



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:14 PM UTC

PDB ID : 1SNU / pdb_00001snu
Title : CRYSTAL STRUCTURE OF THE UNPHOSPHORYLATED
INTERLEUKIN-2 TYROSINE KINASE CATALYTIC DOMAIN
Authors : Brown, K.; Long, J.M.; Vial, S.C.; Dedi, N.; Dunster, N.J.; Renwick, S.B.;
Tanner, A.J.; Frantz, J.D.; Fleming, M.A.; Cheetham, G.M.T.
Deposited on : 2004-03-12
Resolution : 2.50 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

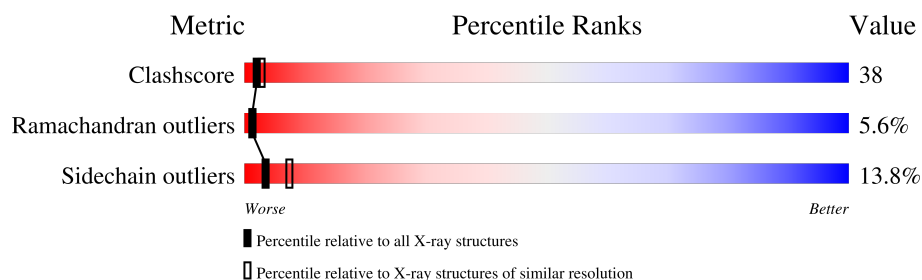
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	264	
1	B	264	

2 Entry composition [i](#)

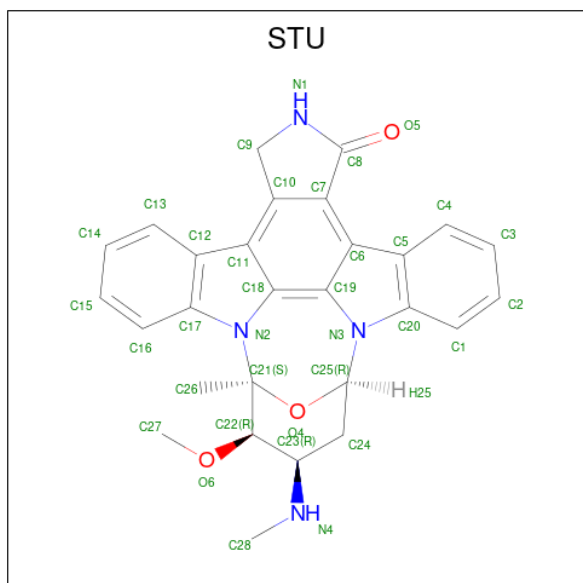
There are 3 unique types of molecules in this entry. The entry contains 4158 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Tyrosine-protein kinase ITK/TSK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	245	Total	C	N	O	S	0	0	0
			1956	1249	326	365	16			
1	B	241	Total	C	N	O	S	0	0	0
			1935	1237	322	360	16			

- Molecule 2 is STAUROSPORINE (CCD ID: STU) (formula: $C_{28}H_{26}N_4O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			35	28	4	3		
2	B	1	Total	C	N	O	0	0
			35	28	4	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	116	Total 116	O 116	0	0
3	B	81	Total 81	O 81	0	0

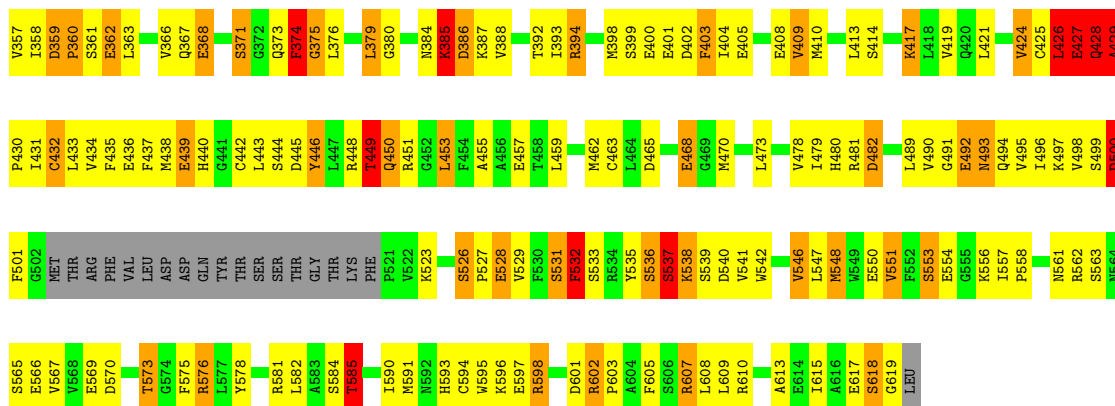
3 Residue-property plots

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. 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. 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.

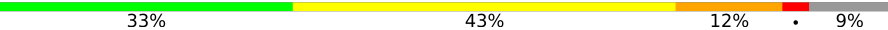
Note EDS was not executed.

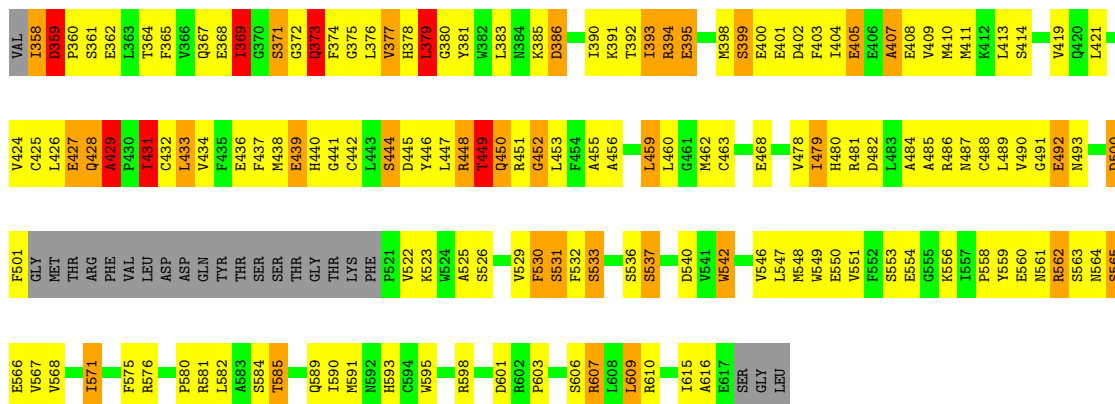
• Molecule 1: Tyrosine-protein kinase ITK/TSK

Chain A: 



