



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:51 AM GMT

PDB ID : 2OIQ
Title : Crystal Structure of chicken c-Src kinase domain in complex with the cancer drug imatinib.
Authors : Seeliger, M.A.; Nagar, B.; Frank, F.; Cao, X.; Henderson, M.N.; Kuriyan, J.
Deposited on : 2007-01-11
Resolution : 2.07 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

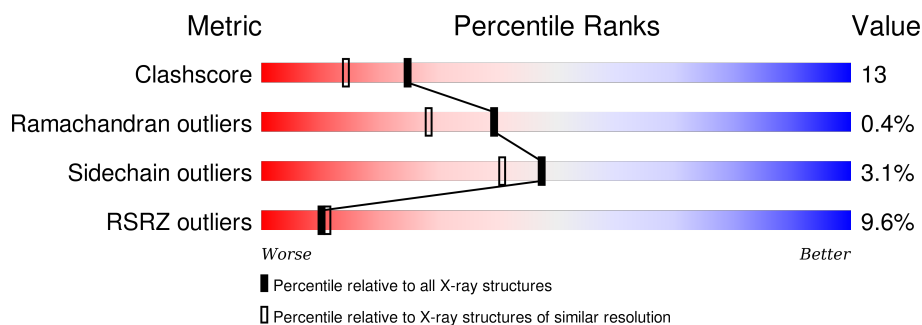
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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))
Clashscore	102246	1910 (2.08-2.04)
Ramachandran outliers	100387	1893 (2.08-2.04)
Sidechain outliers	100360	1893 (2.08-2.04)
RSRZ outliers	91569	1802 (2.08-2.04)

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	286	<div> <div>5%</div> <div>71%</div> <div>21%</div> <div>• 7%</div> </div>
1	B	286	<div> <div>13%</div> <div>66%</div> <div>26%</div> <div>• 7%</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
3	GOL	A	1003	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4560 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.

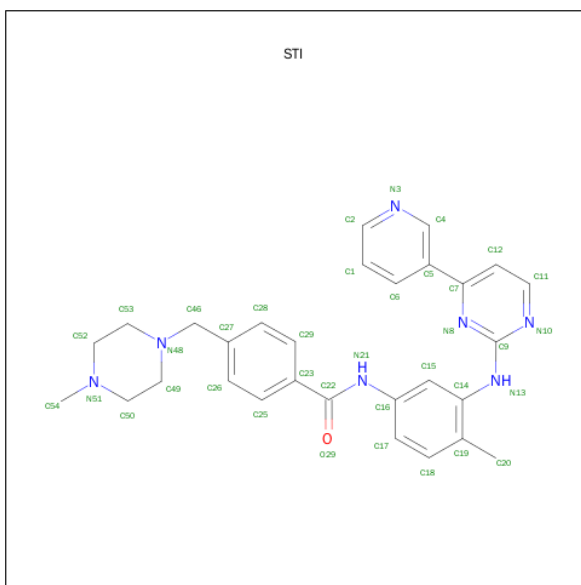
- Molecule 1 is a protein called Proto-oncogene tyrosine-protein kinase Src.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	0	0
			2126	1365	355	389	17			
1	B	265	Total	C	N	O	S	0	0	0
			2135	1371	356	391	17			

There are 6 discrepancies between the modelled and reference sequences:

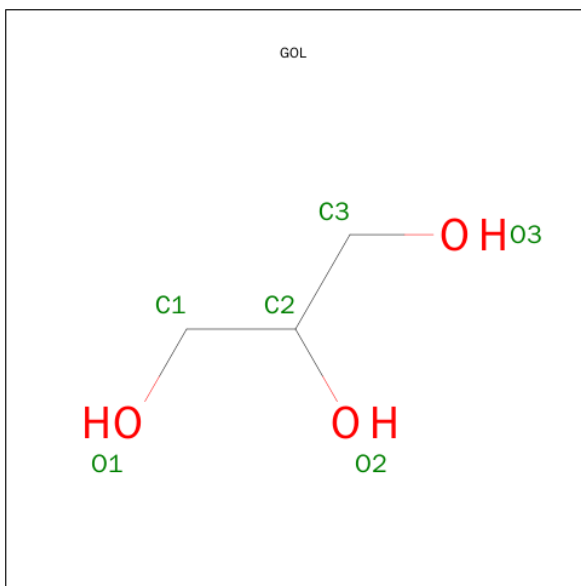
Chain	Residue	Modelled	Actual	Comment	Reference
A	248	GLY	-	CLONING ARTIFACT	UNP P00523
A	249	HIS	-	CLONING ARTIFACT	UNP P00523
A	250	MET	-	INITIATING METHIONINE	UNP P00523
B	248	GLY	-	CLONING ARTIFACT	UNP P00523
B	249	HIS	-	CLONING ARTIFACT	UNP P00523
B	250	MET	-	INITIATING METHIONINE	UNP P00523

