



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 9, 2024 – 12:20 pm GMT

PDB ID : 1W75
Title : Native Orthorhombic form of Torpedo californica acetylcholinesterase (AChE)
Authors : Greenblatt, H.M.; Botti, S.; Argaman, A.; Silman, I.; Sussman, J.L.
Deposited on : 2004-08-29
Resolution : 2.40 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

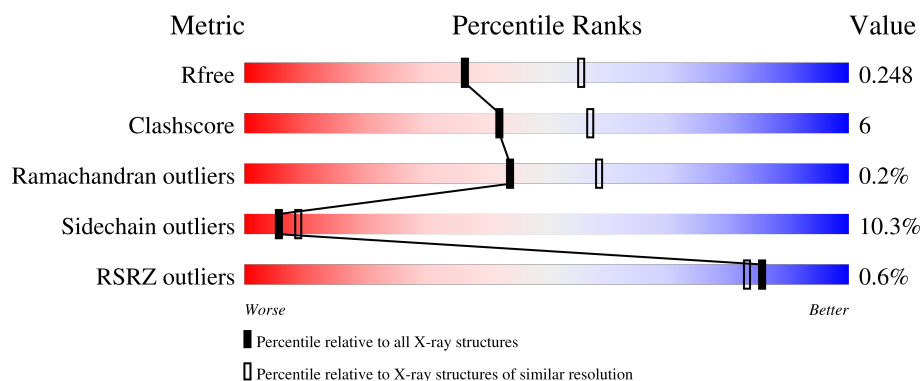
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.40 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}	164625	4642 (2.40-2.40)
Clashscore	180529	5218 (2.40-2.40)
Ramachandran outliers	177936	5158 (2.40-2.40)
Sidechain outliers	177891	5159 (2.40-2.40)
RSRZ outliers	164620	4642 (2.40-2.40)

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	543	 78% 16% . .
1	B	543	 78% 17% . .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8677 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	528	Total	C	N	O	S	0	0	0
			4165	2685	699	759	22			
1	B	532	Total	C	N	O	S	0	0	0
			4204	2708	707	767	22			

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (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		

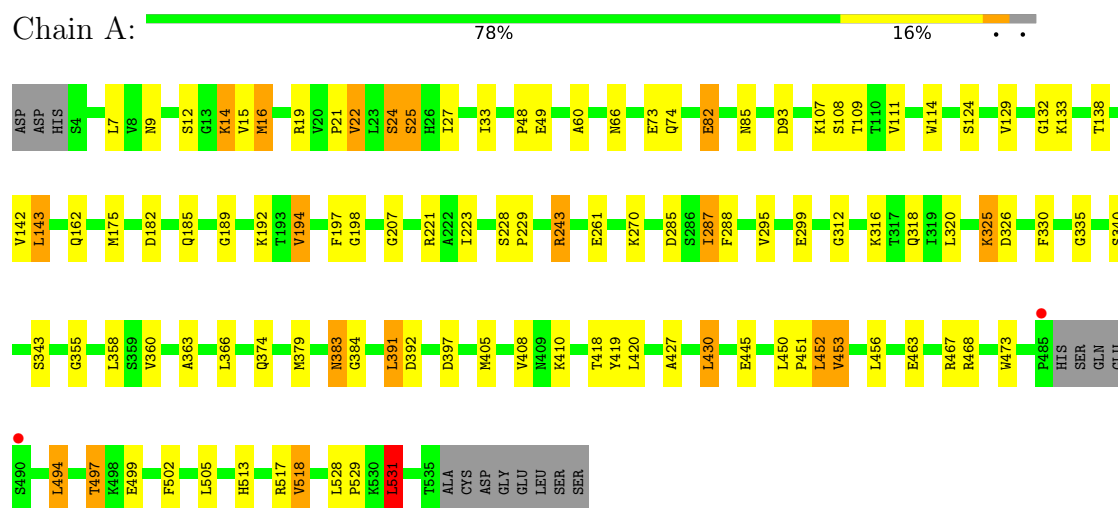
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	127	Total 127	O 127	0	0
3	B	125	Total 125	O 125	0	0

