



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:01 PM GMT

PDB ID : 1W76  
Title : ORTHORHOMBIC FORM OF TORPEDO CALIFORNICA ACETYL-  
CHOLINESTERASE (ACHE) COMPLEXED WITH BIS-ACTING GALAN-  
THAMINE DERIVATIVE  
Authors : Greenblatt, H.M.; Guillou, C.; Guenard, D.; Badet, B.; Thal, C.; Silman, I.;  
Sussman, J.L.  
Deposited on : 2004-08-30  
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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

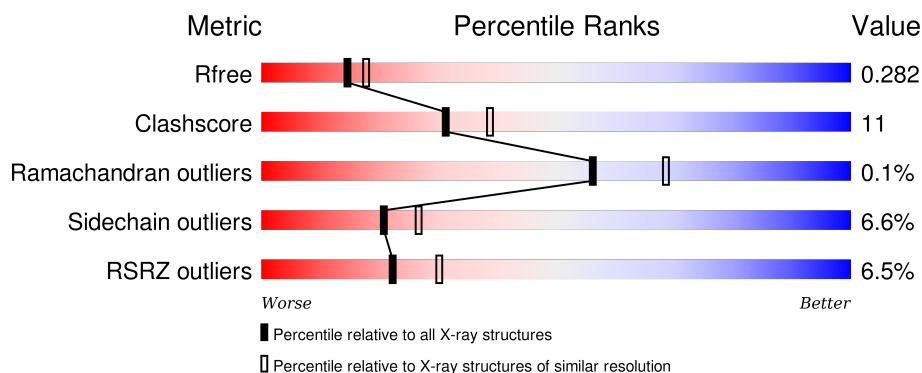
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	543	<div> <div>6%</div> <div>73%</div> <div>20%</div> <div>.</div> <div>.</div> </div>
1	B	543	<div> <div>6%</div> <div>72%</div> <div>22%</div> <div>.</div> <div>.</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8451 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 ACETYLCHOLINESTERASE.

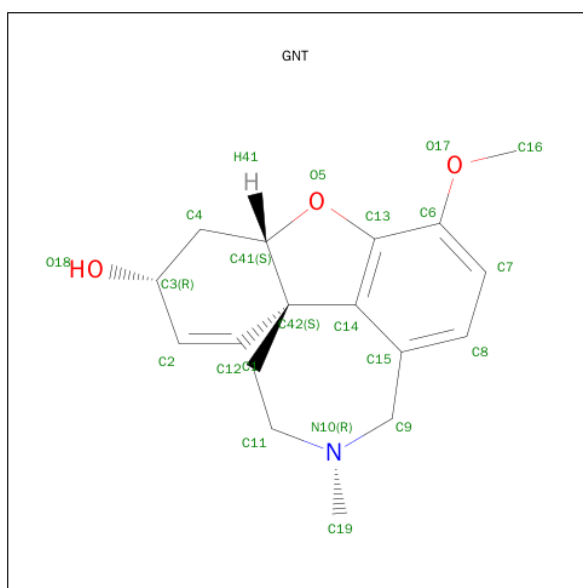
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	522	Total	C	N	O	S	0	0	0
			4118	2654	692	750	22			
1	B	522	Total	C	N	O	S	0	0	0
			4120	2655	692	751	22			

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is (-)-GALANTHAMINE (three-letter code: GNT) (formula:  $C_{17}H_{21}NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			21	17	1	3		
3	B	1	Total	C	N	O	0	0
			21	17	1	3		

