



# Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2QI8  
Title : Crystal structure of drug resistant SRC kinase domain  
Authors : Michalczyk, A.; Rode, H.B.; Gruetter, C.; Rauh, D.  
Deposited on : 2007-07-03  
Resolution : 2.32 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 (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



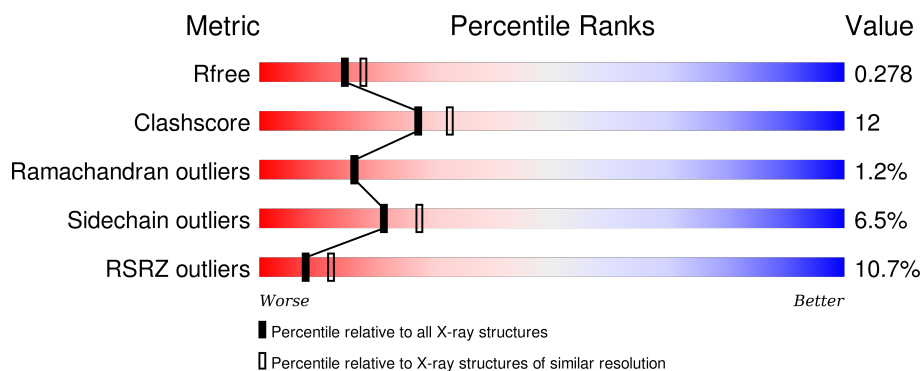
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.32 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	4425 (2.34-2.30)
Clashscore	102246	5057 (2.34-2.30)
Ramachandran outliers	100387	5008 (2.34-2.30)
Sidechain outliers	100360	5007 (2.34-2.30)
RSRZ outliers	91569	4432 (2.34-2.30)

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  $\geq 3$ , 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	286	<div> <div>12%</div> <div>64%</div> <div>22%</div> <div>•</div> <div>11%</div> </div>
1	B	286	<div> <div>7%</div> <div>65%</div> <div>19%</div> <div>•</div> <div>13%</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	GOL	A	100	-	-	-	X



## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4210 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	255	Total	C	N	O	S	0	6	0
			2049	1322	338	371	18			
1	B	249	Total	C	N	O	S	0	1	0
			1983	1273	330	363	17			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	248	GLY	-	CLONING ARTIFACT	UNP P00523
A	249	HIS	-	CLONING ARTIFACT	UNP P00523
A	250	MET	-	CLONING ARTIFACT	UNP P00523
A	338	MET	THR	ENGINEERED	UNP P00523
A	345	CYS	SER	ENGINEERED	UNP P00523
B	248	GLY	-	CLONING ARTIFACT	UNP P00523
B	249	HIS	-	CLONING ARTIFACT	UNP P00523
B	250	MET	-	CLONING ARTIFACT	UNP P00523
B	338	MET	THR	ENGINEERED	UNP P00523
B	345	CYS	SER	ENGINEERED	UNP P00523

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is water.

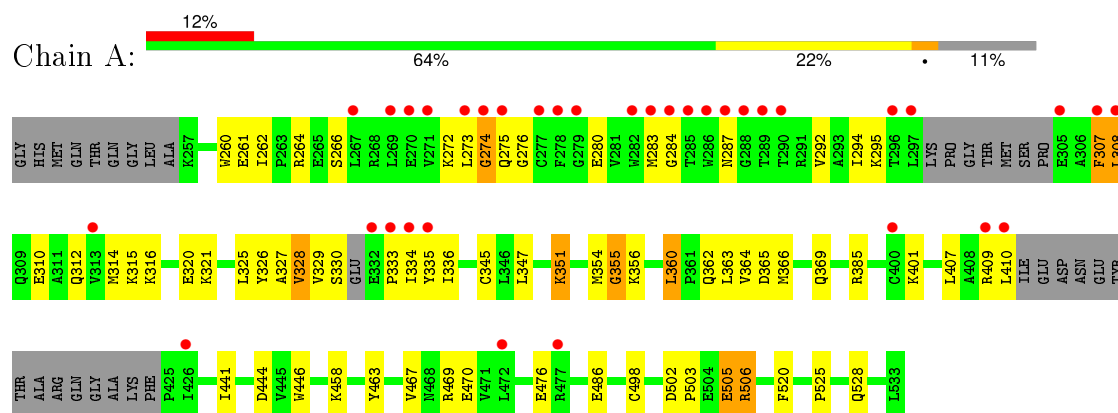
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	76	Total	O	0	0
			76	76		
3	B	96	Total	O	0	0
			96	96		