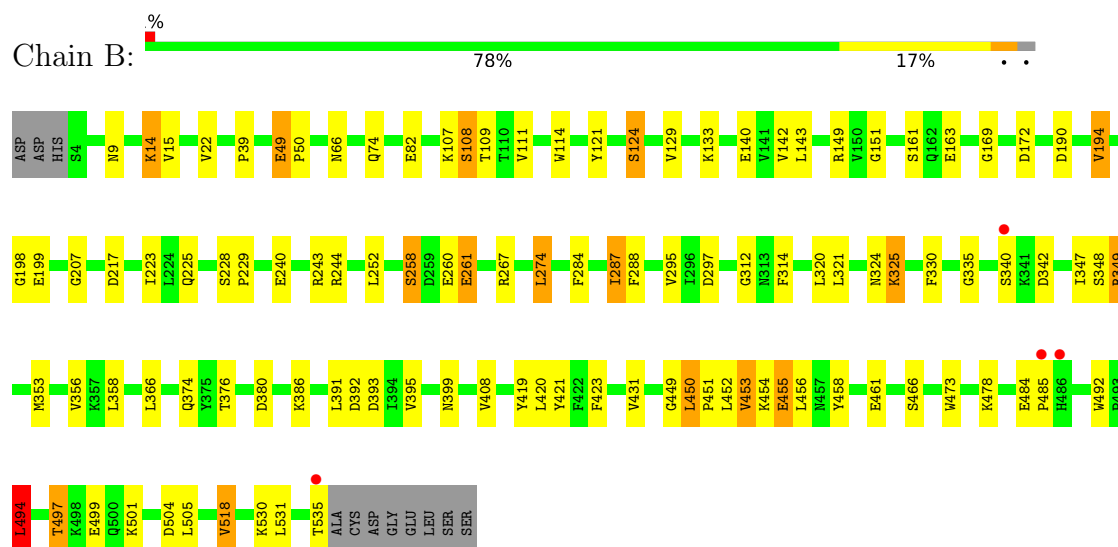
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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, α , β , γ	91.50Å 106.59Å 150.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.40 40.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.5 (40.00-2.40) 94.5 (40.00-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.51 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.204 , 0.247 0.203 , 0.248	Depositor DCC
R_{free} test set	2715 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	34.8	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8677	wwPDB-VP
Average B, all atoms (Å ²)	33.0	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 38.68 % 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 3.5556e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: NAG

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	0.69	0/4286	0.86	8/5823 (0.1%)
1	B	0.68	0/4327	0.83	9/5877 (0.2%)
All	All	0.68	0/8613	0.85	17/11700 (0.1%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	397	ASP	CB-CG-OD2	8.30	125.77	118.30
1	A	518	VAL	CB-CA-C	-7.42	97.31	111.40
1	A	531	LEU	CA-CB-CG	6.99	131.38	115.30
1	B	217	ASP	CB-CG-OD2	6.21	123.89	118.30
1	B	297	ASP	CB-CG-OD2	6.15	123.83	118.30
1	B	518	VAL	CB-CA-C	-5.88	100.22	111.40
1	B	190	ASP	CB-CG-OD2	5.71	123.44	118.30
1	A	93	ASP	CB-CG-OD2	5.71	123.44	118.30
1	A	243	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	B	393	ASP	CB-CG-OD2	5.42	123.18	118.30
1	B	494	LEU	CA-CB-CG	5.34	127.58	115.30
1	A	392	ASP	CB-CG-OD2	5.26	123.04	118.30
1	A	326	ASP	CB-CG-OD2	5.26	123.03	118.30
1	A	182	ASP	CB-CG-OD2	5.13	122.92	118.30
1	B	504	ASP	CB-CG-OD2	5.05	122.84	118.30
1	B	392	ASP	CB-CG-OD2	5.04	122.84	118.30
1	B	342	ASP	CB-CG-OD2	5.04	122.83	118.30

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	4165	0	3992	52	0
1	B	4204	0	4038	51	0
2	A	28	0	26	0	0
2	B	28	0	26	0	0
3	A	127	0	0	4	0
3	B	125	0	0	2	0
All	All	8677	0	8082	102	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 6.