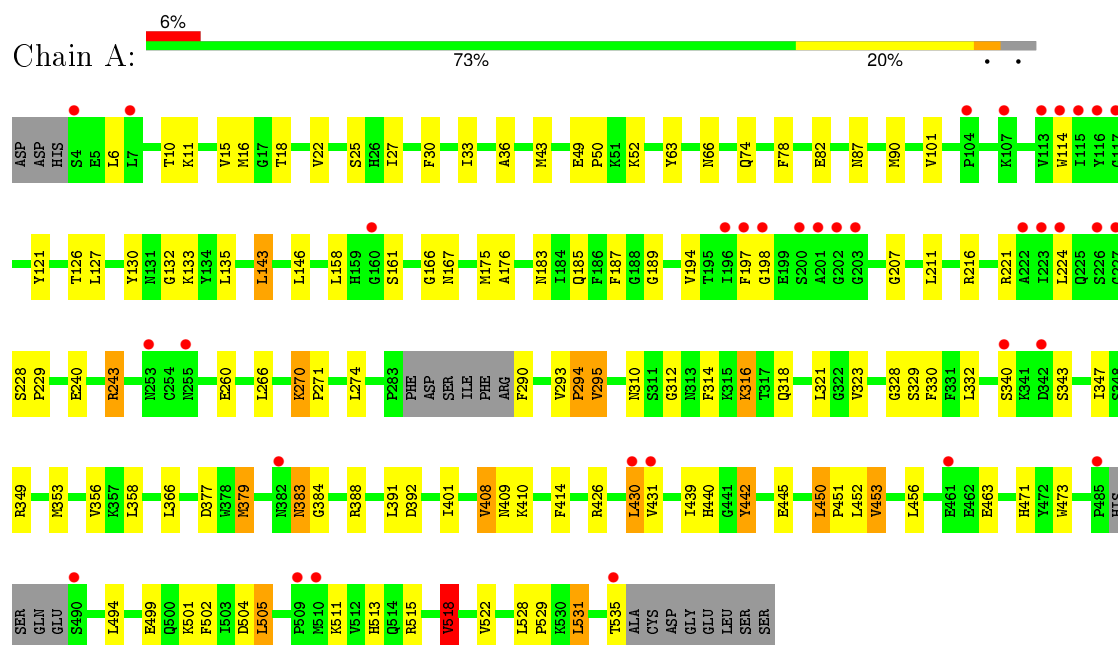
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	54	Total	O	0	0
			54	54		
4	B	61	Total	O	0	0
			61	61		

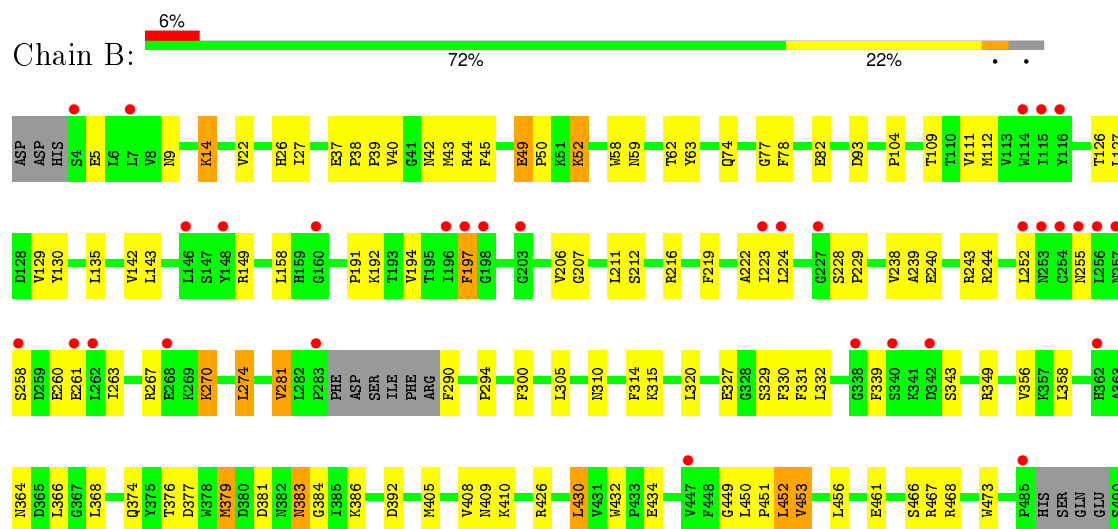
### 3 Residue-property plots

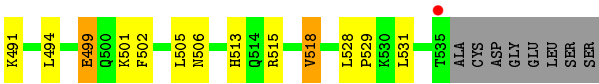
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: ACETYLCHOLINESTERASE