• Molecule 1: Tyrosine-protein kinase ITK/TSK

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	124.40Å 74.20Å 78.80Å 90.00° 94.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	72.4 (20.00-2.50)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.07	Depositor
Refinement program	CNX	Depositor
R, R_{free}	0.237 , 0.295	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4158	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	1.03	9/2000 (0.5%)	1.20	25/2700 (0.9%)
1	B	1.00	4/1979 (0.2%)	1.15	22/2672 (0.8%)
All	All	1.02	13/3979 (0.3%)	1.17	47/5372 (0.9%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	546	VAL	CA-CB	6.23	1.62	1.54
1	B	529	VAL	CA-CB	5.92	1.62	1.54
1	A	541	VAL	CA-CB	5.90	1.60	1.54
1	B	377	VAL	CA-CB	5.87	1.63	1.54
1	A	585	THR	CA-CB	5.79	1.62	1.53
1	A	551	VAL	CA-CB	-5.76	1.47	1.54
1	B	436	GLU	CA-CB	-5.54	1.44	1.53
1	A	468	GLU	CA-CB	-5.36	1.45	1.53
1	A	448	ARG	CA-CB	-5.34	1.45	1.53
1	A	446	TYR	CA-CB	-5.31	1.44	1.53
1	B	434	VAL	CA-CB	-5.22	1.47	1.53
1	A	368	GLU	CA-CB	-5.21	1.46	1.53
1	A	548	MET	CA-CB	-5.18	1.45	1.53

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	369	ILE	N-CA-CB	-13.60	97.25	112.21
1	A	449	THR	N-CA-C	-10.49	95.71	110.50
1	B	449	THR	N-CA-C	-8.66	98.28	110.50
1	A	388	VAL	N-CA-CB	-8.27	102.91	112.34
1	A	539	SER	N-CA-C	-7.49	103.20	111.36
1	A	386	ASP	N-CA-C	7.24	120.32	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	432	CYS	N-CA-C	7.13	119.59	108.96
1	A	362	GLU	N-CA-C	-6.81	104.10	112.88
1	A	379	LEU	N-CA-C	-6.76	98.60	109.96
1	B	379	LEU	N-CA-C	-6.74	98.25	109.24
1	B	429	ALA	N-CA-C	-6.56	95.31	109.81
1	B	429	ALA	CA-C-N	-6.37	111.88	119.84
1	B	429	ALA	C-N-CA	-6.37	111.88	119.84
1	B	377	VAL	N-CA-C	-6.31	99.06	108.46
1	B	530	PHE	CB-CA-C	-6.18	98.11	110.42
1	A	538	LYS	N-CA-C	-6.03	105.00	112.90
1	A	526	SER	N-CA-C	-6.02	103.20	110.13
1	A	375	GLY	N-CA-C	5.96	118.12	112.04
1	A	428	GLN	N-CA-C	5.93	123.43	110.80
1	A	532	PHE	N-CA-C	5.88	120.58	113.17
1	B	359	ASP	N-CA-C	5.85	122.73	109.81
1	B	593	HIS	N-CA-C	-5.82	104.89	112.23
1	A	598	ARG	N-CA-C	5.73	117.20	109.24
1	A	553	SER	N-CA-C	-5.70	106.28	113.18
1	A	594	CYS	N-CA-C	-5.67	105.09	112.23
1	B	536	SER	N-CA-C	-5.66	100.34	108.60
1	B	431	ILE	N-CA-C	-5.57	101.61	109.63
1	A	374	PHE	N-CA-C	-5.54	99.01	110.80
1	B	562	ARG	N-CA-C	5.47	117.71	109.23
1	A	529	VAL	N-CA-C	-5.43	105.83	111.58
1	A	439	GLU	N-CA-C	5.39	122.28	110.80
1	B	542	TRP	N-CA-C	-5.33	105.36	111.07
1	A	429	ALA	N-CA-C	-5.33	98.03	109.81
1	A	455	ALA	N-CA-C	-5.33	101.59	110.17
1	A	602	ARG	CA-C-N	5.30	125.06	119.76
1	A	602	ARG	C-N-CA	5.30	125.06	119.76
1	B	395	GLU	N-CA-C	5.28	118.98	112.54
1	B	434	VAL	N-CA-C	5.26	115.15	107.37
1	B	377	VAL	N-CA-CB	5.23	120.02	111.44
1	A	426	LEU	N-CA-C	-5.23	106.29	113.30
1	B	459	LEU	N-CA-C	-5.23	105.70	111.71
1	B	407	ALA	N-CA-C	-5.11	106.15	112.38
1	B	584	SER	N-CA-C	-5.08	104.16	110.41
1	B	531	SER	N-CA-C	5.07	119.54	112.90
1	A	565	SER	N-CA-C	-5.07	107.26	112.93
1	A	360	PRO	N-CA-C	-5.05	102.03	111.03
1	B	386	ASP	N-CA-C	5.05	117.20	109.07

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	1956	0	1913	153	1
1	B	1935	0	1893	142	0
2	A	35	0	26	3	0
2	B	35	0	26	9	0
3	A	116	0	0	16	0
3	B	81	0	0	10	0
All	All	4158	0	3858	299	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 38.

