



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 07:48 pm GMT

PDB ID : 2Q0B  
Title : Crystal Structure of FGF Receptor 2 (FGFR2) Kinase Domain Harboring the Pathogenic E565A Mutation Responsible for Pfeiffer Syndrome  
Authors : Chen, H.; Mohammadi, M.  
Deposited on : 2007-05-21  
Resolution : 2.90 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](mailto: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.

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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

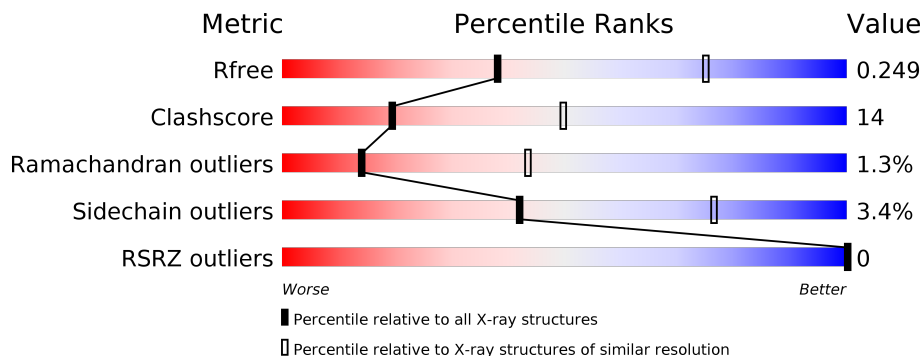
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	1586 (2.90-2.90)
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)
RSRZ outliers	101464	1596 (2.90-2.90)

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  $\geq 3$ , 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	
1	B	324	

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	A	802	-	-	-	X
2	SO4	B	801	-	-	-	X
3	ACP	A	803	-	-	-	X
3	ACP	B	803	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4514 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 Fibroblast growth factor receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	280	Total	C	N	O	S	0	0	0
			2203	1404	376	403	20			
1	B	282	Total	C	N	O	S	0	0	0
			2212	1410	379	403	20			

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	UNP P21802
A	565	ALA	GLU	ENGINEERED	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

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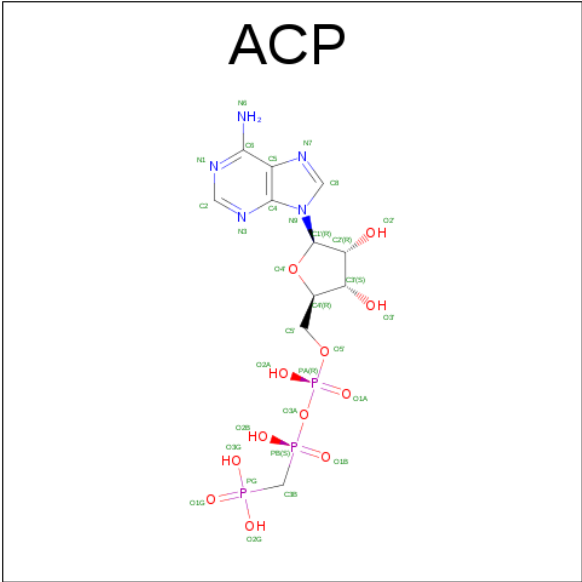
Chain	Residue	Modelled	Actual	Comment	Reference
B	455	SER	-	EXPRESSION TAG	UNP P21802
B	456	GLN	-	EXPRESSION TAG	UNP P21802
B	457	ASP	-	EXPRESSION TAG	UNP P21802
B	491	ALA	CYS	ENGINEERED	UNP P21802
B	565	ALA	GLU	ENGINEERED	UNP P21802

- Molecule 2 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



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		

- Molecule 3 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			10	5	5		
3	B	1	Total	C	N	0	0
			10	5	5		