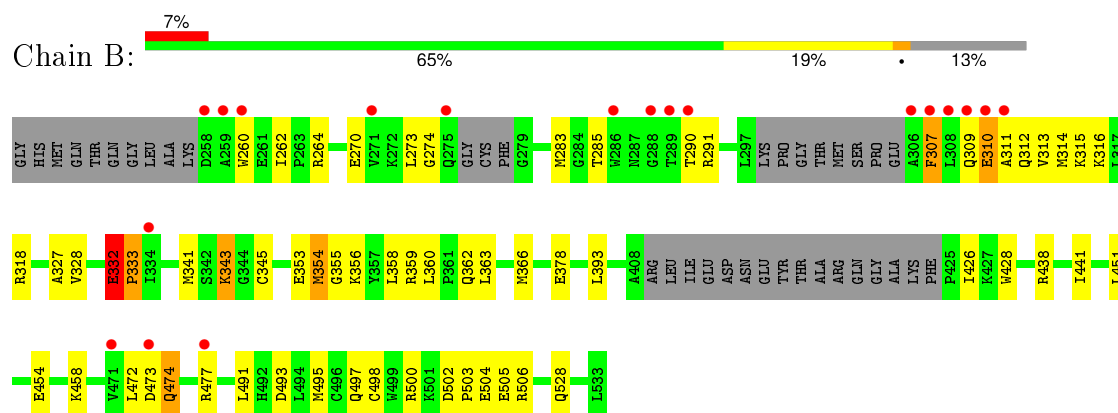
### 3 Residue-property plots

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, $\alpha$ , $\beta$ , $\gamma$	42.00Å 63.02Å 73.95Å 78.78° 88.80° 90.14°	Depositor
Resolution (Å)	72.55 – 2.32 36.69 – 2.32	Depositor EDS
% Data completeness (in resolution range)	93.8 (72.55-2.32) 87.9 (36.69-2.32)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.15 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, $R_{free}$	0.205 , 0.280 0.206 , 0.278	Depositor DCC
$R_{free}$ test set	1546 reflections (5.40%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.8	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.2	EDS
Estimated twinning fraction	0.028 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 30188 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4210	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.64% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL

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	0.76	1/2113 (0.0%)	0.87	2/2858 (0.1%)
1	B	0.75	0/2032	0.83	1/2752 (0.0%)
All	All	0.75	1/4145 (0.0%)	0.85	3/5610 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	3
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	345	CYS	CB-SG	-5.72	1.72	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	506	ARG	NE-CZ-NH1	8.42	124.51	120.30
1	A	506	ARG	NE-CZ-NH2	-6.23	117.19	120.30
1	B	332	GLU	C-N-CD	-5.70	108.07	120.60

There are no chirality outliers.

All (4) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	409	ARG	Peptide
1	B	310	GLU	Peptide
1	B	314	MET	Peptide
1	B	332	GLU	Peptide

## 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	2049	0	2027	56	0
1	B	1983	0	1932	40	0
2	A	6	0	8	1	0
3	A	76	0	0	2	0
3	B	96	0	0	1	0
All	All	4210	0	3967	96	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 12.

