F27-C8	3.18	1.44	1.32
2	A	999	3JZ	C12-N10	3.23	1.53	1.45
2	A	999	3JZ	C11-N9	3.49	1.48	1.40
2	A	999	3JZ	F29-C8	3.79	1.46	1.32
2	A	999	3JZ	C1-C20	4.50	1.47	1.39
2	A	999	3JZ	C5-N10	6.76	1.44	1.34

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	999	3JZ	C12-N10-C5	-7.84	113.43	123.20
2	A	999	3JZ	F27-C8-C6	-5.81	102.46	112.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	999	3JZ	C6-C5-N4	-4.90	114.50	122.10
2	A	999	3JZ	C7-C6-C8	-4.12	115.58	120.52
2	A	999	3JZ	F28-C8-C6	-2.90	107.58	112.68
2	A	999	3JZ	C15-C21-C22	-2.90	119.12	121.96
2	A	999	3JZ	C11-N9-C3	-2.83	121.70	129.19
2	A	999	3JZ	C16-C11-C14	-2.72	116.43	119.69
2	A	999	3JZ	C13-C12-N10	-2.55	104.48	113.65
2	A	999	3JZ	O26-C24-C23	-2.20	124.13	126.93
2	A	999	3JZ	O32-S31-O33	-2.11	115.73	118.66
2	A	999	3JZ	C19-C1-C20	2.01	122.67	118.34
2	A	999	3JZ	C14-C22-C21	2.06	121.28	120.30
2	A	999	3JZ	C12-C13-C17	2.10	125.71	121.05
2	A	999	3JZ	C35-N30-C20	2.35	119.39	117.12
2	A	999	3JZ	C16-C11-N9	2.38	128.42	120.66
2	A	999	3JZ	C23-C22-C21	2.51	110.62	108.50
2	A	999	3JZ	O26-C24-N25	3.14	129.87	125.09
2	A	999	3JZ	O33-S31-N30	4.26	112.47	106.94
2	A	999	3JZ	N2-C3-N4	4.31	131.26	126.67
2	A	999	3JZ	F27-C8-F28	4.39	121.55	105.71
2	A	999	3JZ	O32-S31-C34	7.21	118.67	108.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	999	3JZ	5	0

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 [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	261/277 (94%)	0.09	9 (3%)	49 49	33, 60, 97, 119	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	585	THR	4.6
1	A	586	ARG	3.6
1	A	461	LYS	3.4
1	A	516	ARG	2.3
1	A	688	ASP	2.2
1	A	481	LEU	2.1
1	A	462	ASP	2.1
1	A	630	GLU	2.1
1	A	597	ILE	2.1

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](#)

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	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	3JZ	A	999	35/35	0.95	0.14	-0.48	26,41,58,61	0
3	PO4	A	1	5/5	0.86	0.23	-	104,106,109,113	0

6.5 Other polymers [i](#)

There are no such residues in this entry.