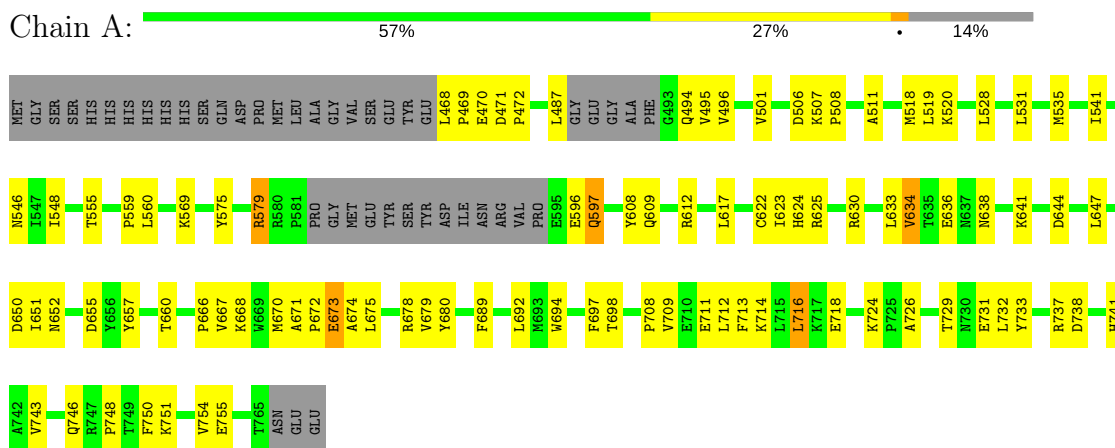
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	29	Total	O	0	0
			29	29		
4	B	30	Total	O	0	0
			30	30		

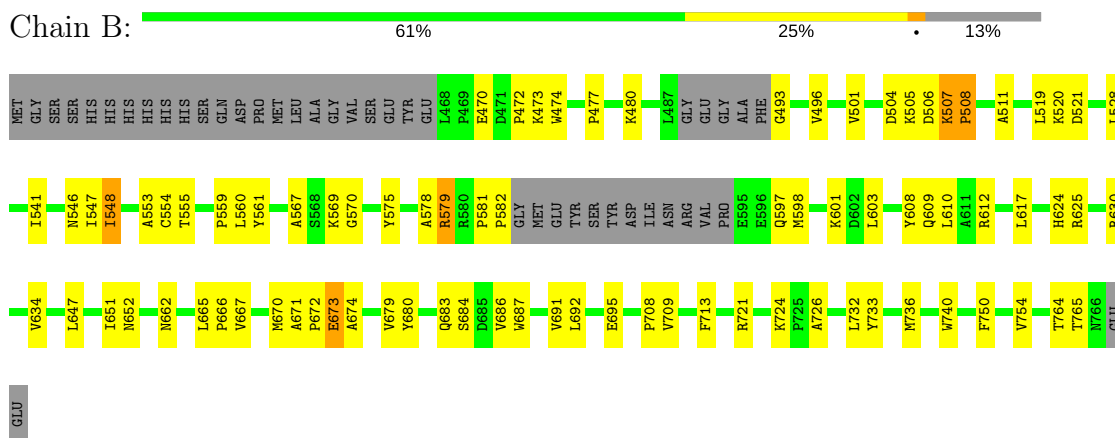
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Fibroblast growth factor receptor 2



#### • Molecule 1: Fibroblast growth factor receptor 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.57Å 116.82Å 63.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.90 49.53 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (25.00-2.90) 94.5 (49.53-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.16	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.37 (at 2.91Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.202 , 0.252 0.201 , 0.249	Depositor DCC
$R_{free}$ test set	817 reflections (4.79%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.9	Xtriage
Anisotropy	0.236	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4514	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.98% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

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	0.36	0/2248	0.62	0/3044
1	B	0.37	0/2258	0.62	0/3060
All	All	0.36	0/4506	0.62	0/6104

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	2203	0	2189	67	0
1	B	2212	0	2193	62	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
3	A	10	0	4	0	0
3	B	10	0	4	1	0
4	A	29	0	0	3	0
4	B	30	0	0	0	0
All	All	4514	0	4390	127	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 14.

