



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 07:50 pm GMT

PDB ID : 4J98
Title : Crystal Structure of FGF Receptor 2 (FGFR2) Kinase Domain Harboring the Gain-of-Function K659Q Mutation.
Authors : Huang, Z.; Chen, H.; Mohammadi, M.
Deposited on : 2013-02-15
Resolution : 2.31 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

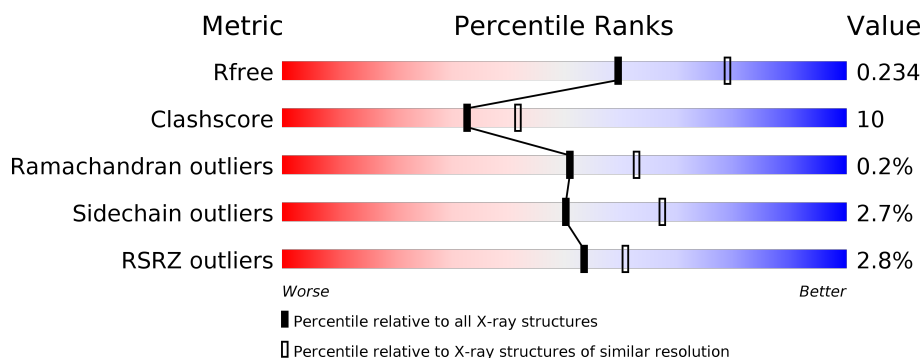
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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	324	<div> <div>3%</div> <div> <div></div> <div>79%</div> <div>13%</div> <div>6%</div> </div> </div>
1	B	324	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>13%</div> <div>6%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	802	-	-	-	X
2	SO4	B	803	-	-	-	X
3	ACP	B	804	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5133 atoms, of which 17 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 Fibroblast growth factor receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	2	0
			2411	1531	406	451	23			
1	B	304	Total	C	N	O	S	0	2	0
			2419	1540	407	449	23			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	445	MET	-	EXPRESSION TAG	UNP P21802
A	446	GLY	-	EXPRESSION TAG	UNP P21802
A	447	SER	-	EXPRESSION TAG	UNP P21802
A	448	SER	-	EXPRESSION TAG	UNP P21802
A	449	HIS	-	EXPRESSION TAG	UNP P21802
A	450	HIS	-	EXPRESSION TAG	UNP P21802
A	451	HIS	-	EXPRESSION TAG	UNP P21802
A	452	HIS	-	EXPRESSION TAG	UNP P21802
A	453	HIS	-	EXPRESSION TAG	UNP P21802
A	454	HIS	-	EXPRESSION TAG	UNP P21802
A	455	SER	-	EXPRESSION TAG	UNP P21802
A	456	GLN	-	EXPRESSION TAG	UNP P21802
A	457	ASP	-	EXPRESSION TAG	UNP P21802
A	491	ALA	CYS	ENGINEERED MUTATION	UNP P21802
A	659	GLN	LYS	ENGINEERED MUTATION	UNP P21802
B	445	MET	-	EXPRESSION TAG	UNP P21802
B	446	GLY	-	EXPRESSION TAG	UNP P21802
B	447	SER	-	EXPRESSION TAG	UNP P21802
B	448	SER	-	EXPRESSION TAG	UNP P21802
B	449	HIS	-	EXPRESSION TAG	UNP P21802
B	450	HIS	-	EXPRESSION TAG	UNP P21802
B	451	HIS	-	EXPRESSION TAG	UNP P21802
B	452	HIS	-	EXPRESSION TAG	UNP P21802
B	453	HIS	-	EXPRESSION TAG	UNP P21802
B	454	HIS	-	EXPRESSION TAG	UNP P21802

Continued on next page...

Continued from previous page...

