



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:34 PM UTC

PDB ID : 5N9W / pdb_00005n9w
Title : Structure of adenylation domain THR1 involved in the biosynthesis of 4-chlorothreonine in Streptomyces SP.OH-5093, apo structure
Authors : Savino, C.; Vallone, B.; Scaglione, A.; Parisi, G.; Montemiglio, L.C.; Fullone, M.R.; Grgurina, I.
Deposited on : 2017-02-27
Resolution : 2.46 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

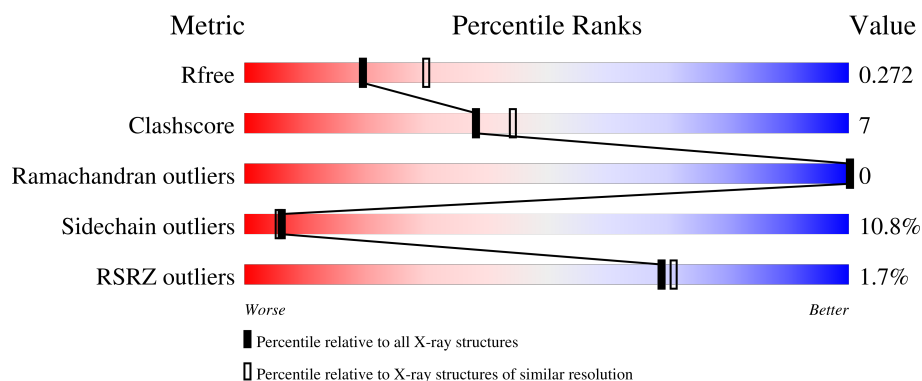
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.46 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	529	67% 20% • 10%
1	B	529	2% 72% 16% • 10%

2 Entry composition [i](#)

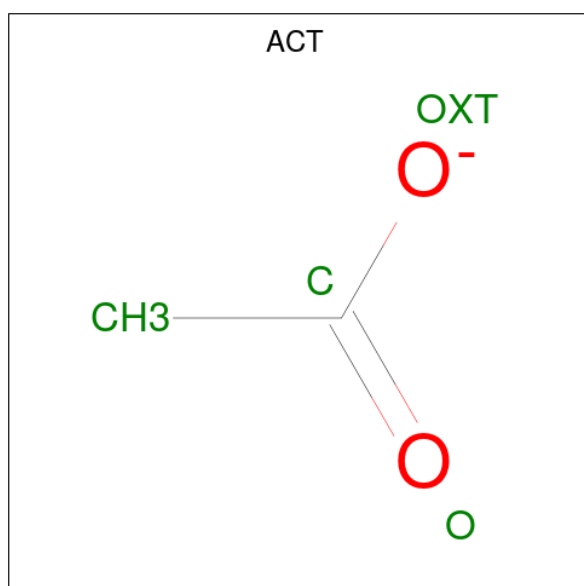
There are 3 unique types of molecules in this entry. The entry contains 7467 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Adenylation domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	477	Total	C	N	O	S	0	1	0
			3691	2335	668	679	9			
1	B	477	Total	C	N	O	S	0	1	0
			3674	2327	665	673	9			