- Molecule 2 is 4-(4-METHYL-PIPERAZIN-1-YLMETHYL)-N-[4-METHYL-3-(4-PYRIDIN-3-YL-PYRIMIDIN-2-YLAMINO)-PHENYL]-BENZAMIDE (three-letter code: STI) (formula: C₂₉H₃₁N₇O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	O	
			37	29	7	1	

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

3	A	1	Total	C	O		
			6	3	3		

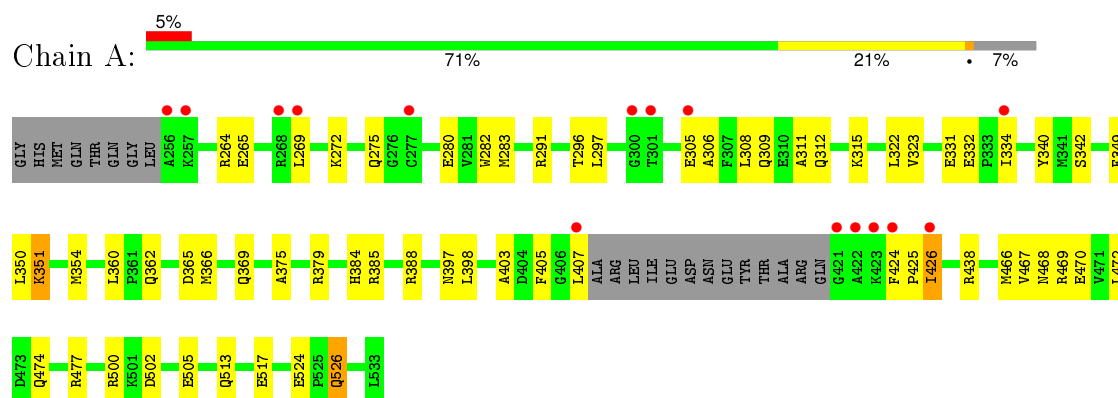
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	136	Total 136	O 136	0	0
4	B	114	Total 114	O 114	0	0

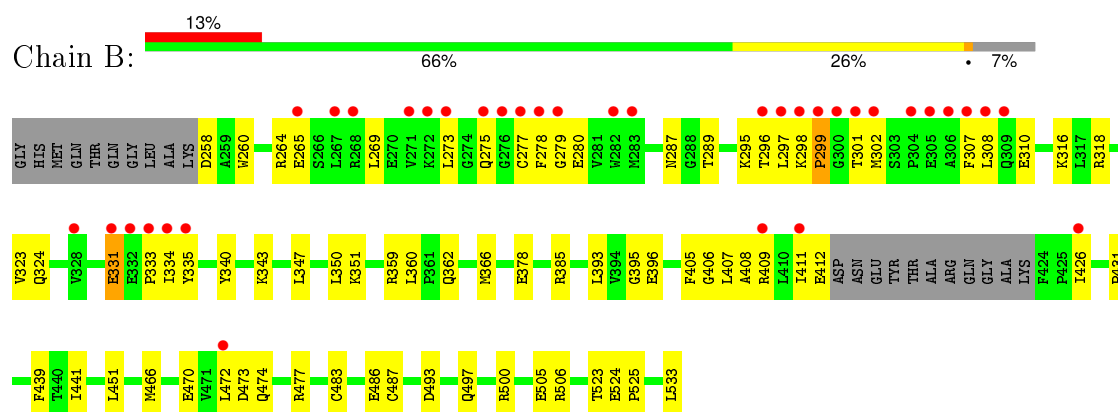
3 Residue-property plots [i](#)

