



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 2, 2026 – 03:40 AM UTC

PDB ID : 2QI8 / pdb_00002qi8
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

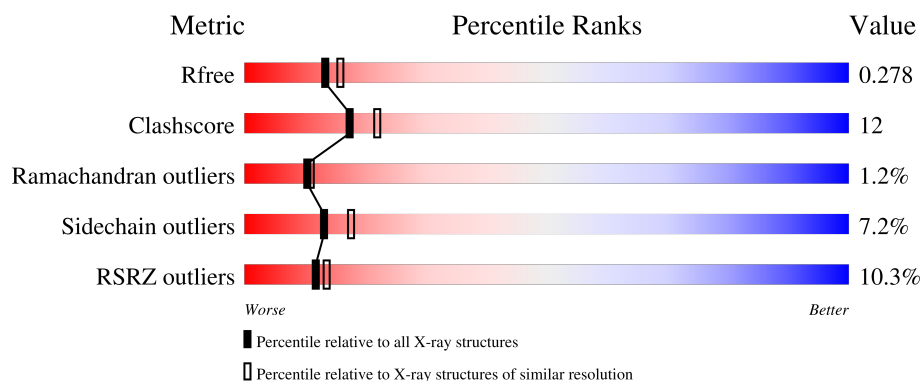
1 Overall quality at a glance

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}	180053	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	13% 63% 22% • 11%
1	B	286	6% 64% 20% • 13%

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 mutation	UNP P00523
A	345	CYS	SER	engineered mutation	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 mutation	UNP P00523
B	345	CYS	SER	engineered mutation	UNP P00523

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

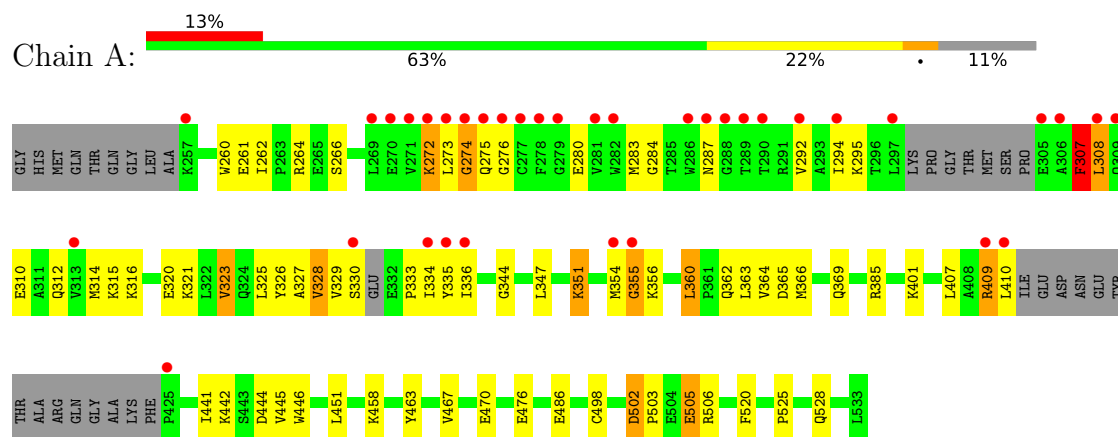
- Molecule 3 is water.

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

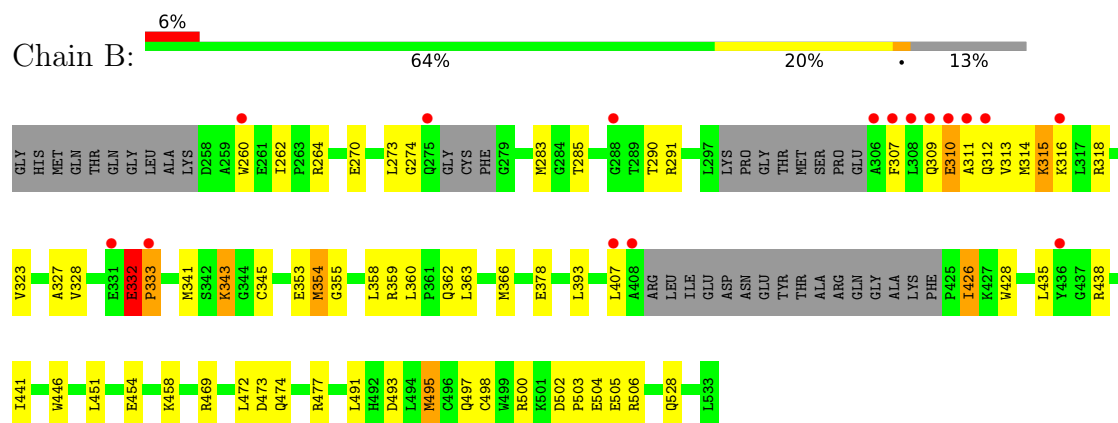
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: 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, α , β , γ	42.00Å 63.02Å 73.95Å 78.78° 88.80° 90.14°	Depositor
Resolution (Å)	72.55 – 2.32 72.52 – 2.32	Depositor EDS
% Data completeness (in resolution range)	93.8 (72.55-2.32) 93.8 (72.52-2.32)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.31Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.205 , 0.280 0.206 , 0.278	Depositor DCC
R_{free} test set	1546 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	30.8	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4210	wwPDB-VP
Average B, all atoms (Å ²)	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.*

