



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:29 PM UTC

PDB ID : 2AOW / pdb_00002aow
Title : Histamine Methyltransferase (Natural Variant I105) Complexed with the Acetylcholinesterase Inhibitor and Alzheimer's Disease Drug Tacrine
Authors : Horton, J.R.; Sawada, K.; Nishibori, M.; Cheng, X.
Deposited on : 2005-08-14
Resolution : 2.97 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
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

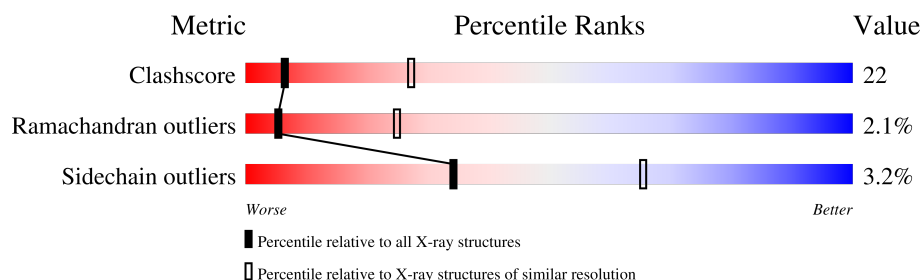
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.97 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	3904 (3.00-2.96)
Ramachandran outliers	187476	3761 (3.00-2.96)
Sidechain outliers	187428	3764 (3.00-2.96)

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	292	
1	B	292	

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
2	THA	A	400	-	X	-	-
2	THA	B	401	-	X	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4495 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.

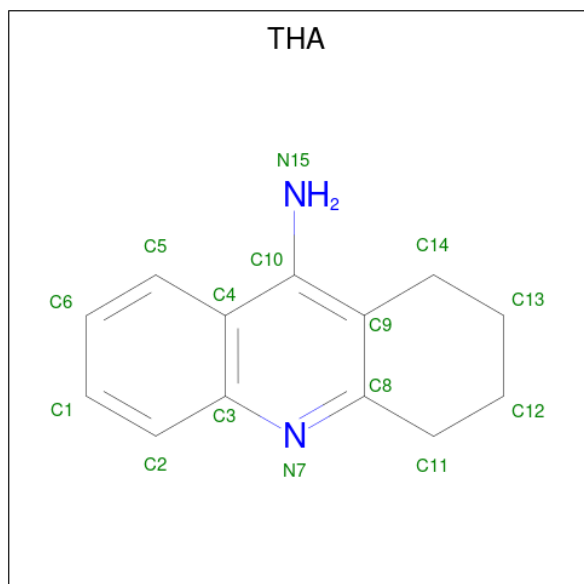
- Molecule 1 is a protein called Histamine N-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	0	0
			2220	1422	356	427	15			
1	B	288	Total	C	N	O	S	0	0	0
			2220	1422	356	427	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	ILE	THR	engineered mutation	UNP P50135
B	105	ILE	THR	engineered mutation	UNP P50135

- Molecule 2 is TACRINE (CCD ID: THA) (formula: C₁₃H₁₄N₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			15	13	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	N	0	0
			15	13	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total	O	0	0
			12	12		
3	B	13	Total	O	0	0
			13	13		

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 6	Depositor
Cell constants a, b, c, α , β , γ	132.96Å 132.96Å 65.21Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.00 – 2.97	Depositor
% Data completeness (in resolution range)	(Not available) (28.00-2.97)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.219 , 0.269	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4495	wwPDB-VP
Average B, all atoms (Å ²)	40.0	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: THA