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 ($RSRZ > 2$). 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	42.08Å 63.37Å 74.47Å 78.99° 89.12° 90.10°	Depositor
Resolution (Å)	50.00 – 2.07 43.45 – 2.07	Depositor EDS
% Data completeness (in resolution range)	93.5 (50.00-2.07) 91.3 (43.45-2.07)	Depositor EDS
R_{merge}	0.00	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.08Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.227 , 0.263 0.228 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	30.8	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.1	EDS
Estimated twinning fraction	0.029 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 44307 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4560	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.41% 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

5.1 Standard geometry

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

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	0.35	0/2178	0.59	0/2947
1	B	0.35	0/2187	0.56	0/2961
All	All	0.35	0/4365	0.58	0/5908

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	2126	0	2115	55	0
1	B	2135	0	2122	55	0
2	A	37	0	31	0	0
3	A	12	0	16	0	0
4	A	136	0	0	1	0
4	B	114	0	0	3	0
All	All	4560	0	4284	110	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 13.

All (110) 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:500:ARG:HD3	1:B:505:GLU:HG2	1.52	0.91
1:A:500:ARG:HD3	1:A:505:GLU:HB3	1.55	0.89
1:A:275:GLN:HG2	1:A:280:GLU:HG2	1.55	0.87
1:B:426:ILE:HG12	1:B:472:LEU:HG	1.62	0.81
1:A:524:GLU:HG3	1:A:526:GLN:HE22	1.48	0.79
1:A:306:ALA:HA	1:A:309:GLN:HE21	1.48	0.77
1:B:278:PHE:HA	1:B:301:THR:HG21	1.71	0.72
1:A:398:LEU:HD12	1:A:398:LEU:N	2.08	0.69
1:A:526:GLN:CD	1:A:526:GLN:H	1.98	0.67
1:A:524:GLU:HG3	1:A:526:GLN:NE2	2.11	0.65
1:A:524:GLU:CG	1:A:526:GLN:HE22	2.10	0.64
1:A:332:GLU:HA	1:A:334:ILE:HD12	1.78	0.64
1:B:298:LYS:HB3	1:B:301:THR:OG1	1.98	0.63
1:A:305:GLU:O	1:A:309:GLN:HG3	1.99	0.63
1:A:323:VAL:HG21	1:A:403:ALA:HB2	1.80	0.63
1:A:283:MET:HG3	1:A:340:TYR:CE1	2.34	0.62
1:A:405:PHE:HB2	1:A:407:LEU:HG	1.82	0.62