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

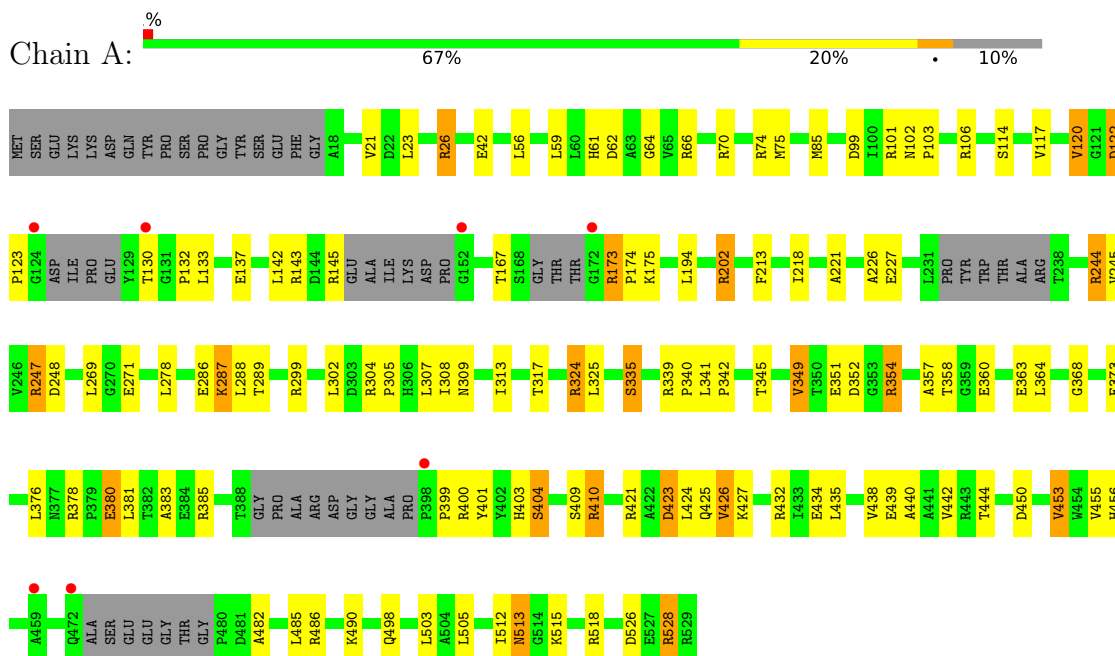
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	44	Total 44	O 44	0	0
3	B	46	Total 46	O 46	0	0

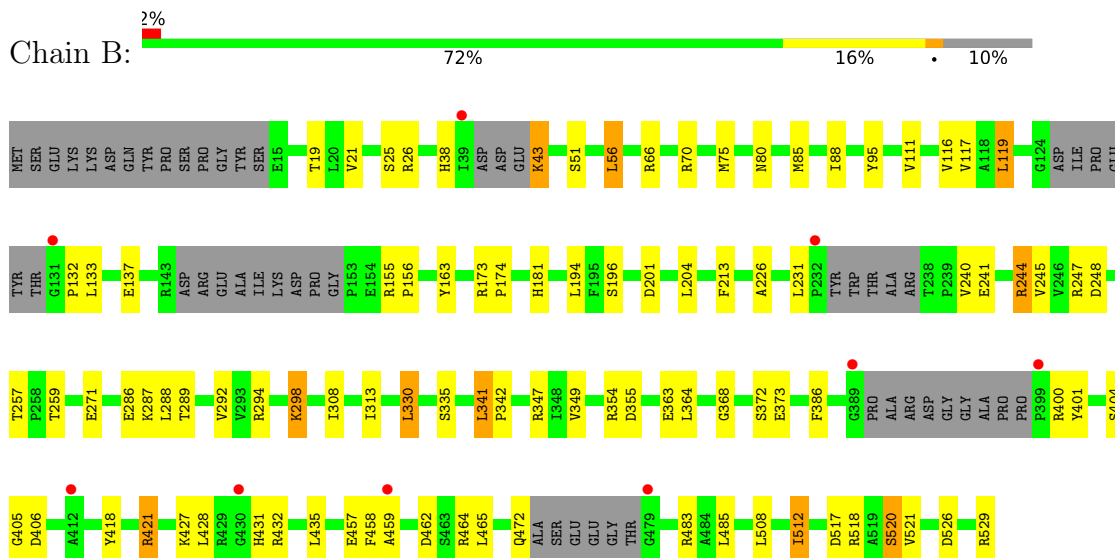
3 Residue-property plots [i](#)