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	0.61	0/2267	0.98	7/3070 (0.2%)
1	B	0.66	0/2267	1.00	9/3070 (0.3%)
All	All	0.64	0/4534	0.99	16/6140 (0.3%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	265	ASP	N-CA-C	6.89	118.87	111.36
1	A	265	ASP	N-CA-C	6.60	118.55	111.36
1	B	254	ALA	CA-C-N	6.20	126.77	120.38
1	B	254	ALA	C-N-CA	6.20	126.77	120.38
1	B	206	GLN	N-CA-C	-5.78	104.90	111.14
1	A	254	ALA	CA-C-N	5.44	125.98	120.38
1	A	254	ALA	C-N-CA	5.44	125.98	120.38
1	A	91	SER	N-CA-C	5.43	117.09	108.67
1	B	91	SER	N-CA-C	5.35	116.96	108.67
1	B	45	GLY	N-CA-C	5.33	120.37	113.27
1	A	206	GLN	N-CA-C	-5.24	105.48	111.14
1	B	89	GLU	CA-C-N	5.18	124.68	119.19
1	B	89	GLU	C-N-CA	5.18	124.68	119.19
1	A	89	GLU	CA-C-N	5.12	124.61	119.19
1	A	89	GLU	C-N-CA	5.12	124.61	119.19
1	B	241	TRP	N-CA-C	-5.08	105.63	111.07

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	2220	0	2109	98	0
1	B	2220	0	2109	94	0
2	A	15	0	14	2	0
2	B	15	0	14	3	0
3	A	12	0	0	1	0
3	B	13	0	0	2	0
All	All	4495	0	4246	191	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 22.