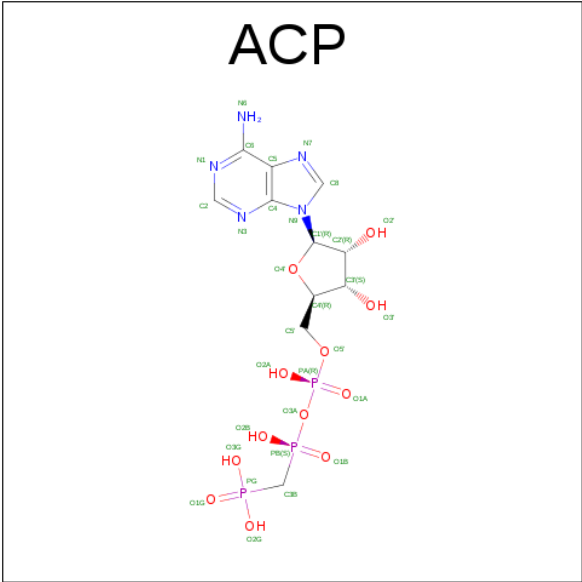
Chain	Residue	Modelled	Actual	Comment	Reference
B	455	SER	-	EXPRESSION TAG	UNP P21802
B	456	GLN	-	EXPRESSION TAG	UNP P21802
B	457	ASP	-	EXPRESSION TAG	UNP P21802
B	491	ALA	CYS	ENGINEERED MUTATION	UNP P21802
B	659	GLN	LYS	ENGINEERED MUTATION	UNP P21802

- Molecule 2 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).

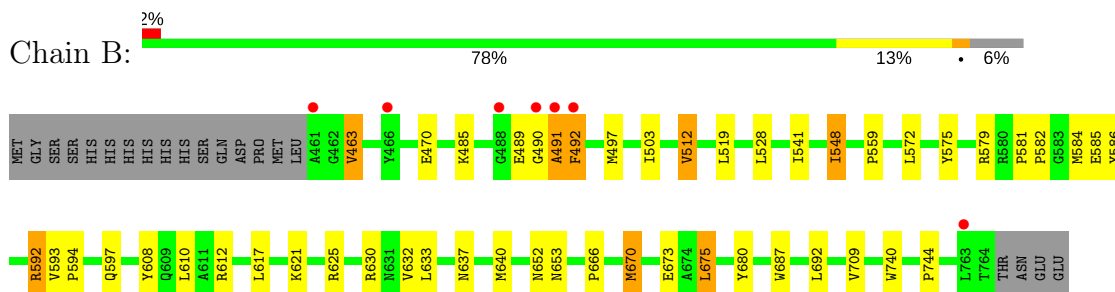


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	B	1	Total	C	H	N	O	P	0	0
			48	11	17	5	12	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	113	Total	O	
			113	113	0
4	B	117	Total	O	
			117	117	0

- Molecule 1: Fibroblast growth factor receptor 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	73.78Å 73.78Å 313.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.44 – 2.31 43.44 – 2.31	Depositor EDS
% Data completeness (in resolution range)	96.7 (43.44-2.31) 94.3 (43.44-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.66 (at 2.32Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.187 , 0.234 0.198 , 0.234	Depositor DCC
R_{free} test set	2000 reflections (5.67%)	DCC
Wilson B-factor (Å ²)	29.3	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5133	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ACP, SO4

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	0.42	0/2469	0.60	1/3344 (0.0%)
1	B	0.43	0/2478	0.59	0/3354
All	All	0.42	0/4947	0.59	1/6698 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	579	ARG	NE-CZ-NH2	-6.70	116.95	120.30

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	2411	0	2379	42	1
1	B	2419	0	2400	53	1
2	A	10	0	0	1	0
2	B	15	0	0	2	0
3	B	31	17	14	8	0
4	A	113	0	0	11	0
4	B	117	0	0	4	0
All	All	5116	17	4793	96	1