#### • Molecule 1: ACETYLCHOLINESTERASE





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.22Å 105.25Å 150.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.17 – 2.30 34.17 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.3 (34.17-2.30) 98.3 (34.17-2.30)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.70 (at 2.31Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.236 , 0.283 0.238 , 0.282	Depositor DCC
$R_{free}$ test set	3188 reflections (4.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.0	Xtriage
Anisotropy	0.808	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 38.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 63895 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8451	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.64 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.9791e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.76	0/4236	0.87	4/5752 (0.1%)
1	B	0.75	0/4238	0.84	2/5754 (0.0%)
All	All	0.76	0/8474	0.85	6/11506 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	518	VAL	CB-CA-C	-6.41	99.21	111.40
1	B	491	LYS	N-CA-C	6.32	128.05	111.00
1	A	328	GLY	N-CA-C	5.75	127.49	113.10
1	B	494	LEU	CA-CB-CG	5.56	128.09	115.30
1	A	494	LEU	CA-CB-CG	5.35	127.60	115.30
1	A	295	VAL	CB-CA-C	-5.18	101.55	111.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	442	TYR	Sidechain



## 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	4118	0	3962	86	0
1	B	4120	0	3967	93	0
2	A	28	0	26	0	0
2	B	28	0	26	0	0
3	A	21	0	21	4	0
3	B	21	0	21	2	0
4	A	54	0	0	3	0
4	B	61	0	0	2	0
All	All	8451	0	8023	177	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 11.