1:A:388:ARG:NH1	1:A:425:PRO:HB3	2.13	0.62
1:A:477:ARG:NH1	1:A:477:ARG:HB2	2.15	0.62
1:B:323:VAL:HG21	1:B:393:LEU:HD12	1.82	0.62
1:B:264:ARG:NH2	1:B:331:GLU:O	2.33	0.61
1:A:311:ALA:O	1:A:315:LYS:HG3	2.01	0.60
1:A:351:LYS:HE3	4:B:534:HOH:O	2.03	0.58
1:B:287:ASN:O	1:B:289:THR:HG23	2.03	0.58
1:B:493:ASP:O	1:B:497:GLN:HG3	2.03	0.58
1:B:359:ARG:H	1:B:362:GLN:NE2	2.02	0.58
1:B:343:LYS:HD3	1:B:395:GLY:O	2.04	0.58
1:A:272:LYS:HE2	1:A:275:GLN:HG3	1.87	0.57
1:A:502:ASP:HB3	1:A:505:GLU:HG3	1.86	0.56
1:B:359:ARG:H	1:B:362:GLN:HE21	1.51	0.56
1:A:467:VAL:HG22	1:A:470:GLU:HG2	1.87	0.56
1:B:385:ARG:HD3	1:B:407:LEU:O	2.06	0.56
1:B:277:CYS:O	1:B:301:THR:HG21	2.06	0.56
1:B:486:GLU:HG2	4:B:594:HOH:O	2.04	0.56
1:B:308:LEU:HD21	1:B:334:ILE:CG2	2.35	0.55
1:B:278:PHE:CE1	1:B:295:LYS:HE3	2.42	0.55
1:B:409:ARG:HH21	1:B:439:PHE:HB2	1.72	0.54
1:B:523:THR:C	1:B:525:PRO:HD3	2.28	0.54
1:A:296:THR:HG22	1:A:297:LEU:N	2.24	0.53
1:B:258:ASP:OD1	1:B:260:TRP:HB2	2.08	0.53
1:B:473:ASP:O	1:B:477:ARG:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:500:ARG:HD3	1:B:505:GLU:CG	2.33	0.53
1:A:264:ARG:NH2	1:A:331:GLU:O	2.42	0.52
1:A:291:ARG:HH11	1:A:291:ARG:HG3	1.75	0.51
1:A:388:ARG:HH12	1:A:425:PRO:HB3	1.75	0.51
1:A:477:ARG:HH11	1:A:477:ARG:HB2	1.76	0.51
1:B:405:PHE:HD1	1:B:408:ALA:CB	2.23	0.51
1:B:297:LEU:HB2	1:B:307:PHE:CE2	2.47	0.50
1:B:405:PHE:HD1	1:B:408:ALA:HB2	1.76	0.50
1:B:483:CYS:SG	1:B:487:CYS:O	2.69	0.50
1:B:524:GLU:N	1:B:525:PRO:HD3	2.26	0.50
1:B:264:ARG:HE	1:B:333:PRO:HG2	1.76	0.49
1:B:318:ARG:HD3	1:B:324:GLN:OE1	2.12	0.49
1:B:296:THR:HG22	1:B:297:LEU:N	2.27	0.49
1:A:362:GLN:O	1:A:366:MET:HG3	2.12	0.49
1:A:513:GLN:O	1:A:517:GLU:HG3	2.12	0.48
1:A:524:GLU:OE2	1:A:526:GLN:NE2	2.46	0.48
1:A:269:LEU:N	1:A:269:LEU:HD22	2.28	0.48
1:B:331:GLU:HA	1:B:331:GLU:OE1	2.14	0.48
1:B:431:PRO:HG2	4:B:635:HOH:O	2.14	0.48
1:A:384:HIS:O	1:A:385:ARG:HB2	2.14	0.48
1:A:306:ALA:HA	1:A:309:GLN:NE2	2.22	0.48
1:A:466:MET:HA	1:A:470:GLU:OE1	2.13	0.48
1:A:323:VAL:CG2	1:A:403:ALA:HB2	2.43	0.47
1:A:308:LEU:O	1:A:312:GLN:HG2	2.15	0.47
1:B:409:ARG:NH2	1:B:439:PHE:O	2.48	0.46