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

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	0.94	1/2113 (0.0%)	1.20	9/2858 (0.3%)
1	B	0.96	0/2032	1.21	5/2752 (0.2%)
All	All	0.95	1/4145 (0.0%)	1.21	14/5610 (0.2%)

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	323	VAL	CA-CB	5.77	1.60	1.54

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	332	GLU	CA-C-N	18.28	142.69	119.84
1	B	332	GLU	C-N-CA	18.28	142.69	119.84
1	A	409	ARG	CA-C-N	6.09	132.66	121.70
1	A	409	ARG	C-N-CA	6.09	132.66	121.70
1	A	409	ARG	N-CA-C	-5.83	100.54	109.41
1	B	435	LEU	N-CA-C	5.69	117.56	111.36
1	B	495	MET	N-CA-C	-5.43	105.28	111.14
1	B	315	LYS	N-CA-C	-5.42	103.23	110.55

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	502	ASP	CA-C-N	5.39	125.46	119.32
1	A	502	ASP	C-N-CA	5.39	125.46	119.32
1	A	307	PHE	CA-C-N	5.16	131.00	121.70
1	A	307	PHE	C-N-CA	5.16	131.00	121.70
1	A	344	GLY	CA-C-N	5.15	128.99	121.31
1	A	344	GLY	C-N-CA	5.15	128.99	121.31

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	59	0
1	B	1983	0	1932	41	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	100	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 (100) 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

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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: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:315:LYS:O	1:B:316:LYS:HB2	1.95	0.64
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:A:310:GLU:HG2	1:A:314[B]:MET:HE2	1.80	0.63
1:B:273:LEU:N	1:B:274:GLY:HA3	2.16	0.61
1:B:309:GLN:HB3	1:B:310:GLU:O	2.00	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:332:GLU:CB	1:B:333:PRO:C	2.80	0.55
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:B:354:MET:HA	1:B:354:MET:HE3	1.90	0.54
1:A:347:LEU:O	1:A:351:LYS:HG2	2.08	0.53
1:A:476:GLU:OE2	1:A:476:GLU:HA	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:TRP:NE1	1:A:315:LYS:HG2	2.24	0.52
1:A:362:GLN:O	1:A:366:MET:HG3	2.08	0.52
1:B:262:ILE:HG12	1:B:327:ALA:HB1	1.91	0.52
1:B:428:TRP:HE1	1:B:454:GLU:CD	2.18	0.51
1:B:318:ARG:NH1	3:B:560:HOH:O	2.37	0.51
1:B:307:PHE:CD2	1:B:307:PHE:C	2.89	0.50
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: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:B:345:CYS:HA	1:B:393:LEU:HD23	1.97	0.47
1:A:260:TRP:CD1	1:A:315:LYS:HG2	2.49	0.47
1:A:275:GLN:HA	1:A:276:GLY:HA3	1.65	0.47
1:A:321:LYS:HA	1:A:401:LYS:HG2	1.97	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:311:ALA:C	1:B:313:VAL:H	2.24	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:283:MET:HG2	1:A:284:GLY:N	2.32	0.44
1:A:308:LEU:H	1:A:336:ILE:HD11	1.81	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:266:SER:HB2	1:A:287:ASN:OD1	2.16	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:502:ASP:HB3	1:A:505:GLU:HB2	2.01	0.43
1:A:294:ILE:H	1:A:294:ILE:HD12	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:HE21	1:B:474:GLN:HB3	1.62	0.43
1:A:441:ILE:O	1:A:444:ASP:HB2	2.19	0.43
1:A:410:LEU:HD23	1:A:410:LEU:HA	1.83	0.42
1:B:378:GLU:HG3	1:B:441:ILE:HG12	2.00	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