All (191) 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:5:MET:HE2	1:A:247:THR:HG21	1.36	1.06
1:B:5:MET:HE2	1:B:247:THR:HG21	1.38	1.05
1:B:82:CYS:HB2	3:B:414:HOH:O	1.61	0.99
1:B:259:ARG:HG2	1:B:259:ARG:HH11	1.28	0.98
1:A:259:ARG:HG2	1:A:259:ARG:HH11	1.28	0.97
1:B:71:LEU:HD21	1:B:85:ASN:HD22	1.29	0.94
1:A:71:LEU:HD21	1:A:85:ASN:HD22	1.35	0.90
1:A:33:GLN:HG3	1:A:69:GLN:HE22	1.36	0.89
1:B:119:THR:OG1	1:B:122:GLU:HG3	1.74	0.88
1:B:33:GLN:HG3	1:B:69:GLN:HE22	1.40	0.86
1:A:119:THR:OG1	1:A:122:GLU:HG3	1.78	0.82
1:B:156:LYS:HG3	1:B:211:LEU:HD22	1.61	0.81
1:A:197:GLN:HG2	1:A:199:ILE:HD13	1.64	0.80
1:B:197:GLN:HG2	1:B:199:ILE:HD13	1.66	0.78
1:A:151:ILE:HB	1:A:152:PRO:HD3	1.64	0.78
1:A:156:LYS:HG3	1:A:211:LEU:HD22	1.67	0.77
1:A:65:GLU:CD	1:A:65:GLU:H	1.95	0.74
1:B:65:GLU:H	1:B:65:GLU:CD	1.96	0.74
1:B:35:PHE:HD2	1:B:36:MET:HE2	1.53	0.74
1:B:151:ILE:HB	1:B:152:PRO:HD3	1.69	0.74
1:B:71:LEU:HD21	1:B:85:ASN:ND2	2.01	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:PHE:HD2	1:A:36:MET:HE2	1.54	0.72
1:B:259:ARG:HG2	1:B:259:ARG:NH1	2.03	0.72
1:B:268:GLU:HG3	1:B:269:PRO:HD2	1.70	0.72
1:A:268:GLU:HG3	1:A:269:PRO:HD2	1.73	0.71
1:A:164:THR:HG22	1:A:165:ASN:OD1	1.91	0.70
1:A:198:TYR:O	1:A:199:ILE:HD12	1.93	0.68
1:B:35:PHE:HD2	1:B:36:MET:CE	2.06	0.68
1:B:94:GLN:NE2	1:B:94:GLN:HA	2.08	0.67
1:A:33:GLN:HG3	1:A:69:GLN:NE2	2.07	0.67
1:A:35:PHE:HD2	1:A:36:MET:CE	2.08	0.67
1:A:151:ILE:HG21	1:A:207:MET:HE1	1.77	0.67
1:B:33:GLN:HG3	1:B:69:GLN:NE2	2.11	0.66
1:B:198:TYR:O	1:B:199:ILE:HD12	1.95	0.66
1:B:164:THR:HG22	1:B:165:ASN:OD1	1.94	0.66
1:A:71:LEU:HD21	1:A:85:ASN:ND2	2.10	0.65
1:A:58:SER:HB3	1:A:140:HIS:CE1	2.32	0.64
1:A:203:ASP:O	1:A:207:MET:HG3	1.98	0.64
1:A:86:GLU:HG2	1:A:114:ALA:HB3	1.79	0.64
1:A:94:GLN:NE2	1:A:94:GLN:HA	2.12	0.64
1:A:46:ARG:HG2	1:A:46:ARG:HH11	1.63	0.63
1:B:268:GLU:CG	1:B:269:PRO:HD2	2.28	0.63
1:A:259:ARG:HH11	1:A:259:ARG:CG	2.08	0.63
1:A:228:ASP:O	1:A:237:GLY:HA3	1.99	0.63
1:B:66:ILE:O	1:B:70:ILE:HG12	2.00	0.62
1:B:183:TRP:HZ2	2:B:401:THA:H5	1.64	0.62
1:B:198:TYR:HE2	3:B:407:HOH:O	1.83	0.62
1:B:228:ASP:O	1:B:237:GLY:HA3	2.00	0.61
1:B:46:ARG:HG2	1:B:46:ARG:HH11	1.65	0.61
1:B:86:GLU:HG2	1:B:114:ALA:HB3	1.83	0.61
1:B:94:GLN:HA	1:B:94:GLN:HE21	1.63	0.61
1:B:126:ARG:HH21	1:B:127:MET:CE	2.13	0.61
1:A:268:GLU:CG	1:A:269:PRO:HD2	2.31	0.60
1:B:5:MET:HE3	1:B:254:ALA:HB2	1.82	0.60
1:A:66:ILE:O	1:A:70:ILE:HG12	2.01	0.60
1:B:219:ASP:O	1:B:220:LEU:HD23	2.02	0.60
1:B:203:ASP:O	1:B:207:MET:HG3	2.02	0.59
1:A:94:GLN:HA	1:A:94:GLN:HE21	1.68	0.59
1:B:228:ASP:HB3	1:B:237:GLY:CA	2.32	0.59
1:A:22:PHE:HD1	1:A:224:MET:HE3	1.65	0.59
1:A:204:LEU:HD23	1:A:288:ILE:HD12	1.85	0.59
1:A:259:ARG:HG2	1:A:259:ARG:NH1	2.04	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:PHE:HD1	1:B:224:MET:HE3	1.68	0.59