All (102) 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:499:GLU:HG2	1:B:501:LYS:HE2	1.50	0.92
1:B:366:LEU:HD23	1:B:531:LEU:HD11	1.56	0.84
1:A:221:ARG:HD3	1:A:318:GLN:OE1	1.83	0.78
1:A:287:ILE:HD11	1:A:335:GLY:HA3	1.66	0.78
1:A:287:ILE:HD11	1:A:335:GLY:CA	2.16	0.75
1:B:497:THR:HB	3:B:2093:HOH:O	1.86	0.75
1:B:287:ILE:HD11	1:B:335:GLY:C	2.07	0.75
1:A:287:ILE:HD11	1:A:335:GLY:C	2.07	0.74
1:B:366:LEU:CD2	1:B:531:LEU:HD11	2.16	0.74
1:A:497:THR:HG22	3:A:2101:HOH:O	1.91	0.71
1:A:383:ASN:C	1:A:383:ASN:HD22	1.93	0.70
1:A:24:SER:O	1:A:25:SER:HB2	1.96	0.66
1:B:450:LEU:O	1:B:453:VAL:HG13	1.99	0.62
1:B:419:TYR:CZ	1:B:494:LEU:HD13	2.37	0.59
1:B:499:GLU:HG2	1:B:501:LYS:CE	2.31	0.56
1:A:453:VAL:HG22	1:A:456:LEU:HG	1.88	0.56
1:B:66:ASN:ND2	1:B:124:SER:HB3	2.20	0.55
1:B:455:GLU:N	1:B:455:GLU:OE2	2.39	0.55
1:B:9:ASN:ND2	1:B:14:LYS:HD3	2.22	0.54
1:A:111:VAL:HB	1:A:194:VAL:HB	1.89	0.54
1:B:453:VAL:HG23	1:B:455:GLU:HG2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:LEU:HD13	1:A:467:ARG:NH2	2.23	0.54
1:A:366:LEU:HD23	1:A:531:LEU:HD13	1.89	0.53
1:A:73:GLU:HA	3:A:2020:HOH:O	2.07	0.53
1:A:138:THR:HG23	3:A:2040:HOH:O	2.09	0.53
1:B:260:GLU:H	1:B:260:GLU:CD	2.11	0.53
1:A:185:GLN:HA	1:A:189:GLY:O	2.09	0.52
1:B:287:ILE:HD11	1:B:335:GLY:HA3	1.92	0.52
1:A:427:ALA:HB3	1:A:430:LEU:HD12	1.91	0.52
1:B:223:ILE:HA	1:B:320:LEU:O	2.09	0.52
1:A:405:MET:HA	1:A:408:VAL:HG12	1.91	0.52
1:A:419:TYR:CZ	1:A:494:LEU:CD1	2.93	0.52
1:A:502:PHE:CZ	1:A:513:HIS:HB2	2.44	0.51
1:B:312:GLY:HA2	1:B:314:PHE:CE2	2.46	0.51
1:B:228:SER:HB2	1:B:229:PRO:HD2	1.92	0.51
1:B:207:GLY:HA3	1:B:229:PRO:HD3	1.94	0.50
