



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 03:31 AM UTC

PDB ID : 1STC / pdb_00001stc
Title : CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUB-UNIT IN COMPLEX WITH STAUROSPORINE
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Deposited on : 1997-10-10
Resolution : 2.30 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

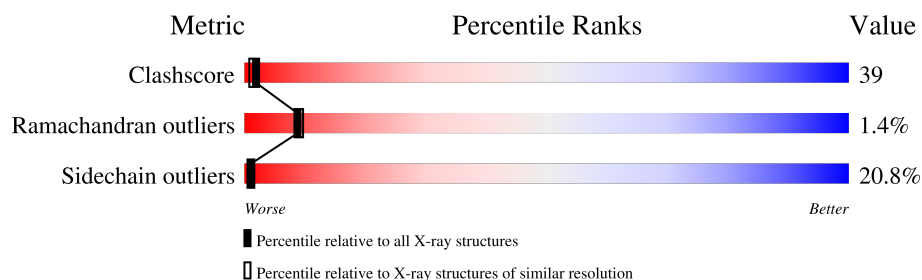
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

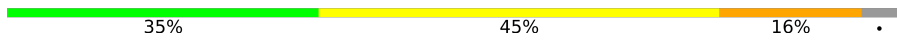
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	E	350	
2	I	20	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3087 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 CAMP-DEPENDENT PROTEIN KINASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	E	336	Total	C	N	O	P	S	0	0	0
			2780	1803	466	500	2	9			

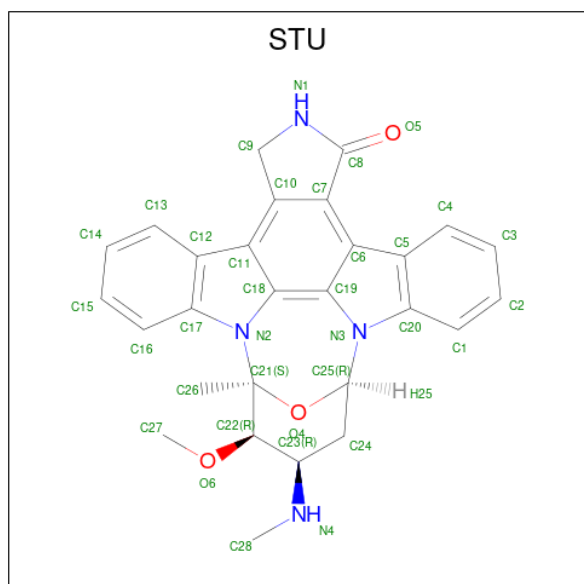
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	10	SEP	SER	conflict	UNP P00517
E	197	TPO	THR	modified residue	UNP P00517
E	338	SEP	SER	modified residue	UNP P00517

- Molecule 2 is a protein called PROTEIN KINASE INHIBITOR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	I	17	Total	C	N	O	0	0	0
			130	78	27	25			

- Molecule 3 is STAUROSPORINE (CCD ID: STU) (formula: $C_{28}H_{26}N_4O_3$).



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

- Molecule 4 is water.

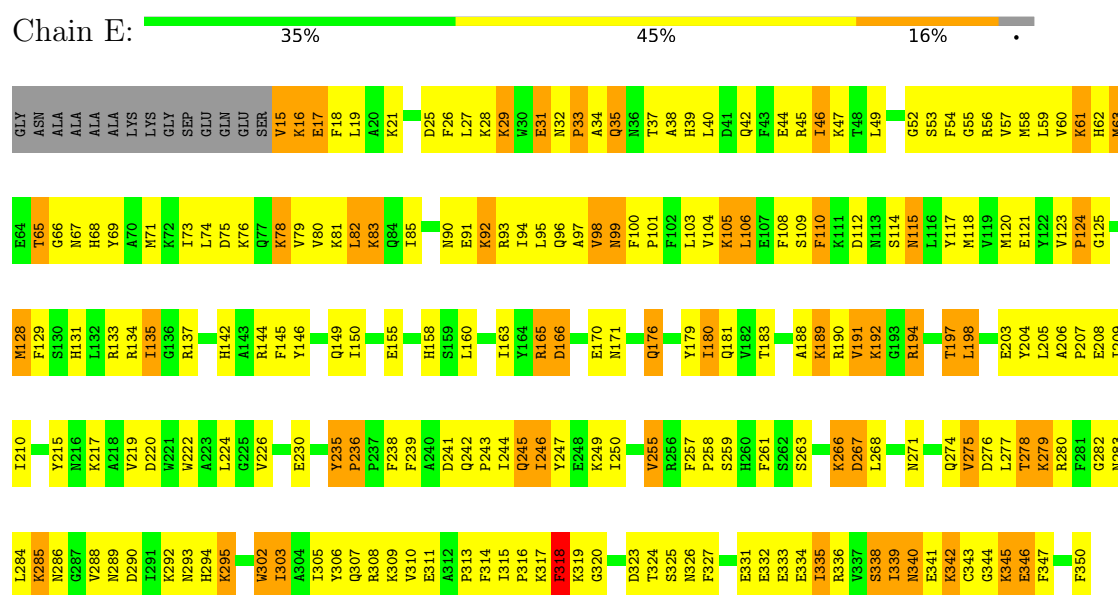
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	127	Total	O	0	0
			127	127		
4	I	15	Total	O	0	0
			15	15		