All (299) 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:607:ARG:HH11	1:A:607:ARG:HB2	1.14	1.07
1:B:360:PRO:HB2	3:B:75:HOH:O	1.61	0.98
1:A:609:LEU:HD23	3:A:34:HOH:O	1.66	0.94
1:B:393:ILE:HG22	1:B:394:ARG:N	1.86	0.89
1:B:393:ILE:HG22	1:B:394:ARG:H	1.36	0.88
1:A:607:ARG:HB2	1:A:607:ARG:NH1	1.90	0.87
1:B:393:ILE:HD11	1:B:403:PHE:CE1	2.11	0.85
1:A:536:SER:O	1:A:537:SER:HB2	1.76	0.85
1:B:459:LEU:HA	1:B:462:MET:HE3	1.57	0.84
1:A:428:GLN:HG3	3:A:100:HOH:O	1.77	0.84
1:B:419:VAL:HG21	1:B:489:LEU:HD12	1.61	0.83
1:A:375:GLY:HA3	1:A:392:THR:O	1.78	0.82
1:A:385:LYS:HE2	1:A:385:LYS:HA	1.61	0.81
1:B:460:LEU:HD21	1:B:615:ILE:O	1.81	0.81
1:A:401:GLU:HG3	1:A:402:ASP:N	1.99	0.78
1:A:426:LEU:C	1:A:428:GLN:H	1.93	0.76
1:A:451:ARG:NH2	1:A:556:LYS:HG3	2.03	0.74
1:B:575:PHE:O	1:B:576:ARG:HD3	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:500:ASP:HB3	3:A:10:HOH:O	1.90	0.72
1:A:526:SER:HB2	1:A:528:GLU:OE2	1.90	0.72
1:A:492:GLU:O	1:A:495:VAL:HG23	1.90	0.71
1:A:419:VAL:HG21	1:A:489:LEU:HD12	1.73	0.71
1:A:492:GLU:CD	1:A:492:GLU:H	1.98	0.70
1:A:569:GLU:O	1:A:573:THR:HG23	1.91	0.70
1:B:403:PHE:CZ	1:B:433:LEU:HD13	2.27	0.69
1:A:430:PRO:HG3	3:A:125:HOH:O	1.92	0.69
1:A:399:SER:HB2	1:A:402:ASP:HB2	1.75	0.69
1:A:360:PRO:HG2	1:A:362:GLU:HG3	1.74	0.69
1:B:365:PHE:CZ	1:B:390:ILE:HG21	2.28	0.68
1:B:378:HIS:HD2	3:B:36:HOH:O	1.76	0.68
1:B:607:ARG:HB2	1:B:607:ARG:HH11	1.58	0.68
1:B:424:VAL:HG12	1:B:433:LEU:HD12	1.76	0.68
1:A:366:VAL:HG23	1:A:380:GLY:HA2	1.76	0.68
1:B:449:THR:O	1:B:450:GLN:HB2	1.91	0.68
1:B:375:GLY:HA3	1:B:392:THR:O	1.94	0.67
1:B:369:ILE:HG22	1:B:377:VAL:CG2	2.23	0.67
1:A:424:VAL:HG13	1:A:433:LEU:HD12	1.77	0.66
1:A:373:GLN:HG2	1:A:394:ARG:HG3	1.78	0.66
1:A:531:SER:HB2	1:A:532:PHE:CD1	2.30	0.65
1:A:610:ARG:CZ	3:A:34:HOH:O	2.44	0.65
1:A:450:GLN:HG3	1:A:453:LEU:HD12	1.77	0.65
1:B:591:MET:HE2	1:B:595:TRP:CH2	2.32	0.65
1:A:553:SER:HB2	1:A:556:LYS:HB2	1.80	0.64
1:B:492:GLU:O	1:B:493:ASN:OD1	2.15	0.64
1:B:547:LEU:C	1:B:547:LEU:HD23	2.23	0.64
1:B:491:GLY:O	1:B:493:ASN:N	2.31	0.63
1:B:393:ILE:HD11	1:B:403:PHE:CD1	2.33	0.63
1:B:565:SER:O	3:B:67:HOH:O	2.16	0.62
1:B:407:ALA:O	1:B:411:MET:HG3	1.98	0.62
1:B:492:GLU:CD	1:B:492:GLU:H	2.07	0.62
1:A:470:MET:CE	1:A:473:LEU:HD12	2.30	0.62
1:B:372:GLY:O	1:B:374:PHE:N	2.33	0.62
1:B:444:SER:HB2	1:B:486:ARG:HA	1.81	0.62
1:B:459:LEU:HD11	1:B:582:LEU:HD13	1.80	0.62
1:A:404:ILE:O	1:A:408:GLU:HG3	2.00	0.61
1:B:358:ILE:HG22	1:B:424:VAL:H	1.66	0.61
1:B:424:VAL:HG12	1:B:433:LEU:CD1	2.30	0.61
1:B:427:GLU:O	1:B:428:GLN:HB2	2.00	0.61
1:A:442:CYS:HA	1:A:489:LEU:HD23	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:581:ARG:NH2	3:B:98:HOH:O	2.33	0.60
1:A:360:PRO:HG2	1:A:362:GLU:CG	2.31	0.60
1:B:598:ARG:HB2	1:B:601:ASP:OD2	2.01	0.60
1:A:615:ILE:HG23	1:A:619:GLY:O	2.02	0.60
1:A:425:CYS:C	1:A:426:LEU:HD23	2.28	0.59
1:A:531:SER:HB2	1:A:532:PHE:CE1	2.37	0.59
1:B:440:HIS:HB2	1:B:490:VAL:O	2.02	0.59
1:A:547:LEU:C	1:A:547:LEU:HD23	2.27	0.59
1:B:369:ILE:HD11	1:B:379:LEU:HG	1.85	0.59
1:A:442:CYS:SG	1:A:445:ASP:HB2	2.42	0.59
1:B:364:THR:O	1:B:380:GLY:HA2	2.03	0.58
1:B:394:ARG:HG3	1:B:395:GLU:N	2.18	0.58
1:B:493:ASN:OD1	1:B:493:ASN:O	2.20	0.58
1:B:368:GLU:CD	1:B:376:LEU:HD22	2.28	0.58
1:B:487:ASN:HA	2:B:621:STU:H272	1.86	0.58
1:A:532:PHE:CD1	1:A:532:PHE:N	2.72	0.58
1:A:429:ALA:HB1	1:A:430:PRO:HD2	1.85	0.57
1:A:570:ASP:O	1:A:575:PHE:HB3	2.04	0.57
1:A:457:GLU:HG3	3:A:182:HOH:O	2.03	0.57
1:A:470:MET:HE1	1:A:473:LEU:HD12	1.87	0.57
1:A:575:PHE:O	1:A:576:ARG:HD3	2.04	0.57
1:A:373:GLN:HG3	1:A:394:ARG:HD2	1.87	0.57
1:A:393:ILE:HG12	1:A:431:ILE:O	2.04	0.57
1:A:459:LEU:HA	1:A:462:MET:HE3	1.87	0.57
1:B:391:LYS:NZ	2:B:621:STU:H15	2.20	0.57
1:A:424:VAL:HG13	1:A:433:LEU:CD1	2.35	0.57
1:A:479:ILE:HD12	1:A:536:SER:O	2.05	0.57
1:A:413:LEU:HD11	1:A:478:VAL:HG21	1.86	0.56
2:A:301:STU:O5	2:A:301:STU:H4	2.05	0.56
1:A:425:CYS:HB2	1:A:432:CYS:SG	2.45	0.56
1:B:532:PHE:O	1:B:533:SER:C	2.47	0.56
1:A:449:THR:O	1:A:450:GLN:CB	2.54	0.56
1:B:393:ILE:CG2	1:B:394:ARG:N	2.59	0.56
1:B:428:GLN:O	1:B:429:ALA:HB3	2.06	0.56
1:B:576:ARG:HG3	1:B:595:TRP:CE3	2.41	0.56
1:A:427:GLU:C	1:A:428:GLN:HG2	2.31	0.56
1:B:360:PRO:HG2	1:B:362:GLU:CD	2.30	0.56
1:A:421:LEU:HD12	1:A:434:VAL:O	2.07	0.55
1:A:421:LEU:HD13	1:A:435:PHE:CD2	2.42	0.55
1:B:400:GLU:O	1:B:404:ILE:HG13	2.06	0.55