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 (96) 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:B:581:PRO:HD2	1:B:584:MET:CE	1.70	1.20
1:B:581:PRO:HD2	1:B:584:MET:HE2	1.36	1.03
1:B:581:PRO:HD2	1:B:584:MET:HE3	1.45	0.97
1:A:481:LEU:HG	4:A:995:HOH:O	1.67	0.95
1:A:572:LEU:HD13	1:A:640:MET:CE	1.97	0.93
1:A:572:LEU:HD13	1:A:640:MET:HE2	1.48	0.92
1:B:572:LEU:HD13	1:B:640:MET:CE	2.06	0.85
2:A:801:SO4:O3	4:A:1005:HOH:O	1.93	0.85
1:A:541:ILE:HD12	1:A:542:GLY:O	1.79	0.82
1:A:579:ARG:HG2	1:A:596:GLU:O	1.81	0.81
1:B:572:LEU:HD13	1:B:640:MET:HE1	1.65	0.79
1:A:630:ARG:NH2	1:A:666:PRO:HG2	1.98	0.78
1:B:630:ARG:NH2	1:B:666:PRO:HG2	1.99	0.77
1:B:652:ASN:HB2	4:B:1002:HOH:O	1.85	0.76
1:A:463:VAL:HG13	1:A:528:LEU:HD23	1.67	0.76
1:A:592:ARG:NH2	1:A:594:PRO:HB3	2.03	0.74
1:B:541:ILE:HD13	1:B:617:LEU:HD11	1.68	0.73
1:B:670:MET:SD	1:B:675:LEU:HD13	2.28	0.73
1:B:503:ILE:HG22	1:B:512:VAL:CG1	2.18	0.73
1:B:608:TYR:CZ	1:B:612:ARG:HD2	2.26	0.71
1:B:485:LYS:HE2	1:B:497:MET:CE	2.21	0.70
1:A:572:LEU:CD1	1:A:640:MET:HE2	2.21	0.70
1:B:608:TYR:CE2	1:B:612:ARG:HD2	2.26	0.69
1:A:612:ARG:HD3	4:A:926:HOH:O	1.92	0.69
1:B:503:ILE:HG22	1:B:512:VAL:HG11	1.75	0.68
1:B:470:GLU:HG3	4:B:1013:HOH:O	1.93	0.68
1:B:485:LYS:HE2	1:B:497:MET:HE1	1.77	0.66
1:A:608:TYR:CZ	1:A:612:ARG:HD2	2.31	0.65
1:A:463:VAL:CG1	1:A:528:LEU:HD23	2.25	0.65
1:B:492:PHE:O	1:B:492:PHE:CD1	2.50	0.65
1:B:637:ASN:HB2	2:B:803:SO4:O2	1.96	0.64
1:A:572:LEU:HD13	1:A:640:MET:HE1	1.80	0.63
1:B:489:GLU:N	3:B:804:ACP:O1A	2.32	0.62
1:B:572:LEU:HD13	1:B:640:MET:HE2	1.83	0.61
1:B:575:TYR:CE2	1:B:579:ARG:NH2	2.68	0.61
1:B:581:PRO:CD	1:B:584:MET:HE2	2.23	0.59
1:B:548:ILE:HG13	1:B:633:LEU:HD12	1.83	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:600:PHE:CZ	1:A:732:LEU:HD12	2.37	0.59
1:A:503:ILE:HG22	1:A:512:VAL:HG13	1.85	0.58
1:A:621:LYS:HD2	1:A:652:ASN:OD1	2.03	0.58
1:B:492:PHE:O	1:B:492:PHE:HD1	1.86	0.58
1:B:585:GLU:HG2	1:B:586:TYR:CD1	2.38	0.58
4:A:964:HOH:O	1:B:709:VAL:HG13	2.02	0.58
1:B:582:PRO:HG2	1:B:592:ARG:HG2	1.85	0.57
1:A:600:PHE:HZ	1:A:732:LEU:HD12	1.70	0.57
1:A:485:LYS:HG2	4:A:967:HOH:O	2.05	0.56