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: CAMP-DEPENDENT PROTEIN KINASE



• Molecule 2: PROTEIN KINASE INHIBITOR



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.99Å 72.82Å 76.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.30	Depositor
% Data completeness (in resolution range)	92.2 (8.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.208 , 0.330	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3087	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	E	0.69	0/2830	1.09	13/3812 (0.3%)
2	I	0.66	0/131	0.88	0/175
All	All	0.69	0/2961	1.08	13/3987 (0.3%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	222	TRP	N-CA-C	-7.79	102.72	111.14
1	E	235	TYR	CA-C-N	7.69	125.27	119.66
1	E	235	TYR	C-N-CA	7.69	125.27	119.66
1	E	95	LEU	N-CA-C	6.89	119.81	111.82
1	E	165	ARG	N-CA-C	6.79	120.74	111.17
1	E	236	PRO	N-CA-C	6.61	116.82	110.47
1	E	282	GLY	N-CA-C	-6.60	106.62	115.21
1	E	250	ILE	N-CA-C	6.51	116.67	110.42
1	E	290	ASP	N-CA-C	-6.50	104.28	111.82
1	E	302	TRP	N-CA-C	6.18	119.67	111.75
1	E	246	ILE	N-CA-C	-5.51	105.24	110.42
1	E	124	PRO	N-CA-C	5.21	121.42	114.18
1	E	123	VAL	N-CA-C	-5.12	102.48	107.55

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	E	2780	0	2761	222	0
2	I	130	0	124	10	0
3	E	35	0	26	3	0
4	E	127	0	0	12	0
4	I	15	0	0	0	0
All	All	3087	0	2911	227	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 39.