1:A:360:PRO:O	1:A:362:GLU:N	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:410:MET:HE2	1:B:501:PHE:O	2.07	0.55
1:A:399:SER:HB2	1:A:402:ASP:H	1.72	0.54
1:A:491:GLY:O	1:A:493:ASN:N	2.39	0.54
1:A:500:ASP:OD2	2:A:301:STU:H273	2.08	0.54
1:B:426:LEU:C	1:B:428:GLN:H	2.16	0.54
1:B:563:SER:O	1:B:567:VAL:HG23	2.08	0.54
1:A:494:GLN:HE21	1:A:494:GLN:HA	1.72	0.53
1:A:421:LEU:HD11	1:A:433:LEU:HG	1.89	0.53
1:A:387:LYS:HE2	1:A:437:PHE:CE2	2.44	0.53
1:A:400:GLU:O	1:A:404:ILE:HG13	2.08	0.53
1:A:375:GLY:N	1:A:393:ILE:O	2.42	0.53
1:B:447:LEU:HD22	1:B:554:GLU:HA	1.91	0.53
1:B:525:ALA:O	1:B:530:PHE:HE2	1.92	0.53
2:A:301:STU:H261	2:A:301:STU:H16	1.91	0.53
1:B:358:ILE:O	1:B:424:VAL:O	2.28	0.52
1:A:440:HIS:HB2	1:A:490:VAL:HB	1.91	0.52
1:B:369:ILE:CD1	1:B:379:LEU:HB2	2.40	0.52
1:B:607:ARG:HB2	1:B:607:ARG:NH1	2.22	0.52
1:A:393:ILE:HD12	1:A:398:MET:CE	2.39	0.52
1:A:443:LEU:HD13	1:A:496:ILE:HD12	1.91	0.52
1:A:367:GLN:NE2	3:A:126:HOH:O	2.41	0.52
1:A:493:ASN:CG	1:A:493:ASN:O	2.52	0.52
1:B:590:ILE:CD1	1:B:615:ILE:HD12	2.39	0.52
1:B:392:THR:OG1	3:B:36:HOH:O	2.18	0.52
1:B:500:ASP:OD2	2:B:621:STU:H273	2.10	0.51
1:A:585:THR:HG22	3:A:136:HOH:O	2.10	0.51
1:A:379:LEU:HD11	1:A:387:LYS:HE3	1.91	0.51
1:B:585:THR:O	1:B:589:GLN:HG3	2.09	0.51
1:A:556:LYS:NZ	3:A:153:HOH:O	2.40	0.51
1:B:522:VAL:HB	1:B:564:ASN:OD1	2.11	0.51
1:B:562:ARG:NH1	1:B:575:PHE:CE2	2.78	0.51
1:A:399:SER:CB	1:A:402:ASP:HB2	2.41	0.51
1:A:463:CYS:SG	1:A:548:MET:HG2	2.51	0.50
1:B:580:PRO:HB2	3:B:11:HOH:O	2.10	0.50
1:A:363:LEU:HD11	1:A:425:CYS:SG	2.51	0.50
1:B:575:PHE:C	1:B:576:ARG:HD3	2.36	0.50
1:A:401:GLU:CG	1:A:402:ASP:N	2.73	0.50
1:A:428:GLN:O	1:A:429:ALA:HB3	2.12	0.50
1:B:525:ALA:O	1:B:530:PHE:CE2	2.65	0.50
1:A:492:GLU:O	1:A:495:VAL:CG2	2.59	0.50
1:B:369:ILE:HG22	1:B:377:VAL:HG23	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:375:GLY:HA2	1:B:393:ILE:O	2.11	0.50
1:A:359:ASP:HB3	1:A:425:CYS:SG	2.52	0.50
1:A:426:LEU:HD22	1:A:431:ILE:CG2	2.41	0.50
1:B:393:ILE:CG2	1:B:394:ARG:H	2.10	0.50
1:B:442:CYS:SG	2:B:621:STU:H282	2.52	0.50
1:A:523:LYS:HD3	1:A:558:PRO:O	2.12	0.50
1:A:538:LYS:NZ	1:A:602:ARG:O	2.37	0.50
1:A:617:GLU:O	1:A:618:SER:CB	2.60	0.49
1:B:360:PRO:HG2	1:B:362:GLU:CG	2.42	0.49
1:B:448:ARG:HH11	1:B:448:ARG:HB2	1.77	0.49
1:B:479:ILE:CD1	1:B:479:ILE:N	2.75	0.49
1:A:593:HIS:ND1	1:A:596:LYS:HE2	2.28	0.49
1:A:493:ASN:O	1:A:493:ASN:OD1	2.29	0.49
2:B:621:STU:O5	2:B:621:STU:H4	2.13	0.49
1:A:449:THR:O	1:A:450:GLN:HB2	2.13	0.49
1:A:591:MET:HE2	1:A:595:TRP:CH2	2.47	0.49
1:B:451:ARG:O	1:B:453:LEU:N	2.45	0.49
1:A:436:GLU:HG3	1:A:436:GLU:O	2.13	0.48
1:B:403:PHE:CE2	1:B:433:LEU:HD13	2.48	0.48
1:A:426:LEU:HD23	1:A:426:LEU:N	2.26	0.48
1:B:425:CYS:HB2	1:B:432:CYS:SG	2.53	0.48
1:A:576:ARG:NH2	1:A:595:TRP:O	2.43	0.48
1:B:606:SER:HB2	1:B:610:ARG:HH12	1.78	0.48
1:A:417:LYS:O	1:A:497:LYS:HA	2.14	0.48
1:A:429:ALA:O	1:A:430:PRO:C	2.55	0.48
1:B:403:PHE:HZ	1:B:433:LEU:HD13	1.78	0.48
1:A:403:PHE:HZ	1:A:426:LEU:HD21	1.78	0.48
1:B:404:ILE:O	1:B:408:GLU:HB2	2.14	0.48
1:B:391:LYS:HZ1	2:B:621:STU:H15	1.78	0.47
1:B:523:LYS:HD3	1:B:558:PRO:O	2.14	0.47
1:B:549:TRP:HB2	1:B:591:MET:HE3	1.96	0.47
1:B:575:PHE:O	1:B:576:ARG:CD	2.61	0.47
1:A:494:GLN:HA	1:A:494:GLN:NE2	2.28	0.47
1:A:499:SER:O	1:A:501:PHE:N	2.47	0.47
1:B:373:GLN:O	1:B:374:PHE:CD1	2.67	0.47
1:B:393:ILE:HD12	1:B:398:MET:HE3	1.97	0.47
1:A:426:LEU:C	1:A:428:GLN:N	2.65	0.47
1:B:563:SER:HB3	1:B:566:GLU:HB2	1.96	0.47
1:B:374:PHE:CD2	1:B:398:MET:HE2	2.49	0.47
1:B:610:ARG:HD3	3:B:3:HOH:O	2.14	0.47
1:A:384:ASN:O	1:A:386:ASP:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:493:ASN:C	1:A:495:VAL:H	2.23	0.47
1:A:605:PHE:HA	1:A:608:LEU:HB2	1.96	0.47
1:A:417:LYS:HE2	1:A:465:ASP:OD1	2.14	0.47
1:B:369:ILE:HD12	1:B:379:LEU:HB2	1.95	0.47
1:B:381:TYR:HA	1:B:386:ASP:O	2.14	0.47
1:B:444:SER:O	1:B:448:ARG:HD3	2.15	0.47
1:A:578:TYR:C	1:A:578:TYR:CD1	2.92	0.46
1:B:427:GLU:O	1:B:428:GLN:CB	2.63	0.46
1:A:393:ILE:HD12	1:A:398:MET:HE3	1.96	0.46
1:A:443:LEU:HD13	1:A:496:ILE:CD1	2.46	0.46
1:A:607:ARG:NH1	3:A:193:HOH:O	2.48	0.46
1:B:486:ARG:HG3	2:B:621:STU:H281	1.97	0.46
1:B:405:GLU:O	1:B:409:VAL:HG23	2.15	0.46
1:B:426:LEU:C	1:B:428:GLN:N	2.73	0.46
1:B:532:PHE:N	1:B:532:PHE:CD1	2.84	0.46
1:B:591:MET:HE2	1:B:595:TRP:HH2	1.79	0.46
1:A:499:SER:C	1:A:501:PHE:N	2.73	0.46