All (177) 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:270:LYS:HA	1:B:270:LYS:HE3	1.31	1.11
1:A:270:LYS:HE3	1:A:271:PRO:HD3	1.38	1.05
1:B:499:GLU:HG2	1:B:501:LYS:HE3	1.49	0.91
1:A:260:GLU:H	1:A:260:GLU:CD	1.76	0.88
1:B:260:GLU:H	1:B:260:GLU:CD	1.85	0.79
1:B:194:VAL:CG2	1:B:219:PHE:HA	2.14	0.78
1:A:310:ASN:OD1	1:A:410:LYS:HE3	1.84	0.78
1:B:270:LYS:CE	1:B:270:LYS:HA	2.13	0.74
1:B:383:ASN:HD22	1:B:383:ASN:C	1.93	0.71
1:A:329:SER:HB3	1:A:392:ASP:OD2	1.90	0.71
1:B:258:SER:OG	1:B:261:GLU:HG2	1.92	0.70
1:A:452:LEU:HD22	1:A:463:GLU:HG3	1.74	0.69
1:A:260:GLU:CD	1:A:260:GLU:N	2.47	0.68
1:B:366:LEU:CD2	1:B:531:LEU:HD11	2.24	0.67
1:B:453:VAL:HG22	1:B:456:LEU:HG	1.76	0.66
1:B:78:PHE:O	1:B:82:GLU:HB2	1.96	0.65
1:B:258:SER:H	1:B:261:GLU:HG3	1.61	0.65
1:B:450:LEU:O	1:B:453:VAL:HG13	1.95	0.65
1:A:36:ALA:HB2	1:A:175:MET:HE2	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:VAL:HG22	1:A:133:LYS:HD2	1.80	0.64
1:A:377:ASP:OD1	1:A:379:MET:HG2	1.99	0.63
1:B:310:ASN:OD1	1:B:410:LYS:HE3	1.99	0.63
1:A:135:LEU:HD23	1:A:143:LEU:HD13	1.81	0.62
1:A:78:PHE:CZ	1:A:431:VAL:HG23	2.33	0.62
1:B:228:SER:HB2	1:B:229:PRO:HD2	1.82	0.62
1:B:515:ARG:O	1:B:518:VAL:HG22	2.00	0.61
1:A:383:ASN:HD22	1:A:383:ASN:C	2.04	0.61
1:A:515:ARG:HB3	1:A:518:VAL:HG22	1.83	0.60
1:A:518:VAL:O	1:A:522:VAL:HG23	2.01	0.60
1:B:22:VAL:HG21	1:B:27:ILE:HG12	1.83	0.60
1:A:471:HIS:HB3	4:A:2049:HOH:O	2.01	0.60
1:A:63:TYR:CD1	1:A:126:THR:HG22	2.36	0.60
1:A:207:GLY:HA3	1:A:229:PRO:HD3	1.84	0.59
1:B:194:VAL:HG22	1:B:219:PHE:HA	1.83	0.59
1:B:206:VAL:CG1	1:B:222:ALA:HB1	2.32	0.59
1:B:366:LEU:HD21	1:B:531:LEU:HD11	1.83	0.59
1:B:528:LEU:HB3	1:B:529:PRO:HD3	1.85	0.59
1:B:349:ARG:HH12	1:B:376:THR:HG23	1.68	0.59
1:B:224:LEU:N	1:B:224:LEU:HD12	2.17	0.59
1:B:252:LEU:HD11	1:B:274:LEU:HD12	1.84	0.59
1:A:312:GLY:O	1:A:316:LYS:NZ	2.36	0.58
1:B:22:VAL:CG2	1:B:27:ILE:HG12	2.34	0.57
1:B:135:LEU:HD23	1:B:143:LEU:HD13	1.85	0.57
1:A:499:GLU:HB3	1:A:501:LYS:HG3	1.87	0.57
1:A:11:LYS:NZ	4:A:2001:HOH:O	2.38	0.57
1:B:44:ARG:O	1:B:45:PHE:HB2	2.05	0.56
1:A:426:ARG:CZ	1:A:430:LEU:HD12	2.36	0.56
1:A:127:LEU:HD12	1:A:130:TYR:CE2	2.41	0.56
1:B:452:LEU:HD13	1:B:467:ARG:NH2	2.21	0.56
1:B:63:TYR:CD1	1:B:126:THR:HG22	2.41	0.56
1:B:49:GLU:HG3	1:B:50:PRO:HD2	1.87	0.56
1:B:255:ASN:ND2	1:B:261:GLU:HB3	2.21	0.55
1:B:260:GLU:N	1:B:260:GLU:CD	2.57	0.55
1:A:290:PHE:CZ	3:A:1538:GNT:H7	2.42	0.55
1:A:349:ARG:O	1:A:353:MET:HG2	2.07	0.55
1:B:127:LEU:HD12	1:B:130:TYR:CE2	2.42	0.55
1:B:9:ASN:ND2	1:B:14:LYS:HD3	2.22	0.54
1:A:347:ILE:HG12	1:A:388:ARG:HB2	1.89	0.54
1:B:290:PHE:CZ	3:B:1538:GNT:H7	2.43	0.54
1:A:50:PRO:HA	1:A:175:MET:HE3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:430:LEU:HD13	1:B:432:TRP:H	1.71	0.54