All (227) 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:E:65:THR:HG22	1:E:67:ASN:H	1.24	0.98
1:E:244:ILE:HD12	1:E:244:ILE:H	1.30	0.96
1:E:303:ILE:H	1:E:303:ILE:HD12	1.32	0.93
1:E:27:LEU:O	1:E:31:GLU:HG2	1.72	0.90
1:E:74:LEU:O	1:E:115:ASN:HB3	1.73	0.88
1:E:131:HIS:HB3	4:E:432:HOH:O	1.75	0.87
1:E:236:PRO:HG3	4:E:363:HOH:O	1.73	0.86
1:E:78:LYS:HE2	1:E:82:LEU:HD11	1.58	0.84
1:E:128:MET:HE1	1:E:180:ILE:HD11	1.61	0.83
1:E:131:HIS:HD2	1:E:134:ARG:HH22	1.23	0.82
1:E:131:HIS:CD2	1:E:134:ARG:HH22	1.97	0.82
1:E:129:PHE:CE2	2:I:18:ARG:HG3	2.15	0.79
1:E:181:GLN:NE2	1:E:308:ARG:HH22	1.82	0.78
1:E:192:LYS:H	1:E:192:LYS:HE2	1.49	0.77
1:E:17:GLU:O	1:E:21:LYS:HD2	1.84	0.77
1:E:39:HIS:ND1	1:E:40:LEU:N	2.33	0.76
1:E:83:LYS:HE3	1:E:83:LYS:O	1.86	0.76
1:E:285:LYS:NZ	1:E:286:ASN:H	1.84	0.75
1:E:85:ILE:HG23	1:E:347:PHE:CE1	2.23	0.73
1:E:285:LYS:H	1:E:285:LYS:HD3	1.54	0.73
1:E:274:GLN:HG2	1:E:279:LYS:HB3	1.73	0.70
1:E:289:ASN:O	1:E:293:ASN:HB2	1.90	0.70
1:E:179:TYR:HB3	1:E:308:ARG:HH21	1.56	0.69
1:E:238:PHE:HA	1:E:249:LYS:HZ3	1.58	0.69
1:E:303:ILE:HD12	1:E:303:ILE:N	2.07	0.69
1:E:163:ILE:HG12	1:E:217:LYS:HG3	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:65:THR:HG22	1:E:67:ASN:N	2.04	0.69
1:E:203:GLU:HB3	4:E:462:HOH:O	1.93	0.69
1:E:276:ASP:OD1	1:E:278:THR:HG22	1.93	0.68
1:E:345:LYS:HG2	1:E:346:GLU:H	1.58	0.68
1:E:39:HIS:O	1:E:42:GLN:HG2	1.93	0.68
1:E:100:PHE:CD1	1:E:101:PRO:HD2	2.28	0.68
1:E:104:VAL:HG21	1:E:183:THR:HB	1.77	0.67
1:E:345:LYS:HG2	1:E:346:GLU:N	2.10	0.67
1:E:341:GLU:O	1:E:342:LYS:HD2	1.95	0.67
1:E:27:LEU:O	1:E:31:GLU:CG	2.42	0.66
1:E:194:ARG:CB	1:E:194:ARG:HH11	2.09	0.66
1:E:75:ASP:OD2	1:E:78:LYS:HB2	1.96	0.66
1:E:285:LYS:NZ	1:E:286:ASN:N	2.44	0.66
1:E:285:LYS:HZ2	1:E:286:ASN:H	1.43	0.65
1:E:37:THR:HG22	1:E:37:THR:O	1.96	0.65
1:E:100:PHE:H	1:E:105:LYS:NZ	1.96	0.64
1:E:176:GLN:HE22	1:E:316:PRO:HB2	1.63	0.64
1:E:334:GLU:HG2	1:E:335:ILE:N	2.13	0.64
1:E:170:GLU:HG2	2:I:18:ARG:HG2	1.80	0.63
1:E:285:LYS:HZ3	1:E:286:ASN:N	1.97	0.62
1:E:135:ILE:HD11	4:E:426:HOH:O	1.98	0.62
1:E:307:GLN:O	1:E:308:ARG:HB2	1.99	0.62
1:E:29:LYS:NZ	1:E:34:ALA:HB2	2.15	0.62
1:E:129:PHE:HE1	1:E:133:ARG:NH1	1.98	0.61
1:E:60:VAL:HG11	1:E:71:MET:HE2	1.83	0.61
1:E:100:PHE:CG	1:E:101:PRO:HD2	2.36	0.61
2:I:5:THR:O	2:I:8:ALA:HB3	2.01	0.61
1:E:90:ASN:O	1:E:94:ILE:HG13	2.00	0.61
1:E:339:ILE:HG13	1:E:340:ASN:CG	2.26	0.60
1:E:176:GLN:HA	1:E:176:GLN:NE2	2.16	0.59