1:B:445:ASP:O	1:B:449:THR:HG23	2.16	0.46
1:B:480:HIS:O	1:B:540:ASP:OD1	2.34	0.46
1:B:546:VAL:O	1:B:550:GLU:HG3	2.16	0.46
1:B:603:PRO:HB3	1:B:607:ARG:HG2	1.98	0.46
1:A:535:TYR:CD1	1:A:535:TYR:N	2.83	0.46
1:A:581:ARG:CG	3:A:7:HOH:O	2.64	0.46
1:A:371:SER:HB3	1:A:376:LEU:HD22	1.97	0.46
1:A:481:ARG:O	1:A:482:ASP:HB2	2.16	0.45
1:A:499:SER:OG	1:A:500:ASP:N	2.47	0.45
1:A:527:PRO:HB2	3:A:64:HOH:O	2.14	0.45
1:B:392:THR:HG22	1:B:432:CYS:HB3	1.98	0.45
1:A:494:GLN:O	1:A:496:ILE:HG12	2.16	0.45
1:A:610:ARG:NH1	3:A:34:HOH:O	2.50	0.45
1:A:373:GLN:O	1:A:374:PHE:HB2	2.15	0.45
1:B:463:CYS:SG	1:B:548:MET:HG2	2.56	0.45
1:A:446:TYR:O	1:A:449:THR:O	2.35	0.45
1:A:526:SER:CB	1:A:528:GLU:OE2	2.61	0.45
1:A:563:SER:O	1:A:566:GLU:HB3	2.16	0.45
1:A:602:ARG:HA	1:A:603:PRO:HD3	1.81	0.45
1:A:438:MET:HE3	1:A:491:GLY:HA3	1.97	0.45
1:A:426:LEU:O	1:A:428:GLN:N	2.49	0.45
1:A:532:PHE:O	1:A:533:SER:C	2.60	0.45
1:A:431:ILE:H	1:A:431:ILE:HG13	1.58	0.45
1:B:428:GLN:O	1:B:429:ALA:CB	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:LYS:NZ	1:A:468:GLU:OE1	2.50	0.44
1:A:451:ARG:HG3	1:A:554:GLU:HB3	1.99	0.44
1:B:459:LEU:CA	1:B:462:MET:HE3	2.40	0.44
1:B:537:SER:O	1:B:540:ASP:HB2	2.17	0.44
1:A:387:LYS:HE2	1:A:437:PHE:CD2	2.52	0.44
1:B:449:THR:O	1:B:450:GLN:CB	2.59	0.44
1:B:484:ALA:O	1:B:485:ALA:C	2.61	0.44
1:A:494:GLN:HE21	1:A:494:GLN:CA	2.30	0.44
1:A:421:LEU:HD13	1:A:435:PHE:CE2	2.53	0.44
1:B:369:ILE:HG22	1:B:377:VAL:HG21	1.99	0.44
1:B:479:ILE:N	1:B:479:ILE:HD13	2.33	0.44
1:B:615:ILE:HD11	3:B:62:HOH:O	2.17	0.44
1:A:385:LYS:HE2	1:A:385:LYS:CA	2.41	0.44
1:A:607:ARG:NH1	1:A:607:ARG:CB	2.71	0.44
1:A:576:ARG:HG3	1:A:595:TRP:CE3	2.53	0.43
1:A:398:MET:SD	1:A:403:PHE:HB2	2.58	0.43
1:B:360:PRO:O	1:B:362:GLU:N	2.52	0.43
1:B:561:ASN:HA	3:B:68:HOH:O	2.19	0.43
1:A:582:LEU:HD23	1:A:582:LEU:HA	1.86	0.43
1:B:360:PRO:HG2	1:B:362:GLU:HG3	2.00	0.43
1:B:383:LEU:C	1:B:385:LYS:N	2.77	0.43
1:A:563:SER:O	1:A:567:VAL:N	2.47	0.43
1:B:562:ARG:HG2	3:B:137:HOH:O	2.18	0.43
1:B:451:ARG:NH2	1:B:556:LYS:HG3	2.34	0.43
1:B:486:ARG:NH1	1:B:486:ARG:HB2	2.34	0.43
1:A:590:ILE:HD12	1:A:615:ILE:HD12	2.02	0.42
1:B:364:THR:O	1:B:380:GLY:CA	2.66	0.42
1:B:446:TYR:CD2	1:B:490:VAL:HG21	2.55	0.42
1:B:459:LEU:HD23	1:B:462:MET:HE1	2.01	0.42
1:B:559:TYR:OH	1:B:571:ILE:HD11	2.19	0.42
1:A:384:ASN:C	1:A:386:ASP:H	2.28	0.42
1:A:598:ARG:HB2	1:A:601:ASP:OD2	2.19	0.42
1:A:375:GLY:CA	1:A:393:ILE:O	2.67	0.42
1:B:413:LEU:HD11	1:B:478:VAL:HG21	2.02	0.42
1:A:480:HIS:O	1:A:540:ASP:OD1	2.38	0.42
1:A:492:GLU:O	1:A:493:ASN:OD1	2.37	0.42
1:A:546:VAL:O	1:A:550:GLU:HG3	2.20	0.42
1:B:377:VAL:HA	1:B:390:ILE:O	2.19	0.42
1:A:581:ARG:HG3	3:A:7:HOH:O	2.19	0.42
1:B:526:SER:HB3	1:B:542:TRP:CB	2.50	0.42
1:A:499:SER:C	1:A:501:PHE:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:486:ARG:HB2	1:B:486:ARG:HH11	1.83	0.42
1:A:357:VAL:N	3:A:2:HOH:O	2.53	0.41
1:A:403:PHE:HZ	1:A:426:LEU:CD2	2.33	0.41
1:A:613:ALA:O	1:A:617:GLU:HG3	2.20	0.41
1:B:399:SER:OG	1:B:402:ASP:HB2	2.20	0.41
1:A:358:ILE:H	1:A:358:ILE:HG12	1.59	0.41
1:A:413:LEU:HD13	1:A:473:LEU:CD2	2.50	0.41
1:B:374:PHE:HD2	1:B:398:MET:HE2	1.83	0.41
1:A:384:ASN:C	1:A:386:ASP:N	2.77	0.41
1:B:441:GLY:HA2	2:B:621:STU:C3	2.50	0.41
1:A:542:TRP:CD1	1:A:542:TRP:C	2.98	0.41
1:B:421:LEU:HD11	1:B:433:LEU:HG	2.00	0.41
1:A:470:MET:HE2	1:A:473:LEU:HD12	1.99	0.41
1:A:428:GLN:HE21	1:A:428:GLN:HB3	1.68	0.41
1:B:455:ALA:O	1:B:456:ALA:C	2.64	0.41
1:B:468:GLU:HG3	1:B:609:LEU:HD11	2.01	0.41
1:A:584:SER:N	3:A:149:HOH:O	2.44	0.41
1:B:371:SER:HB3	1:B:376:LEU:HD23	2.01	0.41
1:B:438:MET:O	1:B:440:HIS:N	2.51	0.41
1:B:439:GLU:O	1:B:439:GLU:HG3	2.21	0.41
1:B:442:CYS:HA	1:B:488:CYS:O	2.21	0.41
1:B:553:SER:OG	1:B:556:LYS:HB2	2.21	0.41
1:A:403:PHE:CZ	1:A:426:LEU:HD21	2.56	0.41
1:B:429:ALA:O	1:B:431:ILE:N	2.54	0.41
1:B:452:GLY:N	1:B:554:GLU:OE2	2.53	0.41
1:B:560:GLU:C	1:B:562:ARG:H	2.29	0.41
2:B:621:STU:H16	2:B:621:STU:H261	2.02	0.41
1:B:367:GLN:O	1:B:378:HIS:HA	2.20	0.41
1:B:369:ILE:HD12	1:B:379:LEU:N	2.36	0.41
1:B:437:PHE:CE2	1:B:439:GLU:HA	2.56	0.41
1:A:405:GLU:O	1:A:409:VAL:HG12	2.20	0.40
1:A:459:LEU:HB3	1:A:551:VAL:HG12	2.02	0.40
1:A:561:ASN:O	1:A:562:ARG:HG3	2.21	0.40
1:B:438:MET:C	1:B:440:HIS:H	2.29	0.40
1:B:426:LEU:HD22	1:B:431:ILE:HD13	2.02	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:408:GLU:OE2	1:A:408:GLU:OE2[2_555]	1.95	0.25