1:A:270:LYS:HE3	1:A:271:PRO:CD	2.26	0.54
1:A:383:ASN:HD22	1:A:384:GLY:N	2.06	0.53
1:B:332:LEU:HD13	1:B:339:PHE:CZ	2.44	0.52
1:B:5:GLU:OE2	1:B:104:PRO:HA	2.08	0.52
1:A:531:LEU:C	1:A:531:LEU:HD12	2.30	0.52
1:A:74:GLN:NE2	4:A:2012:HOH:O	2.41	0.52
1:B:281:VAL:O	1:B:281:VAL:HG23	2.08	0.52
1:B:77:GLY:N	1:B:82:GLU:OE1	2.39	0.52
1:B:329:SER:HB3	1:B:392:ASP:OD2	2.09	0.52
1:A:240:GLU:OE2	1:A:243:ARG:NH1	2.43	0.52
1:B:240:GLU:OE1	1:B:240:GLU:HA	2.09	0.52
1:A:6:LEU:HD13	1:A:18:THR:HA	1.92	0.52
1:A:224:LEU:HD12	1:A:224:LEU:N	2.25	0.51
1:A:453:VAL:HG13	1:A:456:LEU:HD12	1.92	0.51
1:B:37:GLU:OE2	1:B:52:LYS:N	2.35	0.51
1:A:515:ARG:O	1:A:518:VAL:HG22	2.11	0.51
1:B:506:ASN:HB2	4:B:2049:HOH:O	2.11	0.51
1:A:30:PHE:HB3	1:A:33:ILE:HD11	1.92	0.50
1:A:515:ARG:HB3	1:A:518:VAL:CG2	2.41	0.50
1:B:383:ASN:HD22	1:B:384:GLY:N	2.09	0.50
1:B:430:LEU:CD1	1:B:432:TRP:HB2	2.42	0.50
1:B:377:ASP:OD1	1:B:379:MET:HG3	2.11	0.50
1:A:450:LEU:N	1:A:451:PRO:CD	2.75	0.49
1:A:27:ILE:HD11	1:A:133:LYS:HB2	1.95	0.49
1:A:211:LEU:HD23	1:A:314:PHE:HB3	1.94	0.49
1:A:366:LEU:HD21	1:B:531:LEU:HD12	1.94	0.48
1:B:40:VAL:O	1:B:43:MET:HB2	2.12	0.48
1:B:320:LEU:HD23	1:B:320:LEU:C	2.33	0.48
1:A:439:ILE:HG22	1:A:440:HIS:N	2.28	0.48
1:A:340:SER:HB2	1:A:343:SER:HB3	1.95	0.48
1:A:22:VAL:HG21	1:A:27:ILE:HG12	1.95	0.48
1:B:426:ARG:NH1	1:B:434:GLU:HA	2.29	0.48
1:B:270:LYS:CA	1:B:270:LYS:HE3	2.22	0.48
1:B:349:ARG:NH1	1:B:376:THR:HG23	2.28	0.48
1:B:197:PHE:CB	1:B:223:ILE:HB	2.43	0.48
1:A:453:VAL:HG22	1:A:456:LEU:HG	1.96	0.47
1:B:405:MET:O	1:B:408:VAL:HG12	2.14	0.47
1:A:504:ASP:OD2	1:A:513:HIS:NE2	2.41	0.47
1:A:132:GLY:HA3	1:A:143:LEU:HD22	1.96	0.47
1:B:383:ASN:ND2	1:B:383:ASN:C	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:LEU:CD2	1:A:463:GLU:HG3	2.41	0.47
1:A:27:ILE:HD11	1:A:133:LYS:CB	2.45	0.47
1:B:191:PRO:HG2	1:B:192:LYS:HE2	1.97	0.47
1:A:505:LEU:HA	1:A:505:LEU:HD12	1.76	0.46
1:A:10:THR:HB	1:A:183:ASN:OD1	2.16	0.46
1:A:266:LEU:HA	1:A:266:LEU:HD23	1.66	0.46
1:A:228:SER:HB2	1:A:229:PRO:HD2	1.97	0.46
1:B:426:ARG:CZ	1:B:434:GLU:HA	2.46	0.46
1:B:240:GLU:OE2	1:B:243:ARG:NH1	2.49	0.46
1:A:114:TRP:CZ3	1:A:198:GLY:HA2	2.51	0.46
1:A:36:ALA:CB	1:A:175:MET:CE	2.94	0.45
1:B:216:ARG:NH1	1:B:314:PHE:HA	2.32	0.45
1:B:42:ASN:O	1:B:267:ARG:NH2	2.50	0.45
1:A:323:VAL:HG21	1:A:401:ILE:HG12	1.99	0.45
1:B:158:LEU:HD12	1:B:263:ILE:HD11	1.98	0.45
1:B:194:VAL:HG22	4:B:2033:HOH:O	2.16	0.45
1:A:332:LEU:HD11	1:A:392:ASP:HA	1.99	0.45
1:B:450:LEU:N	1:B:451:PRO:CD	2.79	0.45
1:B:515:ARG:HB3	1:B:518:VAL:HG22	1.99	0.45
1:A:270:LYS:HA	1:A:270:LYS:HE3	1.97	0.45
1:B:26:HIS:O	1:B:27:ILE:HG23	2.16	0.45
1:B:216:ARG:HG2	1:B:315:LYS:HB2	1.98	0.45
1:B:109:THR:CG2	1:B:142:VAL:HG23	2.47	0.45