All (127) 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:667:VAL:HG21	1:A:709:VAL:HG13	1.45	0.99
1:A:519:LEU:HD11	1:A:528:LEU:HD13	1.52	0.89
1:B:569:LYS:HB2	1:B:634:VAL:HG13	1.59	0.83
1:B:667:VAL:HG21	1:B:709:VAL:HG13	1.58	0.83
1:A:575:TYR:O	1:A:579:ARG:HD3	1.80	0.81
1:A:708:PRO:HG2	1:A:711:GLU:HG2	1.62	0.80
1:B:507:LYS:N	1:B:508:PRO:HD3	1.97	0.78
1:B:554:CYS:HB2	1:B:561:TYR:HB2	1.66	0.76
1:A:714:LYS:O	1:A:718:GLU:HG3	1.86	0.75
1:B:612:ARG:HH11	1:B:754:VAL:HG11	1.55	0.71
1:B:547:ILE:HD11	1:B:617:LEU:HD13	1.76	0.68
1:B:541:ILE:HD13	1:B:617:LEU:HD11	1.76	0.66
1:A:501:VAL:HG22	1:A:511:ALA:HB2	1.78	0.65
1:B:507:LYS:H	1:B:508:PRO:HD3	1.60	0.65
1:B:683:GLN:O	1:B:686:VAL:HG22	1.95	0.65
1:B:507:LYS:N	1:B:508:PRO:CD	2.62	0.62
1:A:535:MET:HE3	1:A:560:LEU:HD11	1.82	0.62
1:A:667:VAL:CG2	1:A:709:VAL:HG13	2.27	0.61
1:B:667:VAL:CG2	1:B:709:VAL:HG13	2.30	0.61
1:A:671:ALA:HB1	1:A:673:GLU:OE2	2.00	0.61
1:B:671:ALA:HB1	1:B:673:GLU:OE2	2.01	0.60
1:A:697:PHE:CZ	1:A:732:LEU:HD13	2.36	0.60
1:A:729:THR:HG22	1:A:731:GLU:H	1.67	0.59
1:A:630:ARG:NH2	1:A:666:PRO:HG2	2.18	0.59
1:B:519:LEU:HD11	1:B:528:LEU:HD13	1.84	0.59
1:B:647:LEU:HD13	1:B:665:LEU:HD23	1.85	0.59
1:B:569:LYS:HB2	1:B:634:VAL:O	2.02	0.58
1:B:601:LYS:HE3	1:B:765:THR:OG1	2.04	0.58
1:B:547:ILE:CD1	1:B:617:LEU:HD13	2.34	0.57
1:A:657:TYR:HA	1:A:678:ARG:HB2	1.87	0.57
1:A:541:ILE:HD13	1:A:617:LEU:HD11	1.87	0.56
1:A:471:ASP:N	4:A:917:HOH:O	2.39	0.56
1:A:729:THR:HG22	1:A:731:GLU:N	2.21	0.56
1:B:721:ARG:HE	1:B:740:TRP:HB3	1.71	0.56
1:A:548:ILE:HD12	1:A:633:LEU:HD12	1.87	0.55
1:A:494:GLN:HB2	1:A:520:LYS:HG2	1.89	0.55
1:A:625:ARG:HD3	1:A:647:LEU:O	2.07	0.55
1:B:732:LEU:O	1:B:736:MET:HG3	2.08	0.54
1:B:501:VAL:HA	1:B:511:ALA:HA	1.89	0.54
1:B:665:LEU:HD12	1:B:670:MET:HE2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:680:TYR:CE2	1:B:684:SER:HB2	2.44	0.53
1:B:473:LYS:HG3	1:B:474:TRP:CD1	2.44	0.52
1:A:559:PRO:HD3	1:B:708:PRO:HG2	1.90	0.52
1:A:741:HIS:HD2	1:A:746:GLN:O	1.93	0.51
1:A:501:VAL:HA	1:A:511:ALA:HA	1.91	0.51
1:A:746:GLN:HG3	4:A:920:HOH:O	2.10	0.51
1:A:733:TYR:CZ	1:A:737:ARG:HD3	2.46	0.51
1:B:470:GLU:O	1:B:472:PRO:HD3	2.11	0.51
1:A:507:LYS:N	1:A:508:PRO:HD3	2.26	0.51
1:B:674:ALA:HA	1:B:679:VAL:O	2.11	0.50
1:A:531:LEU:HD23	1:A:560:LEU:HD23	1.94	0.50
1:B:612:ARG:HD3	1:B:754:VAL:HG13	1.94	0.50
1:B:724:LYS:HA	1:B:733:TYR:CD1	2.47	0.49
1:A:596:GLU:O	1:A:597:GLN:O	2.31	0.49
1:B:651:ILE:HG23	1:B:652:ASN:OD1	2.12	0.49
1:B:630:ARG:NH2	1:B:666:PRO:HG2	2.27	0.49
1:A:548:ILE:HD12	1:A:633:LEU:CD1	2.42	0.49
1:A:519:LEU:HD11	1:A:528:LEU:CD1	2.36	0.49
1:B:570:GLY:O	1:B:634:VAL:HG12	2.13	0.49
1:B:569:LYS:CB	1:B:634:VAL:HG13	2.35	0.49
1:A:535:MET:HE1	1:A:555:THR:HG22	1.94	0.48
1:B:662:ASN:HB3	1:B:670:MET:CE	2.43	0.48
1:B:477:PRO:HB2	1:B:480:LYS:HG2	1.94	0.48
1:A:750:PHE:O	1:A:754:VAL:HG23	2.12	0.48
1:A:751:LYS:O	1:A:755:GLU:HG3	2.13	0.48