5.3 Torsion angles

5.3.1 Protein backbone

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	241/264 (91%)	204 (85%)	24 (10%)	13 (5%)	1	1
1	B	237/264 (90%)	201 (85%)	22 (9%)	14 (6%)	1	1
All	All	478/528 (90%)	405 (85%)	46 (10%)	27 (6%)	1	1

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	374	PHE
1	A	394	ARG
1	A	482	ASP
1	A	492	GLU
1	A	500	ASP
1	A	618	SER
1	B	373	GLN
1	B	393	ILE
1	B	429	ALA
1	B	439	GLU
1	B	492	GLU
1	A	361	SER
1	A	537	SER
1	B	428	GLN
1	B	452	GLY
1	B	616	ALA
1	A	385	LYS
1	A	439	GLU
1	A	536	SER
1	B	361	SER
1	B	482	ASP
1	B	394	ARG
1	B	481	ARG
1	A	427	GLU
1	A	429	ALA

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Mol	Chain	Res	Type
1	B	359	ASP
1	B	533	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	214/232 (92%)	183 (86%)	31 (14%)	3	6
1	B	212/232 (91%)	184 (87%)	28 (13%)	4	8
All	All	426/464 (92%)	367 (86%)	59 (14%)	3	7

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	359	ASP
1	A	368	GLU
1	A	371	SER
1	A	374	PHE
1	A	385	LYS
1	A	403	PHE
1	A	409	VAL
1	A	410	MET
1	A	414	SER
1	A	417	LYS
1	A	424	VAL
1	A	426	LEU
1	A	427	GLU
1	A	428	GLN
1	A	444	SER
1	A	449	THR
1	A	450	GLN
1	A	453	LEU
1	A	493	ASN
1	A	498	VAL
1	A	500	ASP

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Mol	Chain	Res	Type
1	A	528	GLU
1	A	531	SER
1	A	532	PHE
1	A	537	SER
1	A	557	ILE
1	A	573	THR
1	A	576	ARG
1	A	585	THR
1	A	597	GLU
1	A	607	ARG
1	B	358	ILE
1	B	359	ASP
1	B	369	ILE
1	B	371	SER
1	B	373	GLN
1	B	379	LEU
1	B	399	SER
1	B	401	GLU
1	B	405	GLU
1	B	414	SER
1	B	427	GLU
1	B	431	ILE
1	B	433	LEU
1	B	444	SER
1	B	448	ARG
1	B	449	THR
1	B	450	GLN
1	B	479	ILE
1	B	500	ASP
1	B	531	SER
1	B	537	SER
1	B	551	VAL
1	B	565	SER
1	B	568	VAL
1	B	571	ILE
1	B	585	THR
1	B	607	ARG
1	B	609	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	367	GLN
1	A	373	GLN
1	A	428	GLN
1	A	487	ASN
1	A	494	GLN
1	A	589	GLN
1	A	611	GLN
1	B	367	GLN
1	B	373	GLN
1	B	589	GLN
1	B	611	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 ⓘ

2 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	STU	B	621	-	39,42,42	2.55	20 (51%)	50,68,68	2.59	24 (48%)
2	STU	A	301	-	39,42,42	3.06	24 (61%)	50,68,68	2.36	19 (38%)

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	STU	B	621	-	-	0/4/42/42	-
2	STU	A	301	-	-	0/4/42/42	-