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: Adenylation domain



• Molecule 1: Adenylation domain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	177.63Å 52.81Å 108.86Å 90.00° 105.81° 90.00°	Depositor
Resolution (Å)	46.95 – 2.46 46.95 – 2.46	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.95-2.46) 99.7 (46.95-2.46)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.45Å)	Xtriage
Refinement program	PHENIX dev_1647	Depositor
R, R_{free}	0.197 , 0.270 0.202 , 0.272	Depositor DCC
R_{free} test set	1793 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	37.9	Xtriage
Anisotropy	0.580	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7467	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.22% 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: ACT

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	0.71	3/3778 (0.1%)	0.94	16/5141 (0.3%)
1	B	0.63	0/3761	0.91	7/5117 (0.1%)
All	All	0.67	3/7539 (0.0%)	0.93	23/10258 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	123	PRO	N-CD	8.74	1.59	1.47
1	A	122	ASP	C-N	7.95	1.40	1.33
1	A	120	VAL	C-O	-5.95	1.17	1.24

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	123	PRO	N-CA-C	9.48	125.76	110.21
1	A	317	THR	N-CA-C	7.37	119.53	110.91
1	A	123	PRO	CA-N-CD	-7.16	101.97	112.00
1	B	173	ARG	CA-C-N	6.49	126.72	119.90
1	B	173	ARG	C-N-CA	6.49	126.72	119.90
1	A	122	ASP	CB-CA-C	-6.43	101.13	110.13
1	A	368	GLY	CA-C-N	6.42	126.34	119.28
1	A	368	GLY	C-N-CA	6.42	126.34	119.28
1	A	341	LEU	CA-C-N	6.40	127.84	119.84
1	A	341	LEU	C-N-CA	6.40	127.84	119.84
1	A	103	PRO	CA-C-N	6.27	126.47	119.32
1	A	103	PRO	C-N-CA	6.27	126.47	119.32
1	B	368	GLY	CA-C-N	6.21	126.67	119.47
1	B	368	GLY	C-N-CA	6.21	126.67	119.47
1	B	341	LEU	CA-C-N	5.74	127.01	119.84
1	B	341	LEU	C-N-CA	5.74	127.01	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	123	PRO	N-CD-CG	-5.60	94.80	103.20
1	B	163	TYR	N-CA-C	5.30	116.89	108.79
1	A	505	LEU	CA-C-N	5.16	124.61	119.24
1	A	505	LEU	C-N-CA	5.16	124.61	119.24
1	A	123	PRO	N-CA-CB	-5.05	99.84	103.23
1	A	122	ASP	CA-C-N	-5.01	113.09	120.46
1	A	122	ASP	C-N-CA	-5.01	113.09	120.46

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	A	3691	0	3659	55	1
1	B	3674	0	3650	46	1
2	A	4	0	3	0	0
2	B	8	0	6	0	0
3	A	44	0	0	2	0
3	B	46	0	0	1	0
All	All	7467	0	7318	101	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 7.