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:A:307:PHE:H	1:A:308:LEU:HB2	1.09	1.17
1:B:310:GLU:HB3	1:B:311:ALA:HA	1.18	1.14
1:A:307:PHE:H	1:A:308:LEU:CB	1.77	0.98
1:A:307:PHE:N	1:A:308:LEU:HB2	1.86	0.91
1:A:329:VAL:HG12	1:A:330:SER:H	1.38	0.88
1:B:310:GLU:HB3	1:B:311:ALA:CA	2.02	0.88
1:A:294:ILE:HG22	1:A:295:LYS:H	1.44	0.82
1:A:308:LEU:O	1:A:312:GLN:HG2	1.82	0.80
1:B:310:GLU:CB	1:B:311:ALA:HA	2.07	0.77
1:B:426:ILE:HD13	1:B:472:LEU:HG	1.65	0.77
1:A:486:GLU:H	2:A:100:GOL:H11	1.50	0.74
1:B:260:TRP:HH2	1:B:318:ARG:HH22	1.38	0.70
1:B:358:LEU:O	1:B:359:ARG:NH1	2.25	0.69
1:A:294:ILE:HG22	1:A:295:LYS:N	2.08	0.68
1:A:272:LYS:HE2	1:A:280:GLU:HG3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:LEU:H	1:A:274:GLY:HA3	1.59	0.67
1:A:295:LYS:HE2	1:A:310:GLU:OE2	1.95	0.66
1:A:463:TYR:HA	3:A:572:HOH:O	1.94	0.66
1:B:315:LYS:O	1:B:316:LYS:HB2	1.95	0.65
1:A:385:ARG:HD3	1:A:407:LEU:O	1.97	0.65
1:B:283:MET:SD	1:B:291:ARG:NH1	2.69	0.65
1:B:264:ARG:HH22	1:B:332:GLU:CB	2.09	0.64
1:A:262:ILE:HG12	1:A:327:ALA:HB1	1.79	0.64
1:B:309:GLN:HB3	1:B:310:GLU:O	2.00	0.61
1:B:273:LEU:N	1:B:274:GLY:HA3	2.16	0.61
1:A:328:VAL:HG23	1:A:329:VAL:H	1.66	0.60
1:A:273:LEU:N	1:A:274:GLY:HA3	2.16	0.60
1:B:355:GLY:O	1:B:458:LYS:HE2	2.03	0.58
1:B:273:LEU:H	1:B:274:GLY:HA3	1.67	0.58
1:B:363:LEU:HD11	1:B:458:LYS:HE3	1.87	0.57
1:B:270:GLU:OE2	1:B:285:THR:OG1	2.23	0.57
1:A:294:ILE:CG2	1:A:295:LYS:H	2.14	0.57
1:B:260:TRP:HH2	1:B:318:ARG:NH2	2.03	0.56
1:A:320:GLU:O	1:A:401:LYS:HE2	2.05	0.56
1:B:354:MET:HE3	1:B:354:MET:HA	1.87	0.56
1:A:360:LEU:HD22	1:A:364:VAL:HG23	1.88	0.55
1:A:355:GLY:O	1:A:458:LYS:HE2	2.08	0.54
1:A:283:MET:HG2	1:A:284:GLY:H	1.72	0.54
1:A:272:LYS:HE2	1:A:280:GLU:CG	2.38	0.54
1:A:347:LEU:O	1:A:351:LYS:HG2	2.08	0.53
1:A:476:GLU:HA	1:A:476:GLU:OE2	2.08	0.53
1:A:362:GLN:O	1:A:366:MET:HG3	2.08	0.52
1:A:260:TRP:NE1	1:A:315:LYS:HG2	2.24	0.52
1:B:262:ILE:HG12	1:B:327:ALA:HB1	1.91	0.52
1:B:332:GLU:CB	1:B:333:PRO:C	2.80	0.51
1:B:318:ARG:NH1	3:B:560:HOH:O	2.37	0.51
1:A:328:VAL:CG2	1:A:329:VAL:N	2.74	0.50
1:A:329:VAL:HG12	1:A:330:SER:N	2.18	0.48
1:B:264:ARG:NH2	1:B:332:GLU:CB	2.77	0.48
1:A:328:VAL:HG23	1:A:329:VAL:N	2.29	0.48