1:E:100:PHE:H	1:E:105:LYS:HZ1	1.49	0.59
1:E:35:GLN:HB3	1:E:350:PHE:OXT	2.03	0.58
1:E:257:PHE:HB2	1:E:266:LYS:HD3	1.85	0.58
1:E:305:ILE:HD13	1:E:310:VAL:HG21	1.85	0.58
1:E:61:LYS:HD2	1:E:68:HIS:CE1	2.39	0.58
1:E:181:GLN:OE1	4:E:357:HOH:O	2.17	0.58
1:E:242:GLN:HB2	1:E:245:GLN:NE2	2.19	0.58
1:E:276:ASP:CG	1:E:278:THR:HG22	2.29	0.58
1:E:49:LEU:HD11	1:E:59:LEU:HB2	1.86	0.57
1:E:80:VAL:HG21	1:E:343:CYS:SG	2.43	0.57
1:E:54:PHE:CD2	1:E:55:GLY:N	2.72	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:235:TYR:HB3	2:I:10:PHE:CD2	2.39	0.57
1:E:292:LYS:HA	1:E:302:TRP:CZ2	2.39	0.57
1:E:54:PHE:CG	1:E:55:GLY:N	2.67	0.56
1:E:318:PHE:CD2	1:E:320:GLY:O	2.58	0.56
1:E:96:GLN:NE2	1:E:97:ALA:HB2	2.20	0.56
1:E:45:ARG:C	1:E:46:ILE:HD13	2.31	0.56
2:I:7:TYR:CZ	2:I:11:ILE:HD11	2.41	0.56
1:E:27:LEU:HD22	1:E:31:GLU:OE2	2.06	0.55
1:E:207:PRO:O	1:E:210:ILE:N	2.39	0.55
1:E:238:PHE:HA	1:E:249:LYS:NZ	2.21	0.55
1:E:244:ILE:H	1:E:244:ILE:CD1	2.08	0.55
1:E:319:LYS:HD2	1:E:325:SER:OG	2.07	0.55
1:E:92:LYS:O	1:E:92:LYS:HD3	2.07	0.54
1:E:267:ASP:OD2	1:E:294:HIS:NE2	2.38	0.54
3:E:351:STU:H16	3:E:351:STU:H261	1.90	0.54
1:E:125:GLY:O	1:E:131:HIS:HE1	1.89	0.54
1:E:115:ASN:ND2	1:E:117:TYR:OH	2.41	0.54
1:E:129:PHE:HE1	1:E:133:ARG:HH11	1.55	0.54
1:E:134:ARG:HE	1:E:135:ILE:HD12	1.73	0.54
1:E:207:PRO:HG2	1:E:275:VAL:HG12	1.89	0.54
1:E:142:HIS:CD2	1:E:313:PRO:HG2	2.43	0.53
1:E:57:VAL:HG21	3:E:351:STU:C17	2.38	0.53
1:E:194:ARG:HH11	1:E:194:ARG:HB3	1.73	0.53
1:E:238:PHE:HA	1:E:249:LYS:HE2	1.90	0.53
1:E:74:LEU:O	1:E:115:ASN:CB	2.54	0.53
1:E:150:ILE:CG2	1:E:224:LEU:HD13	2.38	0.53
1:E:181:GLN:NE2	1:E:308:ARG:NH2	2.55	0.53
1:E:243:PRO:HA	1:E:246:ILE:HD12	1.91	0.53
1:E:94:ILE:O	1:E:98:VAL:HG22	2.09	0.52
1:E:106:LEU:CD2	1:E:108:PHE:O	2.57	0.52
1:E:319:LYS:HE3	1:E:326:ASN:HD21	1.74	0.52
1:E:131:HIS:HD2	1:E:134:ARG:NH2	2.02	0.52
1:E:239:PHE:H	1:E:249:LYS:HZ2	1.57	0.52
1:E:65:THR:HG21	1:E:67:ASN:OD1	2.08	0.52
1:E:129:PHE:CE1	1:E:133:ARG:NH1	2.78	0.52
1:E:236:PRO:HB2	4:E:462:HOH:O	2.08	0.52
1:E:58:MET:HE3	1:E:73:ILE:CD1	2.40	0.52
1:E:128:MET:CE	1:E:180:ILE:HD11	2.36	0.52
1:E:246:ILE:O	1:E:247:TYR:C	2.52	0.52
1:E:189:LYS:HD3	1:E:191:VAL:CG1	2.40	0.52
1:E:78:LYS:HA	1:E:81:LYS:HD2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:274:GLN:HG3	1:E:276:ASP:O	2.10	0.51
1:E:158:HIS:HE1	1:E:220:ASP:OD2	1.92	0.51
1:E:82:LEU:O	1:E:83:LYS:HB3	2.10	0.51
1:E:338:SEP:O1P	1:E:340:ASN:ND2	2.44	0.51