All (101) 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:155:ARG:NH2	3:B:701:HOH:O	2.13	0.80
1:A:42:GLU:OE2	1:A:143:ARG:NH2	2.14	0.78
1:B:294:ARG:NH1	1:B:330:LEU:O	2.20	0.74
1:B:174:PRO:HB3	1:B:512:ILE:HG12	1.75	0.68
1:A:244:ARG:NH1	1:A:271:GLU:OE1	2.27	0.68
1:A:247:ARG:HG3	1:A:248:ASP:N	2.09	0.67
1:B:19:THR:HG22	1:B:21:VAL:H	1.61	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:THR:HG22	1:B:259:THR:H	1.64	0.62
1:A:364:LEU:O	1:A:404:SER:OG	2.16	0.62
1:A:202:ARG:HG3	1:A:227:GLU:HB3	1.83	0.61
1:B:75:MET:HE1	1:B:80:ASN:HB2	1.82	0.61
1:B:204:LEU:HD11	1:B:231:LEU:HG	1.82	0.61
1:A:61:HIS:O	1:A:66:ARG:NH2	2.34	0.60
1:A:380:GLU:OE1	1:A:381:LEU:N	2.25	0.59
1:A:102:ASN:OD1	1:A:106:ARG:NH1	2.35	0.59
1:A:442:VAL:HG13	1:A:485:LEU:HD11	1.86	0.58
1:B:427:LYS:HD2	1:B:432:ARG:NH2	2.19	0.57
1:A:513:ASN:OD1	1:A:513:ASN:N	2.27	0.56
1:A:75:MET:CE	1:A:120:VAL:HG12	2.35	0.56
1:A:304:ARG:NH1	3:A:702:HOH:O	2.34	0.55
1:A:490:LYS:HA	1:A:498:GLN:NE2	2.20	0.55
1:A:438:VAL:HB	1:A:453:VAL:HG21	1.89	0.55
1:A:439:GLU:OE2	1:A:518:ARG:NH2	2.40	0.55
1:A:357:ALA:N	1:A:360:GLU:OE1	2.34	0.54
1:B:289:THR:O	1:B:292:VAL:HG12	2.06	0.54
1:A:423:ASP:OD1	1:A:423:ASP:N	2.41	0.54
1:A:114:SER:HA	1:A:376:LEU:HD21	1.89	0.53
1:B:287:LYS:HG3	1:B:418:TYR:HD2	1.74	0.53
1:A:122:ASP:C	1:A:122:ASP:OD2	2.50	0.53
1:A:439:GLU:HG3	1:A:453:VAL:HG13	1.90	0.53
1:B:38:HIS:CG	1:B:43:LYS:HD2	2.44	0.52
1:A:101:ARG:HH22	1:A:512:ILE:HD12	1.73	0.52
1:A:435:LEU:HD22	1:A:453:VAL:HG23	1.92	0.52
1:B:117:VAL:O	1:B:132:PRO:HG2	2.10	0.52
1:A:456:HIS:CE1	1:A:526:ASP:OD1	2.63	0.51
1:B:364:LEU:O	1:B:404:SER:HB3	2.11	0.51
1:B:19:THR:HG21	1:B:156:PRO:HG2	1.93	0.51
1:B:75:MET:HE1	1:B:80:ASN:CB	2.41	0.50
1:B:259:THR:OG1	1:B:286:GLU:OE2	2.22	0.49
1:A:503:LEU:HD11	1:A:528:ARG:HD2	1.95	0.49
1:B:247:ARG:HD2	1:B:248:ASP:OD1	2.12	0.49
1:A:173:ARG:HG2	1:A:173:ARG:HH11	1.78	0.49
1:A:221:ALA:HA	1:A:226:ALA:HB3	1.94	0.49
1:B:427:LYS:HD2	1:B:432:ARG:HH21	1.77	0.49
1:A:167:THR:HG22	1:A:513:ASN:HD21	1.78	0.48
1:B:257:THR:HG22	1:B:259:THR:N	2.26	0.48
1:B:459:ALA:HB3	1:B:462:ASP:HB3	1.96	0.47
1:B:406:ASP:CG	1:B:421:ARG:HE	2.22	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ARG:HE	1:A:26:ARG:HB3	1.53	0.47
1:A:440:ALA:O	1:A:444:THR:HG23	2.15	0.47