1:A:450:LEU:O	1:A:453:VAL:HG13	2.12	0.50
1:B:49:GLU:HG3	1:B:50:PRO:HD2	1.93	0.50
1:A:7:LEU:HB2	1:A:16:MET:CE	2.42	0.49
1:A:15:VAL:HG21	1:A:33:ILE:HG12	1.93	0.49
1:B:287:ILE:HD11	1:B:335:GLY:CA	2.42	0.49
1:B:108:SER:HB2	3:B:2042:HOH:O	2.12	0.49
1:A:228:SER:HB2	1:A:229:PRO:HD2	1.94	0.49
1:B:451:PRO:HA	1:B:458:TYR:CD1	2.48	0.48
1:A:452:LEU:HD22	1:A:463:GLU:HG3	1.95	0.48
1:B:380:ASP:OD2	1:B:386:LYS:NZ	2.42	0.48
1:A:21:PRO:O	1:A:133:LYS:HE3	2.14	0.48
1:B:325:LYS:O	1:B:325:LYS:HG3	2.14	0.47
1:A:132:GLY:HA3	1:A:143:LEU:HD22	1.96	0.47
1:A:360:VAL:HG12	1:A:363:ALA:HB2	1.97	0.47
1:A:207:GLY:HA3	1:A:229:PRO:HD3	1.98	0.46
1:B:240:GLU:O	1:B:244:ARG:HG3	2.16	0.46
1:A:366:LEU:HD21	1:B:531:LEU:HD13	1.98	0.46
1:A:48:PRO:HB2	1:A:175:MET:HE1	1.97	0.46
1:A:66:ASN:ND2	1:A:124:SER:HB3	2.31	0.46
1:A:109:THR:CG2	1:A:142:VAL:HG23	2.45	0.45
1:B:169:GLY:O	1:B:172:ASP:HB2	2.16	0.45
1:A:48:PRO:HB2	1:A:175:MET:CE	2.46	0.45
1:A:408:VAL:CG2	1:A:418:THR:HG21	2.47	0.45
1:A:114:TRP:CZ3	1:A:198:GLY:HA2	2.52	0.45
1:B:109:THR:HG22	1:B:142:VAL:HG23	2.00	0.44
1:B:366:LEU:HD23	1:B:531:LEU:CD1	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:531:LEU:HD12	1:A:531:LEU:C	2.38	0.44
1:B:287:ILE:HD11	1:B:335:GLY:O	2.16	0.44
1:B:349:ARG:O	1:B:353:MET:HG2	2.18	0.44
1:A:355:GLY:HA3	1:A:391:LEU:HD21	2.00	0.44
1:A:383:ASN:HD22	1:A:384:GLY:N	2.15	0.44
1:B:199:GLU:HA	1:B:225:GLN:O	2.18	0.43
1:B:258:SER:OG	1:B:261:GLU:HG2	2.18	0.43
1:A:9:ASN:ND2	1:A:14:LYS:HD3	2.33	0.43
1:A:312:GLY:O	1:A:316:LYS:NZ	2.51	0.43
1:B:163:GLU:HB3	1:B:267:ARG:HH22	1.83	0.43
1:B:252:LEU:HD11	1:B:274:LEU:HD12	2.00	0.43
1:A:383:ASN:C	1:A:383:ASN:ND2	2.67	0.43