1:B:575:TYR:O	1:B:578:ALA:HB3	2.13	0.48
1:A:487:LEU:HB2	1:A:495:VAL:HG12	1.96	0.48
1:A:546:ASN:ND2	1:A:609:GLN:HB3	2.29	0.48
1:B:579:ARG:HG3	1:B:598:MET:HG2	1.95	0.48
1:A:674:ALA:HA	1:A:679:VAL:O	2.14	0.47
1:A:506:ASP:C	1:A:508:PRO:HD3	2.35	0.47
1:B:555:THR:HG22	1:B:560:LEU:CD1	2.44	0.47
1:A:624:HIS:O	1:A:625:ARG:HB2	2.13	0.47
1:A:636:GLU:HA	1:A:636:GLU:OE2	2.15	0.47
1:B:610:LEU:HD13	1:B:692:LEU:HD21	1.97	0.47
1:B:672:PRO:HA	1:B:713:PHE:HE2	1.79	0.47
1:A:470:GLU:O	1:A:472:PRO:HD3	2.15	0.47
1:B:546:ASN:ND2	1:B:609:GLN:HB3	2.30	0.47
1:B:575:TYR:O	1:B:579:ARG:HD3	2.15	0.47
1:A:651:ILE:HG23	1:A:652:ASN:N	2.30	0.46
1:A:506:ASP:C	1:A:507:LYS:HD2	2.35	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:TYR:CZ	1:A:612:ARG:HD3	2.49	0.46
1:B:504:ASP:C	1:B:506:ASP:H	2.18	0.46
1:A:634:VAL:HG23	1:A:638:ASN:HA	1.98	0.46
1:B:477:PRO:HB2	1:B:480:LYS:CG	2.46	0.46
1:A:724:LYS:HG3	1:A:733:TYR:HB2	1.98	0.46
1:A:569:LYS:HB2	1:A:634:VAL:HG22	1.98	0.45
1:B:665:LEU:HD12	1:B:670:MET:CE	2.47	0.45
1:A:487:LEU:HD12	1:A:495:VAL:CG1	2.47	0.45
1:A:743:VAL:HB	1:A:746:GLN:HB2	1.99	0.45
1:B:721:ARG:NE	1:B:740:TRP:HB3	2.31	0.45
1:B:493:GLY:O	1:B:520:LYS:HD2	2.17	0.44
1:A:708:PRO:HB3	1:B:559:PRO:HG3	1.99	0.44
1:A:470:GLU:HA	4:A:917:HOH:O	2.17	0.44
1:B:507:LYS:H	1:B:508:PRO:CD	2.23	0.44
1:B:575:TYR:O	1:B:579:ARG:CD	2.65	0.44
1:B:608:TYR:O	1:B:612:ARG:HG2	2.17	0.44
1:A:535:MET:CE	1:A:560:LEU:HD11	2.47	0.43
1:A:575:TYR:CE1	1:A:634:VAL:HG21	2.53	0.43
1:A:694:TRP:O	1:A:698:THR:HG23	2.19	0.43
1:B:624:HIS:O	1:B:625:ARG:HB2	2.19	0.43
1:A:569:LYS:HB2	1:A:634:VAL:O	2.19	0.43
1:B:567:ALA:O	3:B:803:ACP:H2	2.19	0.43
1:B:579:ARG:N	1:B:579:ARG:HD2	2.34	0.43
1:B:598:MET:HE2	1:B:603:LEU:HD23	2.01	0.43
1:B:691:VAL:O	1:B:695:GLU:HG3	2.19	0.42
1:A:596:GLU:HG2	1:A:596:GLU:O	2.20	0.42
1:B:598:MET:CE	1:B:603:LEU:HD23	2.50	0.42
1:A:496:VAL:HG22	1:A:518:MET:CE	2.49	0.42
1:A:689:PHE:O	1:A:692:LEU:HB3	2.20	0.42
1:A:738:ASP:HB3	1:A:748:PRO:HD3	2.02	0.42
1:A:712:LEU:HG	1:A:716:LEU:HD22	2.01	0.42
1:B:548:ILE:HA	1:B:548:ILE:HD13	1.86	0.42
1:A:468:LEU:HA	1:A:469:PRO:HD3	1.94	0.42
1:A:673:GLU:H	1:A:673:GLU:HG3	1.50	0.42
1:B:687:TRP:C	1:B:687:TRP:CD1	2.93	0.41
1:A:724:LYS:HA	1:A:733:TYR:CD1	2.56	0.41
1:A:675:LEU:HD12	1:A:675:LEU:HA	1.86	0.41
1:B:581:PRO:HA	1:B:582:PRO:HD3	1.87	0.41
1:A:672:PRO:HA	1:A:713:PHE:CE2	2.56	0.41
1:A:670:MET:HE1	1:A:675:LEU:HD13	2.03	0.41
1:B:553:ALA:HA	1:B:561:TYR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:625:ARG:NH1	1:A:647:LEU:O	2.51	0.41
1:B:750:PHE:O	1:B:754:VAL:HG23	2.20	0.41
1:A:623:ILE:HD12	1:A:680:TYR:CD2	2.56	0.40
1:B:724:LYS:HG3	1:B:733:TYR:HB2	2.03	0.40
1:A:668:LYS:HG2	1:A:712:LEU:HD22	2.03	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	274/324 (85%)	256 (93%)	16 (6%)	2 (1%)	25	60
1	B	276/324 (85%)	261 (95%)	10 (4%)	5 (2%)	10	34
All	All	550/648 (85%)	517 (94%)	26 (5%)	7 (1%)	14	43