1:A:358:THR:HG23	1:A:410:ARG:O	2.14	0.47
1:A:399:PRO:HB2	1:A:401:TYR:CE2	2.50	0.47
1:A:85:MET:HE1	1:A:218:ILE:HG21	1.97	0.47
1:A:426:VAL:HG11	1:A:455:VAL:HG21	1.97	0.47
1:B:288:LEU:O	1:B:335:SER:OG	2.29	0.47
1:B:404:SER:OG	1:B:406:ASP:HB2	2.15	0.47
1:B:373:GLU:C	1:B:400:ARG:HH22	2.23	0.47
1:B:386:PHE:HA	1:B:401:TYR:O	2.14	0.46
1:A:339:ARG:HD3	1:A:340:PRO:HD2	1.98	0.46
1:A:373:GLU:O	1:A:400:ARG:NH2	2.48	0.46
1:A:352:ASP:OD1	1:A:354:ARG:NH1	2.49	0.46
1:B:231:LEU:HD21	1:B:245:VAL:HG11	1.98	0.46
1:B:372:SER:OG	1:B:373:GLU:N	2.49	0.45
1:B:88:ILE:HG21	1:B:95:TYR:HB3	1.97	0.45
1:A:482:ALA:O	1:A:486:ARG:HB2	2.16	0.45
1:B:19:THR:HA	1:B:181:HIS:HB3	1.98	0.45
1:B:517:ASP:CG	1:B:520:SER:HB2	2.42	0.45
1:A:278:LEU:HD23	1:A:305:PRO:HG3	1.99	0.45
1:A:287:LYS:HE3	1:A:287:LYS:HB3	1.62	0.44
1:A:309:ASN:HB2	1:A:325:LEU:HD11	1.99	0.44
1:B:241:GLU:OE2	1:B:244:ARG:NE	2.49	0.44
1:B:119:LEU:HD13	1:B:133:LEU:HD13	2.00	0.44
1:B:111:VAL:HG23	1:B:116:VAL:HG22	1.98	0.44
1:B:201:ASP:O	1:B:226:ALA:HB1	2.18	0.43
1:A:380:GLU:O	1:A:383:ALA:HB3	2.18	0.43
1:A:173:ARG:HG2	1:A:173:ARG:NH1	2.33	0.43
1:B:26:ARG:HE	1:B:26:ARG:HB3	1.61	0.43
1:B:347:ARG:NE	1:B:355:ASP:OD1	2.48	0.43
1:B:458:PHE:CE1	1:B:464:ARG:HG3	2.54	0.43
1:B:241:GLU:HA	1:B:244:ARG:HD3	2.01	0.43
1:B:298:LYS:HA	1:B:298:LYS:HD2	1.35	0.43
1:B:349:VAL:HA	1:B:354:ARG:O	2.19	0.42
1:A:378:ARG:HG3	1:A:381:LEU:HD12	2.01	0.42
1:A:302:LEU:O	1:A:324:ARG:NH1	2.53	0.42
1:A:373:GLU:C	1:A:400:ARG:HH22	2.27	0.42
1:A:99:ASP:OD2	1:A:101:ARG:HB2	2.20	0.42
1:B:56:LEU:HD12	1:B:56:LEU:HA	1.87	0.42
1:B:363:GLU:OE2	1:B:405:GLY:N	2.45	0.42
1:A:289:THR:HB	3:A:708:HOH:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:VAL:HG12	1:A:453:VAL:HG11	2.03	0.41
1:A:62:ASP:C	1:A:64:GLY:H	2.29	0.41
1:A:117:VAL:O	1:A:132:PRO:HG2	2.21	0.41
1:B:19:THR:HG23	1:B:181:HIS:ND1	2.36	0.41
1:B:518:ARG:HA	1:B:521:VAL:HG22	2.03	0.41
1:A:349:VAL:HG22	1:A:363:GLU:HB3	2.03	0.41
1:A:512:ILE:HD12	1:A:512:ILE:HA	1.90	0.40
1:B:526:ASP:HA	1:B:529:ARG:HD3	2.01	0.40
1:A:174:PRO:O	1:A:378:ARG:NH2	2.54	0.40
1:A:425:GLN:NE2	1:A:434:GLU:OE2	2.52	0.40
1:B:512:ILE:H	1:B:512:ILE:HG13	1.50	0.40
1:A:288:LEU:O	1:A:335:SER:OG	2.30	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:269:LEU:O	1:B:196:SER:OG[3_445]	2.18	0.02