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	STU	C22-C23	6.20	1.59	1.53
2	A	301	STU	C19-C18	5.74	1.53	1.40
2	A	301	STU	O4-C25	5.71	1.52	1.43
2	B	621	STU	C9-N1	4.82	1.50	1.45
2	A	301	STU	C24-C25	4.69	1.60	1.51
2	B	621	STU	C12-C11	-4.69	1.35	1.46
2	A	301	STU	C5-C20	4.39	1.47	1.41
2	B	621	STU	C3-C4	4.23	1.46	1.38
2	A	301	STU	C4-C5	4.18	1.46	1.40
2	B	621	STU	C19-C18	4.17	1.49	1.40
2	B	621	STU	C11-C10	4.14	1.48	1.40
2	A	301	STU	C12-C11	-4.03	1.37	1.46
2	B	621	STU	C25-N3	4.00	1.49	1.45
2	A	301	STU	C25-N3	3.77	1.48	1.45
2	A	301	STU	O6-C22	3.76	1.48	1.42
2	A	301	STU	C15-C16	3.69	1.45	1.38
2	B	621	STU	C13-C12	3.64	1.45	1.40
2	A	301	STU	C26-C21	3.47	1.55	1.51
2	A	301	STU	C18-N2	3.45	1.43	1.40
2	B	621	STU	C8-N1	3.40	1.37	1.35
2	A	301	STU	C11-C10	3.34	1.47	1.40
2	B	621	STU	C15-C16	3.30	1.44	1.38
2	B	621	STU	C16-C17	3.27	1.44	1.39
2	A	301	STU	C11-C18	3.27	1.47	1.41
2	B	621	STU	C3-C2	3.26	1.45	1.38
2	A	301	STU	C2-C1	3.25	1.44	1.38
2	A	301	STU	C3-C2	3.08	1.45	1.38
2	A	301	STU	C14-C15	3.02	1.44	1.38
2	B	621	STU	C14-C13	2.95	1.44	1.38
2	B	621	STU	C1-C20	2.94	1.44	1.39
2	A	301	STU	C14-C13	2.94	1.43	1.38
2	A	301	STU	C24-C23	2.87	1.57	1.53
2	B	621	STU	C5-C6	-2.80	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	621	STU	C11-C18	2.73	1.46	1.41
2	B	621	STU	C5-C20	2.59	1.45	1.41
2	A	301	STU	C7-C8	-2.58	1.41	1.49
2	A	301	STU	C5-C6	-2.55	1.40	1.46
2	A	301	STU	C8-N1	2.55	1.37	1.35
2	B	621	STU	C14-C15	2.47	1.43	1.38
2	B	621	STU	C4-C5	2.44	1.43	1.40
2	A	301	STU	C1-C20	2.30	1.43	1.39
2	A	301	STU	C3-C4	2.27	1.42	1.38
2	B	621	STU	C7-C8	-2.25	1.42	1.49
2	B	621	STU	C2-C1	2.00	1.42	1.38

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	STU	C27-O6-C22	5.99	124.59	114.46
2	B	621	STU	C6-C5-C20	5.78	112.31	106.49
2	B	621	STU	C19-C18-N2	-5.55	126.67	131.38
2	A	301	STU	C11-C12-C17	5.30	111.82	106.49
2	B	621	STU	C5-C6-C19	-4.82	99.68	106.44
2	B	621	STU	C6-C19-N3	4.75	117.54	109.61
2	A	301	STU	C6-C5-C20	4.54	111.06	106.49
2	A	301	STU	C6-C19-N3	4.30	116.80	109.61
2	B	621	STU	C19-N3-C20	-4.25	102.28	107.90
2	A	301	STU	C19-N3-C20	-4.19	102.35	107.90
2	B	621	STU	C18-C19-N3	-4.09	125.95	129.42
2	A	301	STU	C5-C6-C19	-4.05	100.75	106.44
2	A	301	STU	C12-C11-C10	3.72	139.09	132.33
2	B	621	STU	C10-C9-N1	-3.68	98.17	101.75
2	B	621	STU	C11-C12-C17	3.61	110.13	106.49
2	B	621	STU	C9-C10-C7	3.58	111.20	109.88
2	B	621	STU	C19-N3-C25	3.56	134.59	123.02
2	B	621	STU	O5-C8-N1	3.43	129.16	125.35
2	B	621	STU	C13-C12-C17	3.42	123.19	119.24
2	A	301	STU	C13-C12-C11	-3.40	125.41	133.49
2	B	621	STU	C12-C11-C10	3.30	138.32	132.33
2	B	621	STU	C16-C17-C12	-3.28	117.75	121.59
2	A	301	STU	C18-C19-N3	-3.27	126.65	129.42
2	B	621	STU	C18-N2-C17	-3.10	103.62	107.37
2	A	301	STU	C13-C12-C17	3.05	122.77	119.24
2	B	621	STU	O5-C8-C7	-2.94	124.20	128.47
2	B	621	STU	C7-C6-C19	2.91	122.93	118.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	STU	O5-C8-C7	-2.89	124.28	128.47
2	B	621	STU	C13-C12-C11	-2.86	126.68	133.49
2	B	621	STU	C15-C14-C13	-2.76	116.83	120.24
2	A	301	STU	C7-C6-C19	2.73	122.62	118.04
2	A	301	STU	C18-N2-C17	-2.67	104.14	107.37
2	B	621	STU	C28-N4-C23	2.46	117.33	114.39
2	A	301	STU	C28-N4-C23	2.44	117.30	114.39
2	A	301	STU	C16-C17-C12	-2.35	118.85	121.59
2	B	621	STU	C14-C15-C16	2.24	123.00	120.24
2	A	301	STU	C19-N3-C25	2.23	130.25	123.02
2	A	301	STU	C12-C11-C18	-2.16	103.40	106.44
2	B	621	STU	C11-C18-N2	2.16	111.72	109.38
2	A	301	STU	C4-C5-C6	-2.15	128.37	133.49
2	B	621	STU	C4-C5-C6	-2.07	128.57	133.49
2	B	621	STU	C18-C11-C10	-2.05	117.36	119.77
2	A	301	STU	C7-C8-N1	2.01	108.30	106.38

There are no chirality outliers.

There are no torsion outliers.

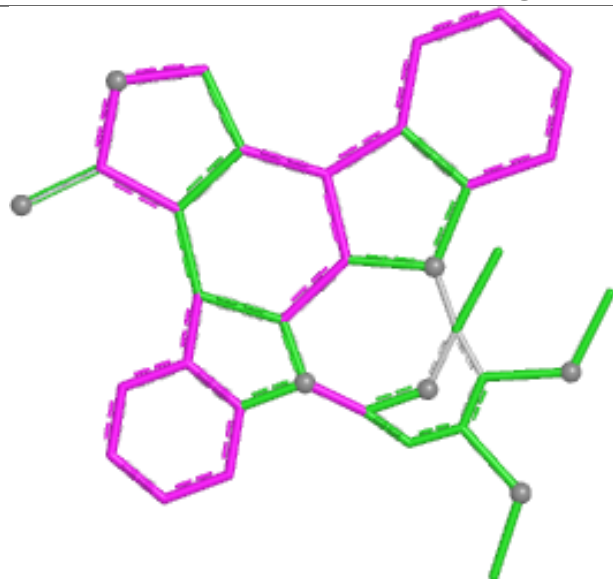
There are no ring outliers.