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	597	GLN
1	B	726	ALA
1	B	597	GLN
1	A	726	ALA
1	B	505	LYS
1	B	508	PRO
1	B	507	LYS

### 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	236/283 (83%)	226 (96%)	10 (4%)	34	69
1	B	236/283 (83%)	230 (98%)	6 (2%)	53	83
All	All	472/566 (83%)	456 (97%)	16 (3%)	42	76

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	579	ARG
1	A	622	CYS
1	A	634	VAL
1	A	641	LYS
1	A	644	ASP
1	A	650	ASP
1	A	655	ASP
1	A	660	THR
1	A	673	GLU
1	A	716	LEU
1	B	496	VAL
1	B	521	ASP
1	B	548	ILE
1	B	579	ARG
1	B	673	GLU
1	B	764	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	620	GLN
1	A	631	ASN
1	A	741	HIS
1	B	494	GLN
1	B	631	ASN
1	B	637	ASN
1	B	653	ASN
1	B	746	GLN
1	B	766	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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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	0.34	0	6,6,6	0.08	0
2	SO4	A	802	-	4,4,4	0.33	0	6,6,6	0.11	0
3	ACP	A	803	-	9,11,33	0.84	0	7,15,52	0.97	0
2	SO4	B	801	-	4,4,4	0.35	0	6,6,6	0.19	0
2	SO4	B	802	-	4,4,4	0.33	0	6,6,6	0.06	0
3	ACP	B	803	-	9,11,33	0.85	0	7,15,52	0.99	0

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	B	802	-	-	0/0/0/0	0/0/0/0
3	ACP	B	803	-	-	0/0/0/38	0/2/2/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	803	ACP	1	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	280/324 (86%)	-0.31	0 100 100	5, 19, 37, 55	0
1	B	282/324 (87%)	-0.32	0 100 100	5, 18, 40, 54	0
All	All	562/648 (86%)	-0.31	0 100 100	5, 19, 38, 55	0

There are no RSRZ outliers to report.

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	SO4	B	801	5/5	0.89	0.23	3.74	56,60,61,61	0
3	ACP	A	803	10/31	0.85	0.34	3.56	54,55,56,56	0
3	ACP	B	803	10/31	0.88	0.29	3.32	40,41,42,43	0
2	SO4	A	802	5/5	0.93	0.27	2.15	77,78,78,79	0
2	SO4	A	801	5/5	0.97	0.13	-1.25	51,51,52,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	B	802	5/5	0.91	0.30	-	99,99,99,99	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.