1:A:126:ARG:HH21	1:A:127:MET:CE	2.16	0.58
1:A:5:MET:HE3	1:A:254:ALA:HB2	1.85	0.58
1:B:204:LEU:HD23	1:B:288:ILE:HD12	1.85	0.58
1:A:191:PRO:HG3	1:A:247:THR:HG23	1.86	0.57
1:B:270:GLU:HG3	1:B:271:PHE:HD1	1.70	0.57
1:B:124:GLN:HG3	1:B:157:PHE:CE2	2.40	0.57
1:A:219:ASP:O	1:A:220:LEU:HD23	2.05	0.57
1:A:34:GLU:HG2	1:A:38:LYS:HD3	1.87	0.55
1:B:22:PHE:CE2	2:B:401:THA:H131	2.41	0.55
1:B:151:ILE:HG21	1:B:207:MET:HE1	1.88	0.55
1:A:228:ASP:HB3	1:A:237:GLY:CA	2.37	0.55
1:A:68:LEU:HD13	1:A:105:ILE:HD12	1.89	0.54
1:B:126:ARG:HH21	1:B:127:MET:HE3	1.72	0.54
1:B:168:MET:HE3	1:B:290:ILE:HD12	1.89	0.54
1:A:126:ARG:HH21	1:A:127:MET:HE3	1.73	0.54
1:B:19:PHE:O	1:B:22:PHE:HB3	2.07	0.54
1:A:210:ASN:ND2	3:A:401:HOH:O	2.40	0.54
1:B:191:PRO:HG3	1:B:247:THR:HG23	1.90	0.54
1:A:270:GLU:HG3	1:A:271:PHE:HD1	1.73	0.53
1:A:259:ARG:CG	1:A:259:ARG:NH1	2.69	0.52
1:A:36:MET:SD	1:A:40:LEU:HD22	2.50	0.52
1:A:55:LYS:HB3	1:A:136:TRP:CE3	2.45	0.52
1:A:124:GLN:HG3	1:A:157:PHE:CE2	2.45	0.52
1:B:55:LYS:HB3	1:B:136:TRP:CE3	2.45	0.52
1:A:108:LEU:O	1:A:111:VAL:HG23	2.10	0.52
1:B:124:GLN:HG3	1:B:157:PHE:CD2	2.44	0.52
1:B:34:GLU:HG2	1:B:38:LYS:HD3	1.91	0.52
1:A:202:ASP:OD1	1:B:99:LYS:NZ	2.39	0.51
1:B:259:ARG:HH11	1:B:259:ARG:CG	2.10	0.51
1:B:236:ASN:HA	1:B:239:LEU:HD12	1.92	0.51
1:A:187:GLY:C	1:A:189:ARG:H	2.17	0.51
1:B:259:ARG:NH1	1:B:259:ARG:CG	2.71	0.51
1:B:58:SER:HB3	1:B:140:HIS:CE1	2.46	0.51
1:B:190:PHE:HB3	1:B:191:PRO:HD2	1.95	0.49
1:A:168:MET:HE3	1:A:290:ILE:HD12	1.94	0.48
1:A:183:TRP:CZ2	2:A:400:THA:H131	2.48	0.48
1:B:35:PHE:CD2	1:B:36:MET:HE2	2.41	0.48
1:B:187:GLY:C	1:B:189:ARG:H	2.21	0.48
1:A:19:PHE:O	1:A:22:PHE:HB3	2.13	0.48
1:A:236:ASN:HA	1:A:239:LEU:HD12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:GLN:HG3	1:A:157:PHE:CD2	2.48	0.48
1:A:65:GLU:CD	1:A:65:GLU:N	2.69	0.47
1:B:36:MET:SD	1:B:40:LEU:HD22	2.54	0.47
1:B:270:GLU:HG3	1:B:271:PHE:CD1	2.47	0.47
1:A:269:PRO:HA	1:A:272:SER:O	2.14	0.47
1:B:269:PRO:HA	1:B:272:SER:O	2.15	0.47
1:B:8:LEU:HD22	1:B:242:ASP:O	2.15	0.47
1:B:228:ASP:HB3	1:B:237:GLY:N	2.29	0.47
1:B:123:TYR:O	1:B:127:MET:HG2	2.13	0.47
1:B:108:LEU:O	1:B:111:VAL:HG23	2.13	0.47
1:B:268:GLU:CD	1:B:269:PRO:HD2	2.40	0.47
1:A:183:TRP:HZ2	2:A:400:THA:H131	1.80	0.47
1:B:119:THR:O	1:B:120:SER:C	2.57	0.47
1:A:44:ILE:HD13	1:A:74:VAL:HG22	1.97	0.46
1:A:89:GLU:O	1:A:117:LYS:HA	2.15	0.46
1:A:171:ILE:HD13	1:A:287:PHE:CE2	2.51	0.46
1:A:58:SER:CB	1:A:140:HIS:CE1	2.97	0.46
1:A:151:ILE:HG21	1:A:207:MET:CE	2.43	0.46
1:A:268:GLU:CD	1:A:269:PRO:HD2	2.41	0.46
1:A:270:GLU:HG3	1:A:271:PHE:CD1	2.48	0.46
1:B:44:ILE:HD13	1:B:74:VAL:HG22	1.98	0.46
1:B:89:GLU:O	1:B:117:LYS:HA	2.16	0.46
1:B:182:LEU:HD12	1:B:182:LEU:C	2.41	0.45
1:B:182:LEU:HD12	1:B:182:LEU:O	2.16	0.45
1:A:123:TYR:O	1:A:127:MET:HG2	2.16	0.45
1:B:98:TYR:O	1:B:102:VAL:HG23	2.15	0.45