1:A:223:ILE:HA	1:A:320:LEU:O	2.19	0.43
1:A:420:LEU:HD23	1:A:502:PHE:HB3	2.00	0.43
1:B:450:LEU:N	1:B:451:PRO:CD	2.82	0.42
1:B:114:TRP:CZ3	1:B:198:GLY:HA2	2.55	0.42
1:B:321:LEU:O	1:B:420:LEU:HA	2.18	0.42
1:B:395:VAL:O	1:B:399:ASN:HB2	2.20	0.42
1:B:121:TYR:HA	1:B:151:GLY:H	1.85	0.42
1:B:347:ILE:HG22	1:B:348:SER:O	2.19	0.42
1:B:453:VAL:HG22	1:B:456:LEU:HG	2.01	0.42
1:A:450:LEU:N	1:A:451:PRO:CD	2.82	0.42
1:A:15:VAL:CG2	1:A:60:ALA:HB2	2.49	0.42
1:B:449:GLY:HA2	1:B:466:SER:OG	2.20	0.42
1:A:132:GLY:CA	1:A:143:LEU:HD22	2.49	0.41
1:A:22:VAL:HG21	1:A:27:ILE:HG12	2.03	0.41
1:A:430:LEU:HD11	3:A:2108:HOH:O	2.19	0.41
1:A:325:LYS:HZ2	1:A:325:LYS:HG2	1.58	0.41
1:B:324:ASN:HA	1:B:423:PHE:O	2.20	0.41
1:A:7:LEU:HB2	1:A:16:MET:HE3	2.03	0.41
1:A:528:LEU:N	1:A:529:PRO:CD	2.83	0.41
1:A:452:LEU:HD13	1:A:467:ARG:CZ	2.51	0.40
1:B:111:VAL:HB	1:B:194:VAL:HB	2.03	0.40
1:B:325:LYS:HZ3	1:B:325:LYS:HG2	1.79	0.40
1:B:484:GLU:HA	1:B:485:PRO:HD2	1.88	0.40
1:B:39:PRO:HG3	1:B:149:ARG:HD3	2.03	0.40
1:B:349:ARG:HH12	1:B:376:THR:HG23	1.87	0.40
1:B:22:VAL:HG13	1:B:133:LYS:HG3	2.02	0.40
1:A:82:GLU:HG3	1:A:85:ASN:HD22	1.87	0.40
1:B:421:TYR:HB3	1:B:492:TRP:CZ2	2.56	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	524/543 (96%)	497 (95%)	25 (5%)	2 (0%)	30	44
1	B	530/543 (98%)	504 (95%)	26 (5%)	0	100	100
All	All	1054/1086 (97%)	1001 (95%)	51 (5%)	2 (0%)	44	59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	25	SER
1	A	24	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	444/474 (94%)	397 (89%)	47 (11%)	5	8
1	B	450/474 (95%)	405 (90%)	45 (10%)	6	9
All	All	894/948 (94%)	802 (90%)	92 (10%)	6	9