1:A:625:ARG:HD3	1:A:647:LEU:O	2.07	0.55
1:B:582:PRO:HG2	1:B:592:ARG:CG	2.37	0.55
1:A:483:LEU:HD23	4:A:995:HOH:O	2.07	0.54
1:B:621:LYS:HD2	1:B:652:ASN:OD1	2.08	0.54
1:A:490:GLY:HA3	4:A:953:HOH:O	2.07	0.54
1:A:751:LYS:NZ	1:A:755:GLU:OE1	2.42	0.52
3:B:804:ACP:H8	3:B:804:ACP:H5'2	1.91	0.52
1:B:630:ARG:HH22	1:B:666:PRO:HG2	1.74	0.52
1:A:630:ARG:HH21	1:A:666:PRO:HG2	1.70	0.52
1:B:541:ILE:CD1	1:B:617:LEU:HD11	2.40	0.52
1:A:670:MET:SD	1:A:675:LEU:HD13	2.51	0.51
1:A:603:LEU:HD21	1:A:699:LEU:CD2	2.41	0.49
1:B:490:GLY:HA3	3:B:804:ACP:O1B	2.12	0.49
1:B:489:GLU:C	3:B:804:ACP:O1A	2.50	0.49
1:A:501:VAL:HG23	4:A:929:HOH:O	2.13	0.49
1:A:662:ASN:OD1	1:B:463:VAL:HG22	2.13	0.49
1:B:503:ILE:CG2	1:B:512:VAL:HG11	2.43	0.49
1:B:519:LEU:HD11	1:B:528:LEU:HD13	1.95	0.49
1:A:503:ILE:HG22	1:A:512:VAL:CG1	2.42	0.48
1:B:491:ALA:CB	3:B:804:ACP:H3B2	2.43	0.48
1:A:603:LEU:HD21	1:A:699:LEU:HD21	1.96	0.48
1:B:612:ARG:HD3	4:B:1014:HOH:O	2.14	0.48
1:A:483:LEU:N	4:A:995:HOH:O	2.46	0.48
1:A:600:PHE:CZ	1:A:732:LEU:CD1	2.96	0.47
1:B:485:LYS:HE2	1:B:497:MET:HE3	1.93	0.47
1:A:541:ILE:CD1	1:A:542:GLY:O	2.58	0.47
1:B:632:VAL:HG11	1:B:640:MET:HE3	1.96	0.47
1:B:687:TRP:CE3	1:B:740:TRP:HA	2.50	0.47
1:A:579:ARG:HB3	1:A:598:MET:HG2	1.96	0.47
1:B:625:ARG:HA	1:B:680:TYR:OH	2.15	0.46
1:B:593:VAL:CG1	1:B:594:PRO:HD2	2.45	0.46
1:B:585:GLU:CD	1:B:585:GLU:H	2.20	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:489:GLU:HG2	1:A:494:GLN:HG3	2.00	0.44
1:B:491:ALA:HB3	3:B:804:ACP:H3B2	2.00	0.44
1:B:548:ILE:HA	1:B:548:ILE:HD13	1.86	0.44
1:B:492:PHE:C	1:B:492:PHE:CD1	2.91	0.43
1:B:491:ALA:HB3	3:B:804:ACP:C3B	2.49	0.43
1:A:538:MET:CE	1:A:548:ILE:O	2.67	0.42
1:B:652:ASN:O	1:B:653:ASN:HB2	2.20	0.42
2:B:801:SO4:O2	4:B:1004:HOH:O	2.21	0.42
1:A:581:PRO:O	1:A:584:MET:HG2	2.20	0.42
1:A:482:THR:C	4:A:995:HOH:O	2.57	0.42
1:A:710:GLU:CG	1:B:559:PRO:HA	2.50	0.42
1:A:697:PHE:CZ	1:A:732:LEU:HD13	2.56	0.41
1:A:710:GLU:HB2	4:A:931:HOH:O	2.20	0.41
1:B:673:GLU:CG	1:B:744:PRO:HG3	2.51	0.41
1:A:625:ARG:HA	1:A:680:TYR:OH	2.21	0.40
1:B:491:ALA:N	3:B:804:ACP:H3B2	2.36	0.40
1:B:610:LEU:HD13	1:B:692:LEU:HD21	2.04	0.40
1:A:519:LEU:HD11	1:A:528:LEU:HD13	2.04	0.40