1:A:268:GLU:OE2	1:A:268:GLU:HA	2.15	0.45
1:B:46:ARG:HG2	1:B:46:ARG:NH1	2.31	0.45
1:A:46:ARG:HG2	1:A:46:ARG:NH1	2.29	0.45
1:A:178:GLY:H	1:A:282:ASN:HB3	1.81	0.45
1:A:228:ASP:HB3	1:A:237:GLY:N	2.32	0.45
1:B:151:ILE:HG21	1:B:207:MET:CE	2.47	0.45
1:A:35:PHE:CD2	1:A:36:MET:HE2	2.42	0.45
1:A:187:GLY:C	1:A:189:ARG:N	2.75	0.45
1:B:242:ASP:OD1	1:B:249:ASN:N	2.49	0.44
1:A:242:ASP:OD1	1:A:249:ASN:N	2.48	0.44
1:A:8:LEU:HD22	1:A:242:ASP:O	2.18	0.44
1:B:5:MET:CE	1:B:254:ALA:HB2	2.47	0.44
1:B:248:CYS:O	1:B:249:ASN:C	2.60	0.44
1:A:98:TYR:O	1:A:102:VAL:HG23	2.18	0.44
1:B:65:GLU:CD	1:B:65:GLU:N	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:268:GLU:OE2	1:B:268:GLU:HA	2.17	0.44
1:B:245:THR:O	1:B:246:GLU:C	2.59	0.44
1:A:119:THR:O	1:A:120:SER:C	2.60	0.43
1:B:40:LEU:HB3	1:B:41:PRO:HD3	2.00	0.43
1:B:231:ILE:O	1:B:234:ASN:HB2	2.17	0.43
1:A:222:SER:HB3	1:A:283:ASN:O	2.18	0.43
1:A:262:LEU:HD23	1:A:262:LEU:HA	1.88	0.43
1:B:178:GLY:H	1:B:282:ASN:HB3	1.83	0.43
1:B:156:LYS:HG3	1:B:211:LEU:CD2	2.42	0.43
1:A:5:MET:CE	1:A:254:ALA:HB2	2.48	0.43
1:A:190:PHE:HB3	1:A:191:PRO:HD2	2.00	0.43
1:B:146:TYR:HB3	2:B:401:THA:H1	2.01	0.42
1:B:171:ILE:HD13	1:B:287:PHE:CE2	2.54	0.42
1:A:40:LEU:HB3	1:A:41:PRO:HD3	2.01	0.42
1:B:11:ASP:O	1:B:12:HIS:C	2.62	0.42
1:A:58:SER:HB3	1:A:140:HIS:NE2	2.34	0.42
1:B:89:GLU:CD	1:B:90:PRO:HD2	2.45	0.42
1:A:248:CYS:O	1:A:249:ASN:C	2.62	0.42
1:B:40:LEU:O	1:B:41:PRO:C	2.60	0.42
1:A:182:LEU:O	1:A:182:LEU:HD12	2.20	0.42
1:A:186:TYR:O	1:A:187:GLY:C	2.63	0.42
1:A:231:ILE:O	1:A:234:ASN:HB2	2.20	0.41
1:B:227:SER:C	1:B:229:CYS:N	2.78	0.41
1:A:40:LEU:O	1:A:41:PRO:C	2.63	0.41
1:A:204:LEU:HD12	1:A:207:MET:HE3	2.01	0.41
1:A:11:ASP:O	1:A:12:HIS:C	2.63	0.41
1:A:223:THR:HB	1:A:280:LEU:HB3	2.03	0.41
1:A:229:CYS:SG	1:A:240:LEU:HB2	2.60	0.41
1:B:66:ILE:HD13	1:B:66:ILE:HA	1.90	0.41
1:A:12:HIS:O	1:A:16:VAL:HG23	2.20	0.41
1:B:68:LEU:HD13	1:B:105:ILE:HD12	2.02	0.41
1:B:107:ASN:O	1:B:108:LEU:HD23	2.20	0.41
1:A:49:ASP:C	1:A:50:THR:HG23	2.46	0.41
1:A:89:GLU:CD	1:A:90:PRO:HD2	2.46	0.41
1:A:187:GLY:O	1:A:189:ARG:N	2.54	0.41
1:A:245:THR:O	1:A:246:GLU:C	2.62	0.41
1:B:89:GLU:OE2	1:B:90:PRO:HD2	2.21	0.41
1:B:151:ILE:HB	1:B:152:PRO:CD	2.45	0.41
1:A:198:TYR:O	1:A:199:ILE:CD1	2.65	0.41
1:A:227:SER:C	1:A:229:CYS:N	2.78	0.41
1:B:95:ILE:O	1:B:99:LYS:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:SER:HB3	1:B:283:ASN:O	2.20	0.40
1:A:69:GLN:O	1:A:72:SER:HB3	2.20	0.40
1:A:151:ILE:HB	1:A:152:PRO:CD	2.42	0.40
1:B:233:GLY:O	1:B:234:ASN:C	2.64	0.40
1:A:48:GLY:HA3	1:A:78:TYR:CZ	2.56	0.40
1:B:142:ILE:HD12	1:B:171:ILE:HD12	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	286/292 (98%)	257 (90%)	23 (8%)	6 (2%)	5	25
1	B	286/292 (98%)	259 (91%)	21 (7%)	6 (2%)	5	25
All	All	572/584 (98%)	516 (90%)	44 (8%)	12 (2%)	5	25