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	SER
1	A	14	LYS
1	A	16	MET
1	A	19	ARG

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Mol	Chain	Res	Type
1	A	22	VAL
1	A	49	GLU
1	A	74	GLN
1	A	82	GLU
1	A	107	LYS
1	A	108	SER
1	A	129	VAL
1	A	143	LEU
1	A	162	GLN
1	A	192	LYS
1	A	194	VAL
1	A	197	PHE
1	A	243	ARG
1	A	261	GLU
1	A	270	LYS
1	A	285	ASP
1	A	287	ILE
1	A	288	PHE
1	A	295	VAL
1	A	299	GLU
1	A	325	LYS
1	A	330	PHE
1	A	340	SER
1	A	343	SER
1	A	358	LEU
1	A	374	GLN
1	A	379	MET
1	A	383	ASN
1	A	391	LEU
1	A	410	LYS
1	A	430	LEU
1	A	445	GLU
1	A	452	LEU
1	A	453	VAL
1	A	468	ARG
1	A	473	TRP
1	A	494	LEU
1	A	497	THR
1	A	499	GLU
1	A	505	LEU
1	A	517	ARG
1	A	518	VAL

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Mol	Chain	Res	Type
1	A	531	LEU
1	B	14	LYS
1	B	15	VAL
1	B	49	GLU
1	B	74	GLN
1	B	82	GLU
1	B	107	LYS
1	B	108	SER
1	B	124	SER
1	B	129	VAL
1	B	140	GLU
1	B	143	LEU
1	B	161	SER
1	B	194	VAL
1	B	243	ARG
1	B	258	SER
1	B	261	GLU
1	B	274	LEU
1	B	284	PHE
1	B	287	ILE
1	B	288	PHE
1	B	295	VAL
1	B	325	LYS
1	B	330	PHE
1	B	340	SER
1	B	349	ARG
1	B	356	VAL
1	B	358	LEU
1	B	374	GLN
1	B	391	LEU
1	B	408	VAL
1	B	431	VAL
1	B	450	LEU
1	B	452	LEU
1	B	453	VAL
1	B	454	LYS
1	B	455	GLU
1	B	461	GLU
1	B	473	TRP
1	B	478	LYS
1	B	494	LEU
1	B	497	THR

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Mol	Chain	Res	Type
1	B	505	LEU
1	B	518	VAL
1	B	530	LYS
1	B	535	THR

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

Mol	Chain	Res	Type
1	A	9	ASN
1	A	68	GLN
1	A	181	HIS
1	A	374	GLN
1	A	383	ASN
1	B	9	ASN
1	B	68	GLN
1	B	74	GLN
1	B	159	HIS
1	B	374	GLN
1	B	457	ASN

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](#)

4 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	B	1536	1	14,14,15	0.67	0	17,19,21	1.68	3 (17%)
2	NAG	A	1536	1	14,14,15	0.53	0	17,19,21	1.72	2 (11%)
2	NAG	A	1537	1	14,14,15	0.68	0	17,19,21	1.82	2 (11%)
2	NAG	B	1537	1	14,14,15	0.68	0	17,19,21	1.80	3 (17%)

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	B	1536	1	-	1/6/23/26	0/1/1/1
2	NAG	A	1536	1	-	4/6/23/26	0/1/1/1
2	NAG	A	1537	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1537	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1537	NAG	O5-C5-C6	4.85	114.81	107.20
2	B	1537	NAG	O5-C5-C6	4.80	114.73	107.20
2	A	1536	NAG	O5-C5-C6	4.46	114.20	107.20
2	A	1536	NAG	C1-O5-C5	4.12	117.78	112.19
2	A	1537	NAG	C1-O5-C5	4.04	117.67	112.19
2	B	1536	NAG	C1-O5-C5	3.93	117.52	112.19
2	B	1537	NAG	C1-O5-C5	3.80	117.35	112.19
2	B	1536	NAG	O5-C5-C6	3.05	111.98	107.20
2	B	1536	NAG	O5-C1-C2	-2.80	106.87	111.29
2	B	1537	NAG	C1-C2-N2	2.30	114.42	110.49

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1537	NAG	O5-C5-C6-O6
2	A	1536	NAG	O5-C5-C6-O6
2	A	1537	NAG	C4-C5-C6-O6
2	B	1537	NAG	O5-C5-C6-O6
2	A	1536	NAG	C4-C5-C6-O6
2	A	1536	NAG	C8-C7-N2-C2
2	A	1536	NAG	O7-C7-N2-C2
2	B	1537	NAG	C4-C5-C6-O6
2	B	1536	NAG	C4-C5-C6-O6

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	528/543 (97%)	-0.43	2 (0%) 89 87	19, 32, 45, 59	0
1	B	532/543 (97%)	-0.40	4 (0%) 82 80	20, 32, 47, 66	0
All	All	1060/1086 (97%)	-0.42	6 (0%) 85 83	19, 32, 46, 66	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	535	THR	4.3
1	B	485	PRO	4.2
1	A	485	PRO	4.1
1	B	486	HIS	3.0
1	A	490	SER	2.3
1	B	340	SER	2.2

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 monosaccharides 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(\AA^2)	Q<0.9
2	NAG	A	1536	14/15	0.74	0.17	67,74,76,76	0
2	NAG	B	1536	14/15	0.74	0.15	63,69,69,69	0
2	NAG	A	1537	14/15	0.79	0.14	57,62,67,68	0
2	NAG	B	1537	14/15	0.83	0.13	48,55,60,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.