1:A:101:VAL:HG11	1:A:187:PHE:O	2.17	0.45
1:B:207:GLY:HA3	1:B:229:PRO:HD3	1.99	0.45
1:B:528:LEU:N	1:B:529:PRO:CD	2.80	0.45
1:B:408:VAL:CG1	1:B:409:ASN:N	2.80	0.45
1:A:430:LEU:HD21	1:A:442:TYR:CD2	2.52	0.44
1:A:321:LEU:HD11	1:A:408:VAL:HG23	2.00	0.44
1:B:453:VAL:HG22	1:B:453:VAL:O	2.16	0.44
1:A:366:LEU:HD21	1:B:531:LEU:CD1	2.48	0.44
1:B:381:ASP:N	1:B:381:ASP:OD1	2.49	0.44
1:A:121:TYR:OH	3:A:1538:GNT:H91	2.18	0.43
1:A:121:TYR:OH	3:A:1538:GNT:H8	2.18	0.43
1:B:244:ARG:HB3	1:B:281:VAL:HG21	2.00	0.43
1:A:321:LEU:HD21	1:A:408:VAL:HG23	1.99	0.43
1:A:528:LEU:N	1:A:529:PRO:CD	2.81	0.43
1:B:364:ASN:O	1:B:368:LEU:HG	2.17	0.43
1:B:502:PHE:CZ	1:B:513:HIS:HB2	2.54	0.43
1:B:327:GLU:OE1	1:B:327:GLU:HA	2.19	0.43
1:A:221:ARG:NH1	1:A:318:GLN:OE1	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:PRO:HG3	1:B:93:ASP:OD1	2.19	0.43
1:A:316:LYS:HG3	1:A:414:PHE:O	2.20	0.42
1:B:383:ASN:ND2	1:B:386:LYS:H	2.18	0.42
1:A:36:ALA:HB2	1:A:175:MET:CE	2.47	0.42
1:A:408:VAL:CG1	1:A:409:ASN:N	2.81	0.42
1:B:332:LEU:HD11	1:B:392:ASP:N	2.34	0.42
1:A:502:PHE:CZ	1:A:513:HIS:HB2	2.54	0.42
1:A:146:LEU:HD22	1:A:176:ALA:HB3	2.02	0.42
1:A:87:ASN:OD1	1:A:87:ASN:N	2.50	0.42
1:B:331:PHE:CZ	3:B:1538:GNT:H163	2.55	0.42
1:A:310:ASN:OD1	1:A:410:LYS:CE	2.62	0.42
1:A:66:ASN:O	1:A:90:MET:HA	2.20	0.42
1:A:78:PHE:HZ	1:A:431:VAL:HG23	1.81	0.41
1:B:112:MET:HB2	1:B:143:LEU:HD12	2.02	0.41
1:A:290:PHE:CZ	3:A:1538:GNT:H162	2.54	0.41
1:B:44:ARG:O	1:B:45:PHE:CB	2.67	0.41
1:B:111:VAL:HB	1:B:194:VAL:HG12	2.02	0.41
1:B:408:VAL:HG13	1:B:409:ASN:N	2.36	0.41
1:B:449:GLY:HA2	1:B:466:SER:OG	2.20	0.41
1:A:531:LEU:C	1:A:531:LEU:CD1	2.88	0.41
1:A:408:VAL:HG12	1:A:409:ASN:N	2.34	0.41
1:B:58:TRP:CD1	1:B:59:ASN:O	2.74	0.41
1:A:158:LEU:O	1:A:161:SER:HB3	2.21	0.41
1:A:185:GLN:HA	1:A:189:GLY:O	2.21	0.41
1:A:293:VAL:HB	1:A:294:PRO:HD2	2.02	0.41
1:B:258:SER:N	1:B:261:GLU:HG3	2.30	0.41
1:A:216:ARG:NH1	1:A:314:PHE:HA	2.35	0.41
1:A:426:ARG:NH2	1:A:430:LEU:HD12	2.36	0.41
1:B:212:SER:HB2	1:B:300:PHE:CD1	2.56	0.41
1:B:197:PHE:HB3	1:B:223:ILE:HB	2.03	0.40
1:A:166:GLY:O	1:A:167:ASN:HB2	2.21	0.40
1:B:211:LEU:HD13	1:B:305:LEU:HD22	2.02	0.40
1:B:238:VAL:HG23	1:B:239:ALA:N	2.35	0.40
1:B:39:PRO:HG3	1:B:149:ARG:HD3	2.03	0.40
1:A:445:GLU:O	1:A:451:PRO: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	A	516/543 (95%)	485 (94%)	30 (6%)	1 (0%)	52	64
1	B	516/543 (95%)	483 (94%)	33 (6%)	0	100	100
All	All	1032/1086 (95%)	968 (94%)	63 (6%)	1 (0%)	56	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	25	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	440/474 (93%)	409 (93%)	31 (7%)	19	23
1	B	441/474 (93%)	414 (94%)	27 (6%)	23	30
All	All	881/948 (93%)	823 (93%)	58 (7%)	21	27