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	107	ASN
1	B	107	ASN
1	A	109	GLU
1	B	109	GLU
1	A	12	HIS
1	A	188	SER
1	A	252	ALA
1	B	12	HIS
1	B	188	SER
1	B	180	ASP
1	B	252	ALA
1	A	276	GLU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	234/260 (90%)	228 (97%)	6 (3%)	40	70
1	B	234/260 (90%)	225 (96%)	9 (4%)	29	61
All	All	468/520 (90%)	453 (97%)	15 (3%)	34	65

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	ARG
1	A	67	ASP
1	A	199	ILE
1	A	204	LEU
1	A	234	ASN
1	A	242	ASP
1	B	46	ARG
1	B	65	GLU
1	B	67	ASP
1	B	105	ILE
1	B	156	LYS
1	B	199	ILE
1	B	204	LEU
1	B	234	ASN
1	B	242	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	HIS
1	A	69	GLN
1	A	85	ASN
1	A	94	GLN
1	A	110	ASN
1	A	197	GLN
1	A	206	GLN

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Mol	Chain	Res	Type
1	B	29	HIS
1	B	69	GLN
1	B	85	ASN
1	B	94	GLN
1	B	110	ASN
1	B	143	GLN
1	B	197	GLN
1	B	206	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	THA	A	400	-	17,17,17	6.77	14 (82%)	22,24,24	3.01	13 (59%)
2	THA	B	401	-	17,17,17	6.84	13 (76%)	22,24,24	3.59	12 (54%)