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:442:LYS:NZ	1:A:506:ARG:O	2.48	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:362:GLN:O	1:B:366:MET:HG3	2.21	0.41
1:B:446:TRP:CD1	1:B:446:TRP:C	2.98	0.41
1:A:307:PHE:N	1:A:308:LEU:CB	2.61	0.41
1:A:445:VAL:O	1:A:446:TRP:C	2.64	0.41
1:B:473:ASP:O	1:B:477:ARG:HG3	2.20	0.41
1:A:273:LEU:HA	1:A:273:LEU:HD23	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%)	10	11
1	B	242/286 (85%)	217 (90%)	22 (9%)	3 (1%)	10	11
All	All	495/572 (86%)	451 (91%)	38 (8%)	6 (1%)	10	11

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	333	PRO
1	B	353	GLU

Continued on next page...

Continued from previous page...

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

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	216/245 (88%)	199 (92%)	17 (8%)	11	15
1	B	207/245 (84%)	192 (93%)	15 (7%)	13	17
All	All	423/490 (86%)	391 (92%)	32 (8%)	13	16

All (32) 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	272	LYS
1	A	307	PHE
1	A	308	LEU
1	A	316	LYS
1	A	323	VAL
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	451	LEU
1	A	505	GLU
1	A	528	GLN
1	B	290	THR
1	B	312	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	323	VAL
1	B	328	VAL
1	B	343	LYS
1	B	354	MET
1	B	360	LEU
1	B	407	LEU
1	B	426	ILE
1	B	438	ARG
1	B	451	LEU
1	B	469	ARG
1	B	493	ASP
1	B	504	GLU
1	B	528	GLN

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

Mol	Chain	Res	Type
1	A	324	GLN
1	A	381	ASN
1	A	397	ASN
1	B	312	GLN
1	B	397	ASN
1	B	528	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	0.39	0	5,5,5	0.72	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	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	100	GOL	C1-C2-C3-O3
2	A	100	GOL	O1-C1-C2-O2
2	A	100	GOL	O2-C2-C3-O3

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 [i](#)

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	255/286 (89%)	0.45	36 (14%) 6 7	15, 27, 72, 81	7 (2%)
1	B	249/286 (87%)	0.28	16 (6%) 25 28	12, 30, 60, 88	3 (1%)
All	All	504/572 (88%)	0.37	52 (10%) 12 13	12, 29, 70, 88	10 (1%)

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	275	GLN	6.5
1	A	277	CYS	6.1
1	B	306	ALA	5.4
1	B	308	LEU	5.0
1	B	307	PHE	4.9
1	B	311	ALA	4.8
1	A	273	LEU	4.4
1	A	306	ALA	4.4
1	A	305	GLU	3.9
1	A	274	GLY	3.8
1	A	409	ARG	3.7
1	A	287	ASN	3.6
1	A	281	VAL	3.6
1	A	354	MET	3.5
1	A	282	TRP	3.5
1	A	355	GLY	3.4
1	B	275	GLN	3.4
1	A	278	PHE	3.3
1	A	271	VAL	3.3
1	A	269	LEU	3.3
1	A	297	LEU	3.2
1	A	335	TYR	3.2
1	A	279	GLY	3.1
1	B	408	ALA	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	312	GLN	3.1
1	A	308	LEU	3.1
1	B	316	LYS	2.8
1	A	286	TRP	2.7
1	B	309	GLN	2.6
1	A	410	LEU	2.6
1	A	330	SER	2.6
1	A	270	GLU	2.5
1	A	309	GLN	2.5
1	B	331	GLU	2.4
1	B	260	TRP	2.4
1	A	272	LYS	2.4
1	A	313	VAL	2.4
1	A	257	LYS	2.3
1	A	289	THR	2.3
1	B	333	PRO	2.3
1	A	276	GLY	2.3
1	B	310	GLU	2.3
1	B	288	GLY	2.2
1	B	407	LEU	2.2
1	A	292	VAL	2.2
1	A	336	ILE	2.2
1	A	425	PRO	2.1
1	A	290	THR	2.1
1	A	334	ILE	2.1
1	A	294	ILE	2.0
1	B	436	TYR	2.0
1	A	288	GLY	2.0

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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
2	GOL	A	100	6/6	0.83	0.15	45,50,51,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.