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	464/529 (88%)	453 (98%)	11 (2%)	0	100	100
1	B	464/529 (88%)	450 (97%)	14 (3%)	0	100	100
All	All	928/1058 (88%)	903 (97%)	25 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	382/420 (91%)	331 (87%)	51 (13%)	4	3
1	B	379/420 (90%)	347 (92%)	32 (8%)	10	12
All	All	761/840 (91%)	678 (89%)	83 (11%)	6	5

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	VAL
1	A	23	LEU
1	A	26	ARG
1	A	56	LEU
1	A	59	LEU
1	A	70	ARG
1	A	74	ARG
1	A	130	THR
1	A	133	LEU
1	A	137	GLU
1	A	142	LEU
1	A	145	ARG
1	A	173	ARG
1	A	175	LYS
1	A	194	LEU
1	A	202	ARG
1	A	213	PHE
1	A	244	ARG
1	A	245	VAL
1	A	247	ARG
1	A	286	GLU
1	A	287	LYS
1	A	299	ARG
1	A	307	LEU
1	A	308	ILE
1	A	313	ILE
1	A	324	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	335	SER
1	A	342	PRO
1	A	345	THR
1	A	349	VAL
1	A	351	GLU
1	A	354	ARG
1	A	380	GLU
1	A	385	ARG
1	A	403	HIS
1	A	404	SER
1	A	409	SER
1	A	410	ARG
1	A	421	ARG
1	A	423	ASP
1	A	424	LEU
1	A	426	VAL
1	A	427	LYS
1	A	432	ARG
1	A	450	ASP
1	A	453	VAL
1	A	513	ASN
1	A	515[A]	LYS
1	A	515[B]	LYS
1	A	528	ARG
1	B	25	SER
1	B	43	LYS
1	B	51	SER
1	B	56	LEU
1	B	66	ARG
1	B	70	ARG
1	B	85	MET
1	B	119	LEU
1	B	137	GLU
1	B	194	LEU
1	B	213	PHE
1	B	240	VAL
1	B	244	ARG
1	B	271	GLU
1	B	298	LYS
1	B	308	ILE
1	B	313	ILE
1	B	330	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	341	LEU
1	B	342	PRO
1	B	421	ARG
1	B	428	LEU
1	B	431	HIS
1	B	435	LEU
1	B	457	GLU
1	B	465	LEU
1	B	472	GLN
1	B	483	ARG
1	B	485	LEU
1	B	508	LEU
1	B	512	ILE
1	B	520	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	GLN
1	A	319	HIS
1	A	346	HIS
1	A	445	HIS
1	A	456	HIS
1	A	498	GLN
1	B	38	HIS
1	B	419	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 [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	ACT	B	602	-	3,3,3	0.94	0	3,3,3	0.96	0
2	ACT	A	601	-	3,3,3	0.75	0	3,3,3	1.13	0
2	ACT	B	601	-	3,3,3	0.90	0	3,3,3	1.11	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	477/529 (90%)	-0.10	7 (1%) 72 74	11, 33, 58, 74	1 (0%)
1	B	477/529 (90%)	-0.10	9 (1%) 66 67	16, 32, 60, 78	1 (0%)
All	All	954/1058 (90%)	-0.10	16 (1%) 69 71	11, 33, 59, 78	2 (0%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	124	GLY	3.4
1	B	389	GLY	3.3
1	B	412	ALA	2.9
1	B	430	GLY	2.7
1	A	172	GLY	2.6
1	B	39	ILE	2.6
1	B	131	GLY	2.5
1	B	459	ALA	2.5
1	B	232	PRO	2.5
1	A	459	ALA	2.4
1	A	472	GLN	2.3
1	A	398	PRO	2.3
1	B	399	PRO	2.2
1	A	152	GLY	2.2
1	B	479	GLY	2.1
1	A	130	THR	2.1

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	ACT	B	602	4/4	0.78	0.18	47,50,51,52	0
2	ACT	B	601	4/4	0.89	0.10	29,30,32,37	0
2	ACT	A	601	4/4	0.89	0.15	48,51,51,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.