1:A:398:LEU:N	1:A:398:LEU:CD1	2.78	0.46
1:A:269:LEU:HD12	1:A:282:TRP:CG	2.50	0.46
1:B:426:ILE:HG12	1:B:472:LEU:CG	2.41	0.46
1:B:269:LEU:HD12	1:B:269:LEU:N	2.31	0.46
1:A:265:GLU:CD	1:A:265:GLU:H	2.19	0.46
1:B:347:LEU:O	1:B:351:LYS:HG2	2.16	0.46
1:B:301:THR:HG22	1:B:302:MET:HG3	1.97	0.45
1:B:278:PHE:CD1	1:B:279:GLY:N	2.84	0.45
1:B:265:GLU:CD	1:B:265:GLU:H	2.20	0.45
1:A:365:ASP:O	1:A:369:GLN:HG3	2.17	0.45
1:A:477:ARG:HH11	1:A:477:ARG:CB	2.29	0.45
1:B:466:MET:HE3	1:B:470:GLU:HG2	1.98	0.44
1:B:310:GLU:HB2	1:B:406:GLY:HA2	1.99	0.44
1:B:378:GLU:HG3	1:B:441:ILE:HG12	1.98	0.44
1:B:331:GLU:C	1:B:334:ILE:HD13	2.38	0.44
1:B:497:GLN:O	1:B:506:ARG:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:469:ARG:HH11	1:A:469:ARG:HG2	1.82	0.44
1:B:466:MET:HE3	1:B:474:GLN:HG3	2.00	0.43
1:B:451:LEU:HD23	1:B:451:LEU:O	2.17	0.43
1:B:362:GLN:O	1:B:366:MET:HG3	2.18	0.43
1:A:269:LEU:HD12	1:A:282:TRP:HB2	2.00	0.43
1:A:332:GLU:HB2	4:A:1118:HOH:O	2.19	0.43
1:B:385:ARG:HD2	1:B:409:ARG:HG2	2.00	0.43
1:B:273:LEU:HD11	1:B:340:TYR:HE1	1.84	0.42
1:A:332:GLU:CA	1:A:334:ILE:HD12	2.45	0.42
1:A:526:GLN:N	1:A:526:GLN:CD	2.68	0.42
1:B:486:GLU:HB2	1:B:533:LEU:HD12	2.02	0.42
1:A:426:ILE:HD13	1:A:472:LEU:HD21	2.00	0.42
1:B:359:ARG:HB2	1:B:362:GLN:HE22	1.85	0.42
1:A:375:ALA:O	1:A:379:ARG:HG3	2.19	0.42
1:B:279:GLY:HA3	1:B:296:THR:O	2.20	0.41
1:A:384:HIS:O	1:A:385:ARG:CB	2.68	0.41
1:A:466:MET:CE	1:A:474:GLN:HG3	2.50	0.41
1:A:269:LEU:N	1:A:269:LEU:CD2	2.83	0.41
1:B:331:GLU:N	1:B:334:ILE:HD13	2.36	0.41
1:A:466:MET:HE1	1:A:474:GLN:HG3	2.02	0.41
1:A:349:PHE:CE1	1:A:354:MET:HG3	2.56	0.41
1:B:334:ILE:O	1:B:335:TYR:HD2	2.02	0.41
1:B:411:ILE:O	1:B:412:GLU:HG3	2.21	0.41
1:A:426:ILE:HG23	1:A:468:ASN:OD1	2.21	0.41
1:A:426:ILE:HD12	1:A:426:ILE:O	2.20	0.41
1:A:438:ARG:HH11	1:A:438:ARG:HB2	1.86	0.41
1:A:296:THR:CG2	1:A:297:LEU:N	2.84	0.40
1:B:275:GLN:HG2	1:B:280:GLU:HG2	2.04	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	261/286 (91%)	251 (96%)	9 (3%)	1 (0%)	39	28
1	B	261/286 (91%)	246 (94%)	14 (5%)	1 (0%)	39	28
All	All	522/572 (91%)	497 (95%)	23 (4%)	2 (0%)	39	28