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	VAL
1	A	16	MET
1	A	43	MET
1	A	49	GLU
1	A	52	LYS

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Mol	Chain	Res	Type
1	A	82	GLU
1	A	143	LEU
1	A	194	VAL
1	A	197	PHE
1	A	243	ARG
1	A	270	LYS
1	A	274	LEU
1	A	294	PRO
1	A	295	VAL
1	A	316	LYS
1	A	330	PHE
1	A	356	VAL
1	A	358	LEU
1	A	379	MET
1	A	383	ASN
1	A	391	LEU
1	A	408	VAL
1	A	430	LEU
1	A	450	LEU
1	A	453	VAL
1	A	473	TRP
1	A	505	LEU
1	A	511	LYS
1	A	518	VAL
1	A	531	LEU
1	A	535	THR
1	B	14	LYS
1	B	49	GLU
1	B	52	LYS
1	B	62	THR
1	B	74	GLN
1	B	129	VAL
1	B	197	PHE
1	B	270	LYS
1	B	274	LEU
1	B	281	VAL
1	B	294	PRO
1	B	330	PHE
1	B	343	SER
1	B	356	VAL
1	B	358	LEU
1	B	374	GLN

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Mol	Chain	Res	Type
1	B	379	MET
1	B	383	ASN
1	B	430	LEU
1	B	452	LEU
1	B	453	VAL
1	B	461	GLU
1	B	468	ARG
1	B	473	TRP
1	B	499	GLU
1	B	505	LEU
1	B	518	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	ASN
1	A	68	GLN
1	A	257	ASN
1	A	362	HIS
1	A	383	ASN
1	A	457	ASN
1	B	9	ASN
1	B	68	GLN
1	B	374	GLN
1	B	383	ASN

### 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 carbohydrates in this entry.



## 5.6 Ligand geometry

6 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	NAG	A	1536	1	14,14,15	0.86	0	15,19,21	1.16	2 (13%)
2	NAG	A	1537	1	14,14,15	0.77	0	15,19,21	0.92	0
3	GNT	A	1538	-	23,24,24	2.85	10 (43%)	31,37,37	2.49	10 (32%)
2	NAG	B	1536	1	14,14,15	0.66	0	15,19,21	0.95	1 (6%)
2	NAG	B	1537	1	14,14,15	0.75	0	15,19,21	1.07	1 (6%)
3	GNT	B	1538	-	23,24,24	2.98	8 (34%)	31,37,37	2.67	11 (35%)

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	NAG	A	1536	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1537	1	-	0/6/23/26	0/1/1/1
3	GNT	A	1538	-	-	0/2/38/38	0/4/4/4
2	NAG	B	1536	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1537	1	-	0/6/23/26	0/1/1/1
3	GNT	B	1538	-	-	0/2/38/38	0/4/4/4

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1538	GNT	C42-C14	-4.90	1.47	1.52
3	A	1538	GNT	C42-C14	-3.88	1.48	1.52
3	A	1538	GNT	C8-C7	2.20	1.42	1.38
3	A	1538	GNT	O5-C13	2.39	1.41	1.38
3	A	1538	GNT	C12-C11	2.58	1.56	1.52
3	B	1538	GNT	C8-C7	2.61	1.43	1.38
3	A	1538	GNT	C13-C14	2.66	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1538	GNT	C2-C1	3.02	1.37	1.32
3	B	1538	GNT	C13-C14	3.12	1.43	1.38
3	B	1538	GNT	C12-C11	3.20	1.57	1.52
3	B	1538	GNT	C3-C2	3.43	1.54	1.49
3	A	1538	GNT	O17-C6	4.01	1.43	1.37
3	B	1538	GNT	O17-C6	4.02	1.43	1.37
3	A	1538	GNT	C3-C2	4.09	1.55	1.49
3	B	1538	GNT	C42-C1	4.44	1.56	1.51
3	A	1538	GNT	C42-C1	5.28	1.57	1.51
3	A	1538	GNT	C4-C3	8.13	1.60	1.52
3	B	1538	GNT	C4-C3	9.02	1.61	1.52