2 monomers are involved in 12 short contacts:

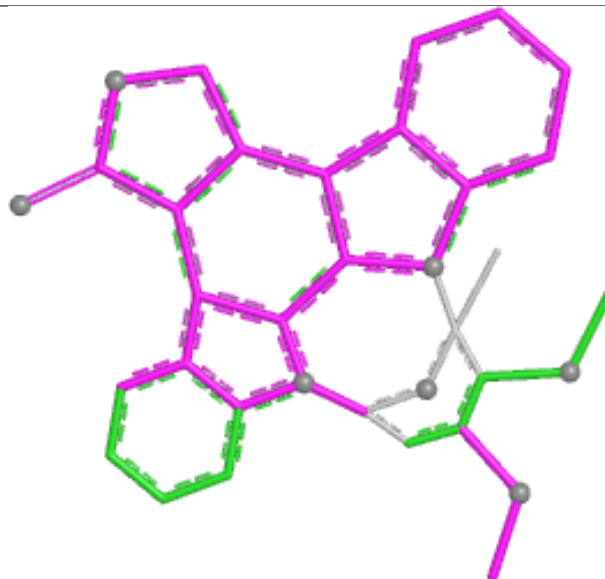
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	621	STU	9	0
2	A	301	STU	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

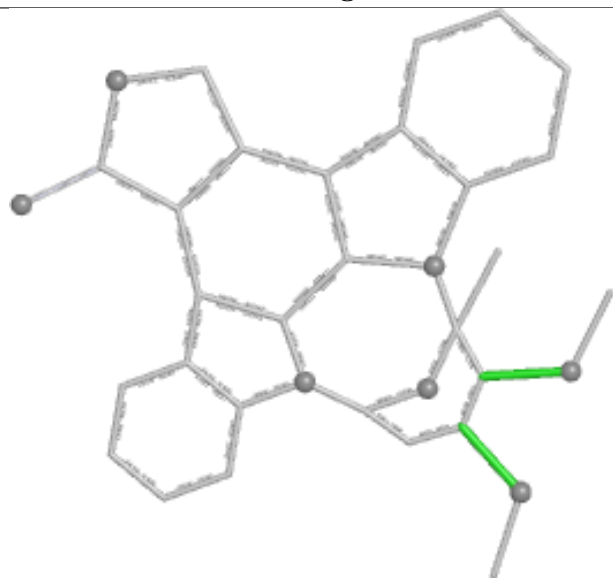
Ligand STU B 621



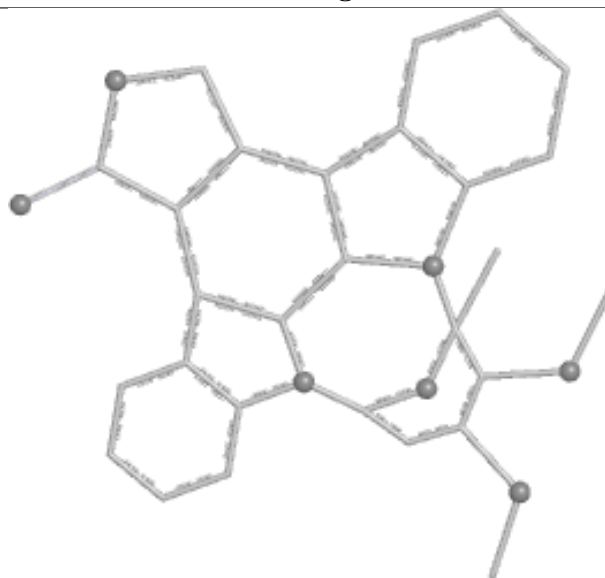
Bond lengths



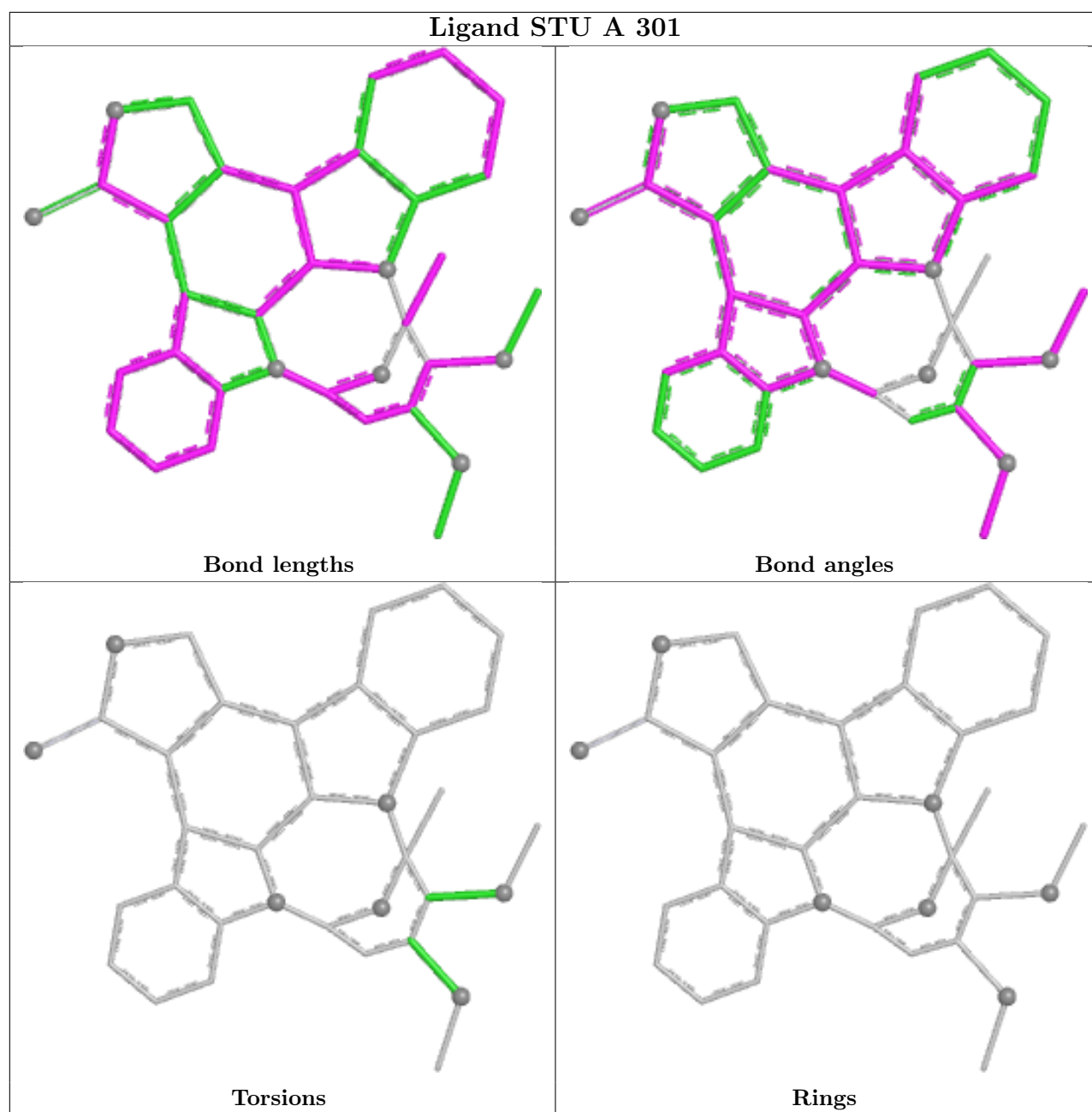
Bond angles



Torsions



Rings



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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.