1:A:329:VAL:CG1	1:A:330:SER:H	2.20	0.48
1:B:345:CYS:HA	1:B:393:LEU:HD23	1.97	0.47
1:A:365:ASP:O	1:A:369:GLN:HG3	2.15	0.47
1:A:446:TRP:HA	1:A:498:CYS:O	2.15	0.47
1:A:260:TRP:CD1	1:A:315:LYS:HG2	2.49	0.47
1:A:321:LYS:HA	1:A:401:LYS:HG2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:428:TRP:HE1	1:B:454:GLU:CD	2.18	0.47
1:A:275:GLN:HA	1:A:276:GLY:HA3	1.65	0.47
1:A:470[B]:GLU:OE2	3:A:566:HOH:O	2.21	0.47
1:A:503:PRO:HA	1:A:506:ARG:CZ	2.46	0.46
1:B:307:PHE:C	1:B:307:PHE:CD2	2.89	0.46
1:A:363:LEU:HD11	1:A:458:LYS:HE3	1.99	0.45
1:B:497:GLN:O	1:B:506:ARG:HG3	2.16	0.45
1:A:467:VAL:HG12	1:A:470[B]:GLU:HB2	1.98	0.45
1:A:308:LEU:H	1:A:336:ILE:HD11	1.81	0.44
1:A:283:MET:HG2	1:A:284:GLY:N	2.32	0.44
1:B:341:MET:HG3	1:B:393:LEU:HB3	1.99	0.44
1:A:314[B]:MET:HB3	1:A:325:LEU:HB2	1.99	0.44
1:A:294:ILE:CG2	1:A:295:LYS:N	2.75	0.44
1:A:520:PHE:O	1:A:525:PRO:HA	2.17	0.44
1:A:266:SER:HB2	1:A:287:ASN:OD1	2.16	0.44
1:A:502:ASP:HB3	1:A:505:GLU:HB2	2.01	0.43
1:A:294:ILE:HD12	1:A:294:ILE:H	1.83	0.43
1:B:491:LEU:O	1:B:495:MET:HG3	2.19	0.43
1:A:273:LEU:N	1:A:274:GLY:CA	2.81	0.43
1:B:315:LYS:O	1:B:316:LYS:CB	2.64	0.43
1:B:474:GLN:HB3	1:B:474:GLN:HE21	1.62	0.43
1:A:441:ILE:O	1:A:444:ASP:HB2	2.19	0.43
1:B:378:GLU:HG3	1:B:441:ILE:HG12	2.00	0.42
1:A:410:LEU:HD23	1:A:410:LEU:HA	1.83	0.42
1:A:329:VAL:HB	1:A:335:TYR:H	1.84	0.42
1:A:272:LYS:HD3	1:A:274:GLY:HA3	2.01	0.42
1:B:495:MET:O	1:B:498:CYS:HB2	2.20	0.42
1:B:500:ARG:NH1	1:B:505:GLU:O	2.52	0.42
1:B:273:LEU:N	1:B:274:GLY:CA	2.81	0.41
1:A:292:VAL:HG12	1:A:326:TYR:CE2	2.55	0.41
1:B:358:LEU:HD13	1:B:363:LEU:HD21	2.02	0.41
1:B:311:ALA:C	1:B:313:VAL:H	2.24	0.41
1:B:362:GLN:O	1:B:366:MET:HG3	2.21	0.41
1:A:307:PHE:N	1:A:308:LEU:CB	2.61	0.41
1:B:473:ASP:O	1:B:477:ARG:HG3	2.20	0.41
1:A:273:LEU:HD23	1:A:273:LEU:HA	1.28	0.40
1:B:343:LYS:HA	1:B:343:LYS:HD3	1.90	0.40
1:B:359:ARG:HA	1:B:359:ARG:HD3	1.77	0.40
1:A:308:LEU:HG	1:A:334:ILE:HG21	2.03	0.40
1:B:502:ASP:HA	1:B:503:PRO:HD3	1.95	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	253/286 (88%)	234 (92%)	16 (6%)	3 (1%)	16	16
1	B	242/286 (85%)	217 (90%)	22 (9%)	3 (1%)	16	16
All	All	495/572 (86%)	451 (91%)	38 (8%)	6 (1%)	16	16