All (1) 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)
1:A:587:SER:OG	1:B:597:GLN:NE2[5_655]	1.89	0.31

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	304/324 (94%)	298 (98%)	6 (2%)	0	100	100
1	B	304/324 (94%)	299 (98%)	4 (1%)	1 (0%)	44	55

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	608/648 (94%)	597 (98%)	10 (2%)	1 (0%)	51 63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	491	ALA

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	261/284 (92%)	254 (97%)	7 (3%)	50 67
1	B	262/284 (92%)	255 (97%)	7 (3%)	50 67
All	All	523/568 (92%)	509 (97%)	14 (3%)	50 67

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	463	VAL
1	A	512	VAL
1	A	579	ARG
1	A	592	ARG
1	A	673	GLU
1	A	675	LEU
1	A	710	GLU
1	B	463	VAL
1	B	492	PHE
1	B	512	VAL
1	B	548	ILE
1	B	592	ARG
1	B	670	MET
1	B	675	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	653	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](#)

6 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	SO4	A	801	-	4,4,4	0.18	0	6,6,6	0.23	0
2	SO4	A	802	-	4,4,4	0.16	0	6,6,6	0.09	0
2	SO4	B	801	-	4,4,4	0.18	0	6,6,6	0.22	0
2	SO4	B	802	-	4,4,4	0.17	0	6,6,6	0.09	0
2	SO4	B	803	-	4,4,4	0.15	0	6,6,6	0.11	0
3	ACP	B	804	-	27,33,33	2.11	6 (22%)	30,52,52	2.30	5 (16%)

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	SO4	A	801	-	-	0/0/0/0	0/0/0/0
2	SO4	A	802	-	-	0/0/0/0	0/0/0/0
2	SO4	B	801	-	-	0/0/0/0	0/0/0/0
2	SO4	B	802	-	-	0/0/0/0	0/0/0/0
2	SO4	B	803	-	-	0/0/0/0	0/0/0/0
3	ACP	B	804	-	-	0/15/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	804	ACP	C2'-C1'	-5.17	1.45	1.53
3	B	804	ACP	C2'-C3'	-4.06	1.42	1.53
3	B	804	ACP	C3'-C4'	-2.45	1.46	1.53
3	B	804	ACP	C6-N6	3.03	1.46	1.34
3	B	804	ACP	C2-N3	3.44	1.37	1.32
3	B	804	ACP	O4'-C1'	5.86	1.49	1.41

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	804	ACP	N3-C2-N1	-9.57	120.52	128.86
3	B	804	ACP	C4'-O4'-C1'	-5.11	104.33	109.77
3	B	804	ACP	PA-O3A-PB	-3.22	122.00	132.39
3	B	804	ACP	C4-C5-N7	-2.21	107.27	109.41
3	B	804	ACP	C2'-C3'-C4'	2.91	108.29	102.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	SO4	1	0
2	B	801	SO4	1	0
2	B	803	SO4	1	0
3	B	804	ACP	8	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	304/324 (93%)	0.02	10 (3%) 47 54	15, 28, 56, 108	0
1	B	304/324 (93%)	-0.13	7 (2%) 61 67	14, 26, 50, 93	0
All	All	608/648 (93%)	-0.06	17 (2%) 53 61	14, 27, 54, 108	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	583	GLY	6.4
1	A	587	SER	5.5
1	A	461	ALA	4.9
1	A	584	MET	4.8
1	A	585	GLU	4.4
1	A	586	TYR	3.3
1	B	461	ALA	3.3
1	B	490	GLY	3.1
1	A	508	PRO	3.1
1	A	506	ASP	2.9
1	B	763	LEU	2.9
1	B	466	TYR	2.7
1	B	492	PHE	2.4
1	A	510	GLU	2.4
1	A	582	PRO	2.3
1	B	491	ALA	2.2
1	B	488	GLY	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(Å ²)	Q<0.9
2	SO4	B	802	5/5	0.94	0.14	2.37	71,72,75,77	0
3	ACP	B	804	31/31	0.77	0.28	2.06	37,70,157,184	0
2	SO4	B	803	5/5	0.83	0.25	2.01	102,103,103,105	0
2	SO4	B	801	5/5	0.92	0.16	1.47	65,71,73,80	0
2	SO4	A	801	5/5	0.89	0.12	0.11	60,70,72,72	0
2	SO4	A	802	5/5	0.94	0.11	-	74,76,77,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.