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	THA	A	400	-	-	-	0/3/3/3
2	THA	B	401	-	-	-	0/3/3/3

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	THA	C8-N7	16.87	1.53	1.32
2	A	400	THA	C8-N7	13.13	1.48	1.32
2	A	400	THA	C1-C2	11.13	1.59	1.36
2	B	401	THA	C6-C5	11.13	1.59	1.36
2	A	400	THA	C6-C5	10.38	1.58	1.36
2	B	401	THA	C1-C2	10.05	1.57	1.36
2	A	400	THA	C9-C8	9.67	1.55	1.40
2	B	401	THA	C9-C8	8.22	1.53	1.40
2	A	400	THA	C2-C3	7.80	1.54	1.41
2	B	401	THA	C2-C3	7.72	1.54	1.41
2	A	400	THA	C6-C1	7.70	1.55	1.38
2	B	401	THA	C5-C4	6.84	1.55	1.42
2	A	400	THA	C4-C3	6.23	1.52	1.42
2	A	400	THA	C5-C4	5.85	1.54	1.42
2	B	401	THA	C6-C1	5.79	1.51	1.38
2	A	400	THA	C10-N15	5.10	1.50	1.36
2	A	400	THA	C10-C4	4.50	1.50	1.44
2	B	401	THA	C3-N7	4.42	1.44	1.37
2	B	401	THA	C10-C4	4.00	1.49	1.44
2	B	401	THA	C4-C3	3.94	1.48	1.42
2	A	400	THA	C14-C9	-3.87	1.45	1.51
2	A	400	THA	C11-C8	-3.57	1.45	1.50
2	B	401	THA	C10-N15	3.47	1.46	1.36
2	A	400	THA	C12-C11	-2.29	1.43	1.51
2	A	400	THA	C10-C9	2.24	1.49	1.41
2	B	401	THA	C11-C8	-2.21	1.47	1.50
2	B	401	THA	C14-C9	-2.21	1.48	1.51

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	THA	C9-C8-N7	-9.20	117.15	123.66
2	A	400	THA	C9-C8-N7	-7.61	118.27	123.66
2	B	401	THA	C6-C1-C2	-5.87	112.55	120.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	THA	C1-C2-C3	-5.84	112.10	120.09
2	B	401	THA	C1-C6-C5	-5.61	112.89	120.40
2	B	401	THA	C8-N7-C3	4.38	122.86	117.67
2	A	400	THA	C2-C3-C4	4.30	123.76	119.13
2	A	400	THA	C1-C6-C5	-4.20	114.78	120.40
2	A	400	THA	C10-C4-C3	4.08	120.50	118.23
2	A	400	THA	C8-N7-C3	3.84	122.22	117.67
2	B	401	THA	C11-C8-N7	3.77	122.58	116.75
2	A	400	THA	C1-C2-C3	-3.33	115.54	120.09
2	B	401	THA	C4-C3-N7	-3.29	119.31	122.80
2	B	401	THA	C12-C11-C8	3.28	118.59	113.48
2	B	401	THA	C13-C14-C9	3.14	119.22	112.84
2	A	400	THA	C6-C1-C2	-3.10	116.25	120.40
2	B	401	THA	C10-C4-C3	3.04	119.93	118.23
2	B	401	THA	C2-C3-N7	2.97	123.03	118.69
2	A	400	THA	C12-C11-C8	2.84	117.90	113.48
2	A	400	THA	C12-C13-C14	2.79	124.37	112.39
2	A	400	THA	C14-C9-C8	-2.79	118.28	120.90
2	A	400	THA	C2-C3-N7	-2.49	115.06	118.69
2	A	400	THA	C6-C5-C4	-2.37	117.71	120.91
2	B	401	THA	C12-C13-C14	2.03	121.12	112.39
2	A	400	THA	C13-C14-C9	2.03	116.96	112.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	400	THA	2	0
2	B	401	THA	3	0

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.