1:E:56:ARG:NH1	1:E:333:GLU:HB2	2.26	0.51
1:E:303:ILE:H	1:E:303:ILE:CD1	2.10	0.51
1:E:319:LYS:CE	1:E:326:ASN:HD21	2.24	0.50
1:E:219:VAL:HB	4:E:392:HOH:O	2.11	0.50
1:E:94:ILE:HD12	1:E:188:ALA:HB3	1.93	0.50
1:E:145:PHE:CE2	1:E:149:GLN:NE2	2.79	0.50
1:E:78:LYS:O	1:E:82:LEU:HD12	2.12	0.50
1:E:238:PHE:HA	1:E:249:LYS:CE	2.41	0.50
1:E:338:SEP:O3P	1:E:339:ILE:HG23	2.11	0.50
1:E:29:LYS:HZ3	1:E:34:ALA:HB2	1.75	0.50
1:E:83:LYS:HB2	4:E:388:HOH:O	2.12	0.49
1:E:324:THR:HG22	1:E:327:PHE:CE2	2.47	0.49
1:E:239:PHE:H	1:E:249:LYS:NZ	2.10	0.49
1:E:129:PHE:CD2	2:I:18:ARG:HG3	2.48	0.49
1:E:129:PHE:CG	1:E:170:GLU:HG3	2.48	0.48
1:E:135:ILE:CG2	1:E:137:ARG:O	2.61	0.48
1:E:207:PRO:CG	1:E:275:VAL:HG12	2.43	0.48
1:E:104:VAL:CG2	1:E:183:THR:HB	2.43	0.48
1:E:163:ILE:HG12	1:E:217:LYS:CG	2.43	0.48
1:E:165:ARG:NH1	1:E:215:TYR:OH	2.46	0.48
1:E:255:VAL:HA	4:E:472:HOH:O	2.12	0.48
1:E:60:VAL:HG22	1:E:69:TYR:O	2.14	0.48
1:E:110:PHE:CD1	1:E:110:PHE:N	2.81	0.48
1:E:150:ILE:HG22	1:E:224:LEU:HD13	1.95	0.48
1:E:76:LYS:HG2	1:E:347:PHE:CE2	2.49	0.47
1:E:118:MET:O	1:E:120:MET:HE2	2.14	0.47
1:E:257:PHE:CB	1:E:266:LYS:HD3	2.44	0.47
1:E:83:LYS:O	1:E:83:LYS:CG	2.61	0.47
1:E:155:GLU:HG3	1:E:288:VAL:HG21	1.94	0.47
1:E:208:GLU:OE2	1:E:277:LEU:HD21	2.14	0.47
1:E:236:PRO:HD2	2:I:10:PHE:CE1	2.49	0.47
1:E:306:TYR:CD1	1:E:306:TYR:C	2.92	0.47
1:E:112:ASP:OD1	1:E:112:ASP:N	2.48	0.47
1:E:142:HIS:HD2	1:E:313:PRO:HG2	1.80	0.47
1:E:99:ASN:HA	1:E:105:LYS:HE3	1.96	0.47
1:E:246:ILE:O	1:E:249:LYS:N	2.47	0.47
1:E:15:VAL:HG13	1:E:19:LEU:CD1	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:57:VAL:HG21	3:E:351:STU:N2	2.30	0.47
1:E:65:THR:CG2	1:E:67:ASN:OD1	2.62	0.47
1:E:192:LYS:HE2	1:E:192:LYS:N	2.24	0.47
1:E:204:TYR:CE1	1:E:226:VAL:HG12	2.50	0.47
1:E:241:ASP:C	1:E:242:GLN:HG2	2.39	0.47
1:E:142:HIS:NE2	1:E:146:TYR:CE2	2.83	0.47
1:E:324:THR:HG22	1:E:327:PHE:CD2	2.50	0.47
1:E:134:ARG:HE	1:E:135:ILE:CD1	2.28	0.46
1:E:198:LEU:HD13	1:E:209:ILE:HG22	1.97	0.46
1:E:206:ALA:O	1:E:207:PRO:C	2.59	0.46
1:E:29:LYS:HE2	1:E:33:PRO:HA	1.97	0.46
1:E:105:LYS:HD2	4:E:360:HOH:O	2.13	0.46
1:E:56:ARG:HH22	1:E:332:GLU:HA	1.80	0.46
1:E:92:LYS:HD3	1:E:92:LYS:C	2.40	0.46
1:E:342:LYS:O	1:E:343:CYS:HB2	2.15	0.46
1:E:179:TYR:HB3	1:E:308:ARG:NH2	2.26	0.46
1:E:274:GLN:O	1:E:280:ARG:NH2	2.36	0.45
1:E:33:PRO:HA	1:E:96:GLN:OE1	2.16	0.45
1:E:346:GLU:H	1:E:346:GLU:HG2	1.32	0.45
1:E:276:ASP:OD2	1:E:278:THR:HG22	2.16	0.45