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1538	GNT	C4-C41-C42	-6.70	110.89	115.22
3	A	1538	GNT	C4-C41-C42	-5.84	111.44	115.22
3	B	1538	GNT	C14-C42-C41	-4.93	97.21	99.97
3	A	1538	GNT	C14-C42-C41	-4.85	97.25	99.97
3	B	1538	GNT	C41-C4-C3	-4.61	106.67	113.16
3	B	1538	GNT	O18-C3-C2	-4.21	103.07	109.94
3	A	1538	GNT	C41-C4-C3	-4.17	107.28	113.16
3	B	1538	GNT	C13-O5-C41	-4.09	99.52	105.34
3	A	1538	GNT	C13-O5-C41	-4.07	99.54	105.34
3	B	1538	GNT	C12-C42-C1	-3.96	107.24	112.21
3	A	1538	GNT	O18-C3-C2	-3.67	103.95	109.94
3	A	1538	GNT	C12-C42-C1	-3.66	107.61	112.21
2	B	1536	NAG	C2-N2-C7	-3.07	119.09	123.04
3	B	1538	GNT	C41-C42-C1	-2.44	109.47	111.05
2	A	1536	NAG	C4-C3-C2	-2.15	107.89	111.23
3	A	1538	GNT	C41-C42-C1	-2.14	109.66	111.05
2	A	1536	NAG	C2-N2-C7	-2.12	120.31	123.04
3	B	1538	GNT	C7-C6-C13	-2.06	116.72	120.33
3	B	1538	GNT	C12-C42-C14	2.29	118.07	114.51
3	A	1538	GNT	C12-C42-C14	2.30	118.09	114.51
2	B	1537	NAG	C1-O5-C5	2.65	115.61	112.25
3	A	1538	GNT	C12-C42-C41	3.03	115.44	110.68
3	B	1538	GNT	C12-C42-C41	3.33	115.91	110.68
3	A	1538	GNT	O5-C41-C4	5.50	115.31	109.72
3	B	1538	GNT	O5-C41-C4	5.59	115.40	109.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1538	GNT	4	0
3	B	1538	GNT	2	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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	522/543 (96%)	0.30	35 (6%)	21 29	23, 42, 60, 75	0
1	B	522/543 (96%)	0.28	33 (6%)	23 31	26, 42, 62, 79	0
All	All	1044/1086 (96%)	0.29	68 (6%)	22 30	23, 42, 62, 79	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	535	THR	6.7
1	B	257	ASN	6.1
1	A	4	SER	5.0
1	A	115	ILE	4.9
1	B	362	HIS	4.6
1	B	342	ASP	4.6
1	B	255	ASN	4.5
1	B	4	SER	4.4
1	B	160	GLY	4.1
1	B	262	LEU	4.1
1	B	258	SER	4.1
1	B	254	CYS	4.0
1	A	485	PRO	3.9
1	B	115	ILE	3.9
1	B	252	LEU	3.8
1	B	256	LEU	3.8
1	A	223	ILE	3.7
1	A	490	SER	3.5
1	A	224	LEU	3.4
1	B	261	GLU	3.4
1	A	253	ASN	3.3
1	A	509	PRO	3.3
1	A	114	TRP	3.2
1	B	114	TRP	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	104	PRO	3.0
1	A	202	GLY	2.9
1	A	197	PHE	2.9
1	B	197	PHE	2.8
1	A	201	ALA	2.8
1	A	342	ASP	2.8
1	A	198	GLY	2.8
1	A	430	LEU	2.7
1	A	255	ASN	2.7
1	A	227	GLY	2.7
1	B	340	SER	2.6
1	A	226	SER	2.6
1	B	338	GLY	2.5
1	B	116	TYR	2.5
1	A	510	MET	2.5
1	A	116	TYR	2.5
1	B	196	ILE	2.4
1	B	146	LEU	2.4
1	A	107	LYS	2.4
1	A	431	VAL	2.4
1	A	340	SER	2.3
1	B	283	PRO	2.3
1	B	203	GLY	2.3
1	A	196	ILE	2.3
1	B	224	LEU	2.3
1	A	7	LEU	2.2
1	A	200	SER	2.2
1	B	253	ASN	2.2
1	B	198	GLY	2.2
1	B	227	GLY	2.2
1	A	382	ASN	2.2
1	B	7	LEU	2.2
1	A	113	VAL	2.1
1	A	203	GLY	2.1
1	A	461	GLU	2.1
1	B	268	GLU	2.1
1	B	485	PRO	2.1
1	B	447	VAL	2.1
1	A	117	GLY	2.1
1	A	160	GLY	2.1
1	A	222	ALA	2.1
1	B	223	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	148	TYR	2.0
1	A	535	THR	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	GNT	A	1538	21/21	0.85	0.23	0.79	40,45,48,50	0
3	GNT	B	1538	21/21	0.90	0.18	0.34	40,44,47,48	0
2	NAG	B	1537	14/15	0.86	0.18	-	52,58,62,62	0
2	NAG	A	1537	14/15	0.82	0.19	-	50,60,64,64	0
2	NAG	A	1536	14/15	0.80	0.26	-	61,63,65,66	0
2	NAG	B	1536	14/15	0.81	0.29	-	63,65,66,70	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.