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	299	PRO
1	A	342	SER

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	228/245 (93%)	220 (96%)	8 (4%)	43	35
1	B	230/245 (94%)	224 (97%)	6 (3%)	54	48
All	All	458/490 (94%)	444 (97%)	14 (3%)	47	41

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

Mol	Chain	Res	Type
1	A	322	LEU
1	A	350	LEU
1	A	351	LYS
1	A	360	LEU
1	A	397	ASN
1	A	424	PHE
1	A	426	ILE
1	A	526	GLN
1	B	299	PRO
1	B	316	LYS
1	B	331	GLU
1	B	350	LEU
1	B	360	LEU
1	B	396	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	309	GLN
1	A	397	ASN
1	B	362	GLN

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](#)

3 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	STI	A	1001	-	41,41,41	2.42	24 (58%)	56,56,56	2.04	10 (17%)
3	GOL	A	1002	-	5,5,5	0.24	0	5,5,5	0.25	0
3	GOL	A	1003	-	5,5,5	0.25	0	5,5,5	0.23	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	STI	A	1001	-	-	0/20/30/30	0/5/5/5
3	GOL	A	1002	-	-	0/4/4/4	0/0/0/0
3	GOL	A	1003	-	-	0/4/4/4	0/0/0/0

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	STI	C4-N3	2.04	1.38	1.34
2	A	1001	STI	C11-N10	2.07	1.39	1.34
2	A	1001	STI	C20-C19	2.08	1.55	1.51
2	A	1001	STI	C1-C2	2.08	1.43	1.37
2	A	1001	STI	C12-C7	2.21	1.44	1.38
2	A	1001	STI	C49-N48	2.25	1.53	1.46
2	A	1001	STI	C2-N3	2.27	1.40	1.33
2	A	1001	STI	C9-N13	2.28	1.40	1.36
2	A	1001	STI	C7-N8	2.46	1.38	1.34
2	A	1001	STI	C1-C6	2.53	1.44	1.38
2	A	1001	STI	C52-N51	2.60	1.52	1.46
2	A	1001	STI	C17-C16	2.69	1.43	1.39
2	A	1001	STI	C28-C27	3.01	1.45	1.38
2	A	1001	STI	C50-N51	3.05	1.53	1.46
2	A	1001	STI	C6-C5	3.05	1.45	1.39
2	A	1001	STI	C29-C23	3.16	1.44	1.39
2	A	1001	STI	C17-C18	3.17	1.44	1.38
2	A	1001	STI	C9-N10	3.25	1.38	1.34
2	A	1001	STI	C4-C5	3.45	1.45	1.39
2	A	1001	STI	C26-C27	3.60	1.46	1.38
2	A	1001	STI	C26-C25	3.61	1.45	1.38
2	A	1001	STI	C15-C16	3.90	1.46	1.39
2	A	1001	STI	C14-C19	4.11	1.48	1.40
2	A	1001	STI	C25-C23	4.68	1.47	1.39

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	STI	N10-C9-N8	-6.61	119.62	126.67
2	A	1001	STI	C12-C11-N10	-3.17	120.28	123.90
2	A	1001	STI	C14-N13-C9	-2.67	122.18	129.22
2	A	1001	STI	O29-C22-C23	-2.11	117.37	120.97
2	A	1001	STI	C20-C19-C14	2.05	123.50	121.36
2	A	1001	STI	N13-C9-N10	2.24	122.79	116.01
2	A	1001	STI	C27-C46-N48	2.68	118.35	113.16
2	A	1001	STI	C2-N3-C4	3.17	122.68	116.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	STI	C11-N10-C9	6.33	120.99	115.49
2	A	1001	STI	C7-N8-C9	7.99	122.45	116.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

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	265/286 (92%)	0.40	15 (5%) 27 30	21, 36, 66, 88	0
1	B	265/286 (92%)	0.63	36 (13%) 4 4	20, 37, 90, 104	0
All	All	530/572 (92%)	0.52	51 (9%) 10 11	20, 37, 80, 104	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	422	ALA	10.3
1	B	277	CYS	8.8
1	B	278	PHE	7.6
1	A	407	LEU	6.8
1	A	256	ALA	6.5
1	B	297	LEU	6.2
1	B	306	ALA	6.2
1	B	301	THR	5.9
1	A	423	LYS	5.7
1	B	302	MET	5.3
1	B	411	ILE	4.9
1	A	424	PHE	4.7
1	B	299	PRO	4.4
1	B	300	GLY	4.3
1	B	268	ARG	4.3
1	A	257	LYS	4.2
1	B	298	LYS	3.9
1	B	296	THR	3.8
1	A	421	GLY	3.8
1	B	304	PRO	3.7
1	A	305	GLU	3.6
1	A	300	GLY	3.3
1	B	267	LEU	3.3
1	B	273	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	272	LYS	3.3
1	B	307	PHE	3.2
1	B	279	GLY	3.1
1	B	309	GLN	3.0
1	B	305	GLU	3.0
1	B	283	MET	2.9
1	A	426	ILE	2.9
1	A	277	CYS	2.8
1	B	271	VAL	2.8
1	B	334	ILE	2.8
1	B	335	TYR	2.7
1	A	301	THR	2.6
1	B	331	GLU	2.5
1	B	308	LEU	2.5
1	B	426	ILE	2.5
1	B	332	GLU	2.5
1	A	334	ILE	2.3
1	A	268	ARG	2.3
1	B	275	GLN	2.3
1	B	282	TRP	2.3
1	B	276	GLY	2.3
1	B	409	ARG	2.2
1	B	333	PRO	2.2
1	B	328	VAL	2.2
1	B	265	GLU	2.1
1	B	472	LEU	2.1
1	A	269	LEU	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 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
3	GOL	A	1003	6/6	0.94	0.15	2.15	45,46,48,48	0
3	GOL	A	1002	6/6	0.95	0.14	1.28	33,36,37,38	0
2	STI	A	1001	37/37	0.95	0.12	-0.12	26,33,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.