1:E:83:LYS:O	1:E:83:LYS:HG2	2.16	0.45
1:E:219:VAL:HG23	1:E:220:ASP:N	2.32	0.45
1:E:279:LYS:C	1:E:284:LEU:HD21	2.42	0.45
2:I:7:TYR:CE2	2:I:11:ILE:HD11	2.51	0.45
1:E:134:ARG:HH21	1:E:135:ILE:HD13	1.82	0.45
1:E:166:ASP:O	1:E:171:ASN:ND2	2.49	0.45
1:E:189:LYS:NZ	1:E:197:TPO:O3P	2.49	0.44
1:E:58:MET:HE3	1:E:73:ILE:HD11	2.00	0.44
1:E:83:LYS:O	1:E:83:LYS:CE	2.62	0.44
1:E:124:PRO:HG2	1:E:176:GLN:OE1	2.18	0.44
1:E:58:MET:CE	1:E:73:ILE:HD13	2.47	0.44
1:E:75:ASP:O	1:E:79:VAL:HG23	2.17	0.44
1:E:205:LEU:HD23	4:E:403:HOH:O	2.18	0.44
1:E:335:ILE:HD12	1:E:335:ILE:HA	1.91	0.44
1:E:26:PHE:CD1	1:E:160:LEU:HD13	2.53	0.43
1:E:343:CYS:O	1:E:346:GLU:HG2	2.17	0.43
1:E:267:ASP:O	1:E:271:ASN:ND2	2.51	0.43
1:E:76:LYS:HG2	1:E:347:PHE:CD2	2.53	0.43
1:E:112:ASP:C	1:E:114:SER:H	2.27	0.43
2:I:7:TYR:O	2:I:11:ILE:HD12	2.19	0.43
1:E:37:THR:O	1:E:37:THR:CG2	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:45:ARG:HA	1:E:60:VAL:HG12	2.00	0.43
1:E:34:ALA:C	1:E:35:GLN:HG3	2.38	0.43
1:E:105:LYS:N	1:E:105:LYS:CD	2.82	0.43
1:E:32:ASN:O	1:E:33:PRO:O	2.36	0.43
1:E:106:LEU:HD21	1:E:108:PHE:O	2.19	0.43
1:E:15:VAL:HG12	1:E:16:LYS:N	2.34	0.42
1:E:176:GLN:NE2	1:E:316:PRO:HG2	2.34	0.42
1:E:65:THR:CG2	1:E:67:ASN:CG	2.92	0.42
1:E:31:GLU:HG2	1:E:31:GLU:H	1.58	0.42
1:E:32:ASN:N	1:E:33:PRO:CD	2.82	0.42
1:E:52:GLY:HA3	1:E:54:PHE:CE1	2.55	0.42
1:E:58:MET:HE3	1:E:73:ILE:HD13	2.01	0.42
1:E:62:HIS:O	1:E:66:GLY:N	2.42	0.42
1:E:295:LYS:HZ3	1:E:295:LYS:HG3	1.70	0.42
1:E:341:GLU:C	1:E:342:LYS:HD2	2.43	0.42
1:E:135:ILE:HG22	1:E:137:ARG:O	2.20	0.42
1:E:338:SEP:P	1:E:340:ASN:HD22	2.42	0.42
1:E:103:LEU:HB2	1:E:105:LYS:NZ	2.35	0.41
1:E:163:ILE:HG13	1:E:191:VAL:HG23	2.01	0.41
1:E:258:PRO:HD2	1:E:261:PHE:CD2	2.55	0.41
1:E:314:PHE:C	1:E:315:ILE:HD12	2.44	0.41
1:E:280:ARG:O	1:E:283:ASN:HB3	2.21	0.41
1:E:285:LYS:HZ3	1:E:285:LYS:HG2	1.78	0.41
1:E:21:LYS:HB3	4:E:458:HOH:O	2.20	0.41
1:E:37:THR:O	1:E:38:ALA:HB2	2.19	0.41
1:E:146:TYR:CD1	1:E:180:ILE:HD12	2.56	0.41
1:E:189:LYS:HD3	1:E:191:VAL:HG13	2.02	0.41
1:E:230:GLU:CD	2:I:19:ARG:HH22	2.26	0.41
1:E:285:LYS:HZ3	1:E:286:ASN:CG	2.28	0.41
1:E:336:ARG:HD3	1:E:336:ARG:C	2.46	0.41
1:E:144:ARG:O	1:E:145:PHE:C	2.64	0.41
1:E:318:PHE:HD2	1:E:320:GLY:O	2.01	0.41
1:E:343:CYS:HB3	1:E:346:GLU:HG3	2.03	0.40
1:E:15:VAL:HG13	1:E:19:LEU:HD12	2.04	0.40
1:E:15:VAL:O	1:E:18:PHE:N	2.55	0.40
1:E:285:LYS:NZ	1:E:286:ASN:ND2	2.69	0.40
1:E:103:LEU:O	1:E:105:LYS:HD3	2.21	0.40