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	333	PRO
1	B	353	GLU
1	A	274	GLY
1	A	355	GLY
1	A	333	PRO
1	B	332	GLU

### 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	216/245 (88%)	201 (93%)	15 (7%)	19	24
1	B	207/245 (84%)	193 (93%)	14 (7%)	20	25
All	All	423/490 (86%)	394 (93%)	29 (7%)	21	24

All (29) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	261[A]	GLU
1	A	261[B]	GLU
1	A	264	ARG
1	A	307	PHE
1	A	308	LEU
1	A	316	LYS
1	A	328	VAL
1	A	351	LYS
1	A	354	MET
1	A	356[A]	LYS
1	A	356[B]	LYS
1	A	360	LEU
1	A	469	ARG
1	A	505	GLU
1	A	528	GLN
1	B	290	THR
1	B	307	PHE
1	B	312	GLN
1	B	328	VAL
1	B	343	LYS
1	B	354	MET
1	B	356	LYS
1	B	360	LEU
1	B	438	ARG
1	B	451	LEU
1	B	474	GLN
1	B	493	ASP
1	B	504	GLU
1	B	528	GLN

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	324	GLN
1	A	381	ASN
1	A	397	ASN
1	B	397	ASN
1	B	474	GLN

### 5.3.3 RNA ⓘ

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](#)

1 ligand is 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	GOL	A	100	-	5,5,5	0.31	0	5,5,5	0.71	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	GOL	A	100	-	-	0/4/4/4	0/0/0/0

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
2	A	100	GOL	1	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 ⓘ

### 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, 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	255/286 (89%)	0.61	35 (13%) 4 6	15, 28, 72, 81	1 (0%)
1	B	249/286 (87%)	0.44	19 (7%) 17 24	12, 31, 60, 88	2 (0%)
All	All	504/572 (88%)	0.53	54 (10%) 8 12	12, 29, 70, 88	3 (0%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	308	LEU	7.5
1	A	277	CYS	4.9
1	A	288	GLY	4.9
1	A	334	ILE	4.7
1	A	282	TRP	4.6
1	A	271	VAL	4.5
1	A	297	LEU	4.2
1	B	289	THR	3.8
1	A	287	ASN	3.7
1	A	270	GLU	3.7
1	A	335	TYR	3.7
1	A	333	PRO	3.6
1	B	259	ALA	3.4
1	A	273	LEU	3.3
1	B	290	THR	3.2
1	B	309	GLN	3.1
1	A	290	THR	3.0
1	A	296	THR	3.0
1	A	278	PHE	3.0
1	B	306	ALA	3.0
1	A	409	ARG	3.0
1	A	410	LEU	3.0
1	A	477	ARG	2.9
1	A	285	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	477	ARG	2.8
1	B	334	ILE	2.8
1	A	275	GLN	2.8
1	A	307	PHE	2.8
1	A	284	GLY	2.7
1	A	286	TRP	2.7
1	A	269	LEU	2.7
1	B	288	GLY	2.7
1	B	271	VAL	2.7
1	B	473	ASP	2.7
1	A	308	LEU	2.6
1	A	305	GLU	2.6
1	A	279	GLY	2.6
1	A	283	MET	2.6
1	B	258	ASP	2.5
1	B	471	VAL	2.4
1	B	275	GLN	2.4
1	B	307	PHE	2.4
1	A	289	THR	2.4
1	A	313	VAL	2.4
1	A	267	LEU	2.3
1	A	274	GLY	2.3
1	A	332	GLU	2.3
1	B	310	GLU	2.3
1	B	311	ALA	2.3
1	B	260	TRP	2.3
1	B	286	TRP	2.2
1	A	426	ILE	2.1
1	A	472	LEU	2.0
1	A	400	CYS	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 [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( $\text{\AA}^2$ )	Q<0.9
2	GOL	A	100	6/6	0.72	0.26	16.97	45,50,51,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.