There are no symmetry-related clashes.

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	E	332/350 (95%)	297 (90%)	30 (9%)	5 (2%)	8	8
2	I	15/20 (75%)	15 (100%)	0	0	100	100
All	All	347/370 (94%)	312 (90%)	30 (9%)	5 (1%)	9	9

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	33	PRO
1	E	318	PHE
1	E	63	MET
1	E	166	ASP
1	E	344	GLY

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	E	295/302 (98%)	231 (78%)	64 (22%)	1	1
2	I	12/15 (80%)	12 (100%)	0	100	100
All	All	307/317 (97%)	243 (79%)	64 (21%)	1	1

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	15	VAL

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Mol	Chain	Res	Type
1	E	16	LYS
1	E	17	GLU
1	E	25	ASP
1	E	28	LYS
1	E	29	LYS
1	E	31	GLU
1	E	35	GLN
1	E	44	GLU
1	E	46	ILE
1	E	47	LYS
1	E	53	SER
1	E	61	LYS
1	E	63	MET
1	E	65	THR
1	E	78	LYS
1	E	82	LEU
1	E	83	LYS
1	E	91	GLU
1	E	92	LYS
1	E	93	ARG
1	E	98	VAL
1	E	99	ASN
1	E	105	LYS
1	E	106	LEU
1	E	109	SER
1	E	110	PHE
1	E	115	ASN
1	E	121	GLU
1	E	128	MET
1	E	135	ILE
1	E	176	GLN
1	E	180	ILE
1	E	189	LYS
1	E	190	ARG
1	E	191	VAL
1	E	192	LYS
1	E	194	ARG
1	E	198	LEU
1	E	245	GLN
1	E	255	VAL
1	E	259	SER
1	E	263	SER

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Mol	Chain	Res	Type
1	E	266	LYS
1	E	267	ASP
1	E	268	LEU
1	E	275	VAL
1	E	278	THR
1	E	279	LYS
1	E	285	LYS
1	E	295	LYS
1	E	303	ILE
1	E	309	LYS
1	E	311	GLU
1	E	317	LYS
1	E	318	PHE
1	E	323	ASP
1	E	331	GLU
1	E	335	ILE
1	E	339	ILE
1	E	340	ASN
1	E	342	LYS
1	E	345	LYS
1	E	346	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	32	ASN
1	E	42	GLN
1	E	68	HIS
1	E	77	GLN
1	E	99	ASN
1	E	115	ASN
1	E	131	HIS
1	E	158	HIS
1	E	176	GLN
1	E	181	GLN
1	E	245	GLN
1	E	271	ASN
1	E	283	ASN
1	E	286	ASN
1	E	293	ASN
1	E	326	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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
1	TPO	E	197	1	8,10,11	1.56	1 (12%)	10,14,16	1.29	2 (20%)
1	SEP	E	338	1	8,9,10	1.44	1 (12%)	7,12,14	1.38	1 (14%)

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
1	TPO	E	197	1	-	2/9/11/13	-
1	SEP	E	338	1	-	4/6/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	338	SEP	P-OG	-3.16	1.50	1.60
1	E	197	TPO	P-OG1	-2.91	1.54	1.59

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	338	SEP	O3P-P-O2P	2.50	117.19	107.80
1	E	197	TPO	O2P-P-O1P	2.23	119.52	110.83
1	E	197	TPO	O3P-P-OG1	-2.22	97.19	105.85

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	E	197	TPO	O-C-CA-CB
1	E	338	SEP	N-CA-CB-OG
1	E	338	SEP	CA-CB-OG-P
1	E	338	SEP	CB-OG-P-O1P
1	E	338	SEP	CB-OG-P-O2P
1	E	197	TPO	N-CA-CB-CG2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	197	TPO	1	0
1	E	338	SEP	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	$\# Z > 2$
3	STU	E	351	-	39,42,42	1.16	3 (7%)	50,68,68	0.89	2 (4%)

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
3	STU	E	351	-	-	2/4/42/42	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	351	STU	C25-N3	2.86	1.48	1.45
3	E	351	STU	C16-C17	2.14	1.42	1.39
3	E	351	STU	C4-C5	2.11	1.43	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	351	STU	C27-O6-C22	3.39	120.19	114.46
3	E	351	STU	C16-C17-C12	-2.15	119.08	121.59

There are no chirality outliers.

All (2) torsion outliers are listed below:

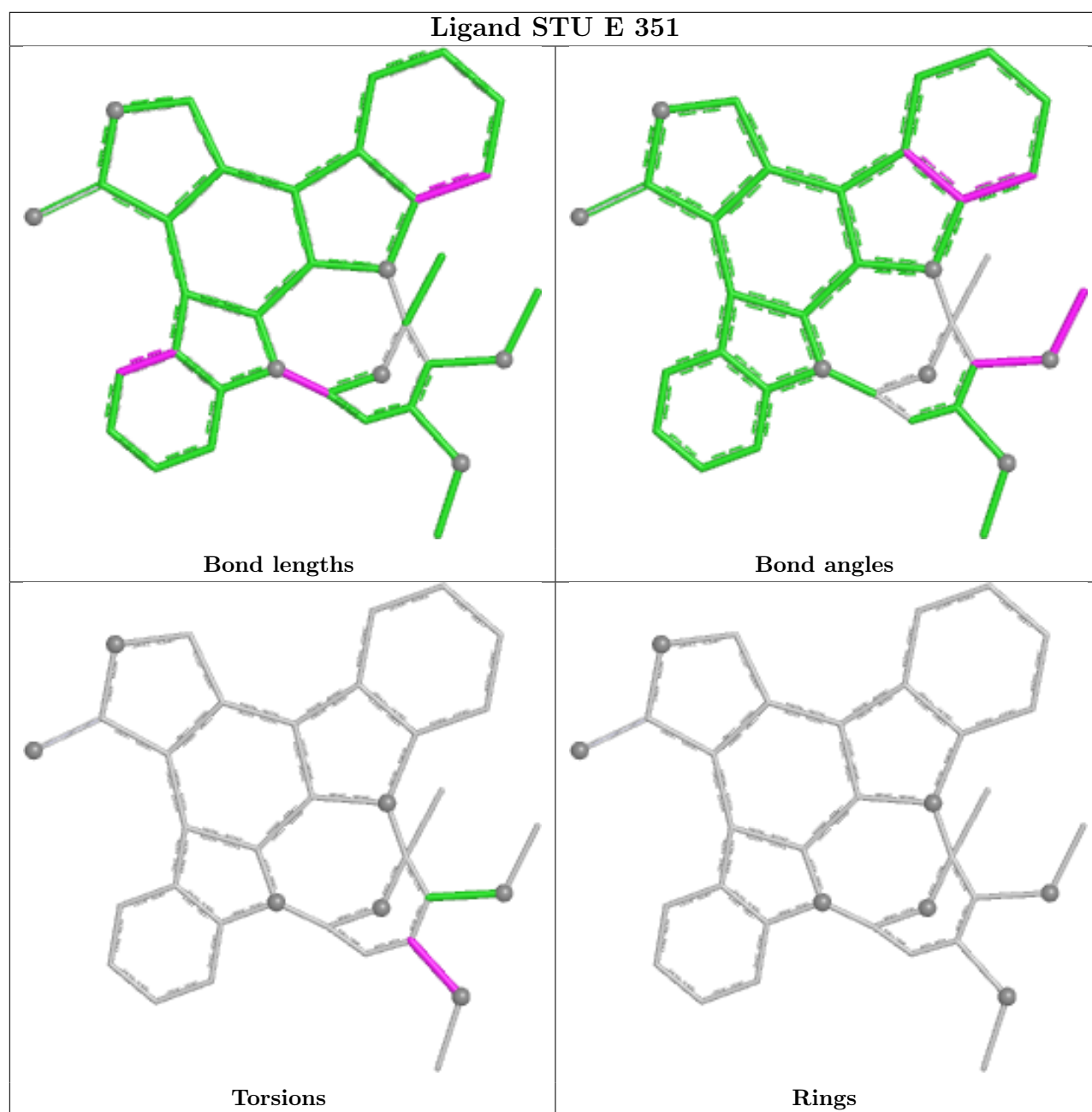
Mol	Chain	Res	Type	Atoms
3	E	351	STU	C24-C23-N4-C28
3	E	351	STU	C22-C23-N4-C28

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	351	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.



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.